

GenCore version 5.1.6  
Run on: March 5, 2005, 23:01:24 ; Search time 182.5 Seconds  
(without alignments)  
4624.171 Million cell updates/sec

Title: US-10-015-385A-193  
Perfect score: 2066  
Sequence: 1 caagcagtcattcccttgg.....aggggcaaaaaaaaaa 1091  
Scoring table: BLOSUM62  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 4211384  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	ABG66676	standard; protein; 254 AA.		
DE	Human novel polypeptide #11.			
PN	WO200244340-A2.			
PD	06-JUN-2002.			
PA	(HYSE-) HYSEQ INC.			
Best Local Similarity:	85.52%	Mismatches: 0		
Query Match:	66.58%	Indels: 43		
RESULT 2				
ID	AAB21304	standard; protein; 248 AA.		
DE	Human KLK-L5 protein #4.			
PN	WO200053776-A2.			
PD	14-SEP-2000.			
PA	(MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 3				
ID	AAB24428	standard; protein; 248 AA.		
DE	Human PRO1303 protein sequence SEQ ID NO:203.			
PN	WO200032221-A2.			
PD	08-JUN-2000.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 4				
ID	AAB24032	standard; protein; 248 AA.		
DE	Human PRO1303 protein sequence SEQ ID NO:33.			
PN	WO200053750-A1.			
PD	14-SEP-2000.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 5				
ID	AA99393	standard; protein; 248 AA.		
DE	Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.			
PN	WO200012708-A2.			
PD	09-MAR-2000.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches: 0		
Query Match:	66.51%	Indels: 0		
RESULT 6				
ID	AAM23994	standard; protein; 248 AA.		
DE	Human EST encoded protein SEQ ID NO: 1519.			
PN	WO200154477-A2.			
PD	02-AUG-2001.			

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PA	(HYSE-) HYSEQ INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 7					
ID	AAB66142	standard; protein; 248 AA.			
DE	Protein of the invention #54.				
PN	WO200078961-A1.				
PD	28-DEC-2000.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 8					
ID	ABO33635	standard; protein; 248 AA.			
DE	Novel human secreted and transmembrane protein PRO1303.				
PN	US2003073130-A1.				
PD	17-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 9					
ID	ABO44488	standard; protein; 248 AA.			
DE	Human secreted/transmembrane protein PRO1303.				
PN	US2003044841-A1.				
PD	06-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 10					
ID	ABO33512	standard; protein; 248 AA.			
DE	Novel human secreted and transmembrane protein PRO1303.				
PN	US2003073129-A1.				
PD	17-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 11					
ID	ADC18063	standard; protein; 248 AA.			
DE	Human PRO polypeptide #54.				
PN	US2003064925-A1.				
PD	03-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 12					
ID	ADD70709	standard; protein; 248 AA.			
DE	Human secreted/transmembrane protein PRO1303.				
PN	US2003096235-A1.				
PD	29-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 13					
ID	ADD39786	standard; protein; 248 AA.			
DE	Human secreted/transmembrane protein PRO1303.				
PN	US2003083462-A1.				
PD	01-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 14					
ID	ADD70232	standard; protein; 248 AA.			
DE	Human secreted/transmembrane protein PRO1303.				
PN	US2003054406-A1.				
PD	20-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%	Mismatches:			
Query Match:	66.51%	Indels:			
RESULT 15					
ID	ADD38353	standard; protein; 248 AA.			
DE	Human secreted/transmembrane protein PRO1303.				
PN	US2003096955-A1.				
PD	22-MAY-2003.				
PA	(GETH ) GENENTECH INC.				

Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 16	
ID ADD19309 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003096954-A1.	
PD 22-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 17	
ID ADD38832 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003092061-A1.	
PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 18	
ID ADD40263 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082627-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 19	
ID ADE50484 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003069179-A1.	
PD 10-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 20	
ID ADE20096 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003092883-A1.	
PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 21	
ID ADE50007 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082626-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 22	
ID ADE21565 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003082628-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 23	
ID ADF29990 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003204053-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 24	
ID ADF55883 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003204054-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 25	
ID ADH9387 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003065142-A1.	
PD 03-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 26	
ID ADE96567 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003195347-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 27	
ID ADF25878 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003199675-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 28	
ID ADF24777 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003198993-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 29	
ID ADF29513 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003203401-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 30	
ID ADE97044 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003195334-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 31	
ID ADH03082 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003216562-A1.	
PD 20-NOV-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 32	
ID ADH04036 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003220471-A1.	
PD 27-NOV-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0
RESULT 33	
ID ADH03559 standard; protein; 248 AA.	
DE Human secreted/transmembrane protein PRO1303.	
PN US2003224478-A1.	
PD 04-DEC-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 66.51%	Indels: 0



RESULT 34  
ID ADH04513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.51% Indels: 0  
RESULT 35  
ID ADH61514 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.51% Indels: 0  
RESULT 36  
ID ADN10927 standard; protein; 248 AA.  
DE Human Kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.51% Indels: 0  
RESULT 37  
ID ADL94713 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.51% Indels: 0  
RESULT 38  
ID ADT94373 standard; protein; 248 AA.  
DE Human Kik-L5 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.51% Indels: 0  
RESULT 39  
ID AAB21303 standard; protein; 254 AA.  
DE Human Kik-L5 protein #3.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 85.19% Mismatches: 0  
Query Match: 66.43% Indels: 43  
RESULT 40  
ID ADN10926 standard; protein; 254 AA.  
DE Human Kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 85.19% Mismatches: 0  
Query Match: 66.43% Indels: 43  
RESULT 41  
ID ADP56174 standard; protein; 254 AA.  
DE Human PRO protein sequence SEQ ID NO:2150.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 85.19% Mismatches: 0  
Query Match: 66.43% Indels: 43  
RESULT 42  
ID AAO29516 standard; protein; 248 AA.  
DE Human Kallikrein-like protein 5 (18817).  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 99.60% Mismatches: 1  
Query Match: 66.17% Indels: 0  
RESULT 43

ID AAB21301 standard; protein; 184 AA.  
DE Human Kik-L5 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 49.32% Indels: 0  
RESULT 44  
ID AAY28642 standard; protein; 162 AA.  
DE Human secreted protein from CDNA clone HKAFV61.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 64.11% Mismatches: 3  
Query Match: 39.25% Indels: 86  
RESULT 45  
ID AAY32852 standard; protein; 260 AA.  
DE Human serine protease protein sequence.  
PN JP11225765-A.  
PD 24-AUG-1999.  
PA (SUNR ) SUNTORY LTD.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 46  
ID AAY41744 standard; protein; 260 AA.  
DE Human PRO322 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 47  
ID AAY03220 standard; protein; 260 AA.  
DE Amino acid sequence of human tumour antigen derived gene-14 protein.  
PN WO9909138-A1.  
PD 25-FEB-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 48  
ID AAB21322 standard; protein; 260 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 49  
ID AAB44300 standard; protein; 260 AA.  
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 50  
ID AAY51131 standard; protein; 260 AA.  
DE Human neuropsin protein.  
PN JP11318461-A.  
PD 24-NOV-1999.  
PA (SHIO/) SHIOZAKA S.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 51  
ID AAU12369 standard; protein; 260 AA.  
DE Human PRO322 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 52

ID AAB53087 standard; protein; 260 AA.  
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 53  
ID ABG23373 standard; protein; 260 AA.  
DE Novel human diagnostic protein #23364.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 54  
ID ABB84852 standard; protein; 260 AA.  
DE Human PRO322 protein sequence SEQ ID NO:72.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 55  
ID AAU81959 standard; protein; 260 AA.  
DE Human PRO322.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 56  
ID ABB95458 standard; protein; 260 AA.  
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 57  
ID ADI17076 standard; protein; 260 AA.  
DE Human NOVX protein homologue SeqID 612.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 58  
ID ABO17813 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 59  
ID ABO25246 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003004102-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 60  
ID ABU81067 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 61  
ID ABU72252 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 62  
ID ADA05702 standard; protein; 260 AA.  
DE Human NOV11h protein SEQ ID NO:62.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 63  
ID ABU66767 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 64  
ID ABU84932 standard; protein; 260 AA.  
DE Human secreted and transmembrane PRO polypeptide #8.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 65  
ID ABU59848 standard; protein; 260 AA.  
DE Novel secreted and transmembrane protein PRO322.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 66  
ID ABU61130 standard; protein; 260 AA.  
DE Human PRO322 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 67  
ID ABO25038 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein (PRO) #198.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 68  
ID ABU80399 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein PRO322.  
PN US2003004102-A1.

PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 69  
ID ADBU7043 standard; protein; 260 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 70  
ID ADA45915 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 71  
ID ADA76346 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 72  
ID ADA18996 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 73  
ID ADA61619 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 74  
ID ADB19404 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 75  
ID ADB27945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 76  
ID ADA86424 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 77  
ID ADB15988 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087350-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 78  
ID ADA4774 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 79  
ID ADA67569 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 80  
ID ADB30576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 81  
ID ADA85872 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 82  
ID ADA97084 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 83  
ID ADA79388 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 84  
ID ADA87527 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 85  
ID ADB16729 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 86  
ID ADA91821 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 87  
ID ADB14884 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 88  
ID ADA24934 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 89  
ID ADB18845 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 90  
ID ADA94060 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 91  
ID ADB19956 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 92  
ID ADB13268 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 93  
ID ABO43346 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 94  
ID ABO19701 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 95  
ID ADA12595 standard; protein; 260 AA.  
DE Human secreted/transmembrane polypeptide PRO322.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13

Query Match: 30.61% Indels: 13  
RESULT 96  
ID ADA74522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 97  
ID ADB24755 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 98  
ID ADA82279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 99  
ID ADA75242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 100  
ID ADA85320 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 101  
ID ADA84768 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 102  
ID ADB30024 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 103  
ID ADA80552 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 104  
ID ADA75794 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13

RESULT 105  
ID ADA47019 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 106  
ID ADB25315 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 107  
ID ADA93491 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 108  
ID ADB26841 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 109  
ID ADB31128 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 110  
ID ADA61056 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 111  
ID ADB24203 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 112  
ID ADA96532 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 113  
ID ADA81104 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 114  
ID ADB28497 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 115  
ID ADB26289 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 116  
ID ADB21774 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 117  
ID ABO19592 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane polypeptide #60.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 118  
ID ADA77553 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 119  
ID ADB18293 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 120  
ID ADA86976 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 121  
ID ADA88079 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 122  
ID ADA46467 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 123  
ID ADB28497 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13

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PN US2003082699-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 124
ID ADB29049 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 125
ID ADA77001 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 126
ID ADA8631 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 127
ID ADA97636 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 128
ID ADB27393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 129
ID ADB22326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 130
ID ADA67017 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 131
ID ADB22878 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077111-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 132
ID ADB23651 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 133
ID ADA92373 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 134
ID ADB15436 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 135
ID ADB38688 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 136
ID ADB38136 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 137
ID ADB66608 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 138
ID ADB9688 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 139
ID ADB90420 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 140
ID ADB80561 standard; protein; 260 AA.
DE Ovarian cancer-associated protein #63.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 141
ID ADB39521 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13

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Query Match: 30.61% Indels: 13
RESULT 142
ID ADB73901 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 143
ID ADB47144 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 144
ID ADB86751 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 145
ID ADB76617 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 146
ID ADB77356 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 147
ID ADB34513 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 148
ID ADB35617 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 149
ID ADB33961 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 150
ID ADB35065 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 151
ID ADB36169 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 152
ID ADB46564 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 153
ID ADC44043 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 154
ID ADC61803 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 155
ID ADC63767 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 156
ID ADC66867 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 157
ID ADC68991 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 158
ID ADC63051 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 159
ID ADC68116 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 160
```

ID ADC41436 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003072745-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 30.61% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 161  
ID ADC67491 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073131-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 162  
ID ADC67491 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073131-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 163  
ID ADC42060 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003104998-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 164  
ID ADC50437 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092106-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 165  
ID ADC71984 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092107-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 166  
ID ADC59963 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092105-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 167  
ID ADC52970 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087365-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 168  
ID ADC57324 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087366-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 169  
ID ADC60515 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087367-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 170  
ID ADC50990 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087361-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 171  
ID ADC65517 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087362-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 172  
ID ADC54615 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087363-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 173  
ID ADC53576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087364-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 174  
ID ADC59099 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087359-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 175  
ID ADC55977 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087360-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 176  
ID ADC58547 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087346-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 177  
ID ADD03221 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092104-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 178  
ID ADC90213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.



PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 179  
ID ADC69632 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 180  
ID ADC48521 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 181  
ID ADD10050 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 182  
ID ADD04625 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 183  
ID ADC80581 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 184  
ID ADD09100 standard; protein; 260 AA.  
DE Human kallikrein 8 protein SEQ ID NO:2.  
PN WO2003085404-A1.  
PD 16-OCT-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 185  
ID ADD11088 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 186  
ID ADD10361 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 187  
ID ADC47969 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194771-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 188  
ID ADC80029 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 189  
ID ADD11321 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 190  
ID ADD09498 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 191  
ID ADD41211 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 192  
ID ADD52350 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 193  
ID ADD33090 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 194  
ID ADD33642 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 195  
ID ADD37114 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 196  
ID ABW00074 standard; protein; 260 AA.  
DE Human tumour antigen derived gene-14 (TAGD-14) protein.  
PN US2002037581-A1.  
PD 28-MAR-2002.

PA (UABR-) UAB RES FOUND.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 197  
ID ADD51798 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 198  
ID ADD02597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 199  
ID ADD02031 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 200  
ID ADD54213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 201  
ID ADE49429 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 202  
ID ADD92530 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 203  
ID ADD91426 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 204  
ID ADE04040 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 205  
ID ADE32337 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 206  
ID ADE22269 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 207  
ID ADD79493 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 208  
ID ADE35483 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 209  
ID ADE16597 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 210  
ID ADD73212 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 211  
ID ADE42029 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 212  
ID ADE17846 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 213  
ID ADD91978 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 214  
ID ADE33441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96

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Query Match: 30.61% Indels: 13
RESULT 215
ID ADE33993 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 216
ID ADD80045 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 217
ID ADD93082 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 218
ID ADD72570 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 219
ID ADE19502 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 220
ID ADE18950 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 221
ID ADE43146 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 222
ID ADD95935 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 223
ID ADE22821 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 224
ID ADD78939 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 225
ID ADE32889 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 226
ID ADE42581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 227
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 228
ID ADD80597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 229
ID ADD89625 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 230
ID ADE40909 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 231
ID ADE04708 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 232
ID ADE92837 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 233
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
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ID ADF47235 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195333-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 234  
ID ADG21546 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207355-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 235  
ID ADG23187 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207384-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 236  
ID ADF97522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207370-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 237  
ID ADG80586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207373-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 238  
ID ADG52992 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216561-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 239  
ID ADG60312 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003206915-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 240  
ID ADG80034 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207372-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 241  
ID ADH55326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207381-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 242  
ID ADH55878 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207379-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 243  
ID ADI61072 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003077700-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 244  
ID ADI64097 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207385-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 245  
ID ADH81959 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207388-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 246  
ID ADH81407 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207377-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 247  
ID ADH82576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087355-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 248  
ID ADN15975 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087353-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 249  
ID ADN16604 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087385-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 250  
ID ADN39182 standard; protein; 260 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.  
PN WO2003042661-A2.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 251  
ID ADN15423 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.

PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 252  
ID ADN14871 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 253  
ID ADI65046 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 254  
ID ADI63545 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US200307387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 255  
ID ADC81133 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 256  
ID ADD76581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 257  
ID ADD87945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 258  
ID ADD86349 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 259  
ID ADE75797 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 260  
ID ADE48729 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 261  
ID ADE41322 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 262  
ID ADE23373 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 263  
ID ADE23925 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092410-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 264  
ID ADE24568 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 265  
ID ADD87393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 266  
ID ADE89259 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 267  
ID ADE18398 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 268  
ID ADE88707 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 269  
ID ADE89830 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003130181-A1.  
PD 10-JUL-2003.

PA (ASHK/) ASHKENAZI A J. PD 23-OCT-2003. Mismatches: 96  
PA (BAKE/) BAKER K P. PA (GETH ) GENENTECH INC. Indels: 13  
PA (BOTS/) BOTSTEIN D. Best Local Similarity: 48.08%  
PA (DESN/) DESNOYERS L. Query Match: 30.61%  
PA (EATO/) EATON D L. RESULT 276  
PA (FERR/) FERRARA N. ID ADE93389 standard; protein; 260 AA.  
PA (FILV/) FILVAROFF E. DE Human PRO polypeptide #198.  
PA (FONG/) FONG S. PN US2003199060-A1.  
PA (GAOW/) GAO W. PD 23-OCT-2003.  
PA (GERB/) GERBER H. PA (GETH ) GENENTECH INC. Mismatches: 96  
PA (GERR/) GERRITSEN M E. Best Local Similarity: 48.08%  
PA (GODD/) GODDARD A. Query Match: 30.61% Indels: 13  
PA (GODO/) GODOWSKI P J. ID ADF24354 standard; protein; 260 AA.  
PA (GIRM/) GIRMALDI J C. DE Human secreted/transmembrane protein, PRO322.  
PA (GURN/) GURNEY A L. PN US2003204055-A1.  
PA (HILL/) HILLAN K J. PD 30-OCT-2003.  
PA (KLJA/) KLJAVIN I J. PA (GETH ) GENENTECH INC. Mismatches: 96  
PA (KUOS/) KUO S S. Best Local Similarity: 48.08% Indels: 13  
PA (NAPI/) NAPIER M A. Query Match: 30.61%  
PA (PANJ/) PAN J. RESULT 278  
PA (PAON/) PAONI N F. ID ADF40786 standard; protein; 260 AA.  
PA (ROYM/) ROY M A. DE Human secreted/transmembrane protein, PRO322.  
PA (SHEL/) SHELTON D L. PN US2003199021-A1.  
PA (STEW/) STEWART T A. PD 23-OCT-2003.  
PA (TUNA/) TUNAS D. PA (GETH ) GENENTECH INC. Mismatches: 96  
PA (WILL/) WILLIAMS P M. Best Local Similarity: 48.08% Indels: 13  
PA (WOOD/) WOOD W I. Query Match: 30.61%  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 270  
ID ADF61470 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 271  
ID ADF40162 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 272  
ID ADF45958 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 273  
ID ADE94727 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 274  
ID ADE91138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 275  
ID ADE95279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199052-A1.

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PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 276  
ID ADE93389 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 277  
ID ADF24354 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 278  
ID ADF40786 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 279  
ID ADF23730 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 280  
ID ADF33713 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 281  
ID ADF34970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 282  
ID ADF27180 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 283  
ID ADF27816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 96  
Best Local Similarity: 48.08% Indels: 13  
Query Match: 30.61%  
RESULT 284  
ID ADE92285 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199051-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 285  
 ID ADE90586 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199063-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 286  
 ID ADF41410 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003199435-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 287  
 ID ADF33089 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003211091-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 288  
 ID ADF25455 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003211092-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 289  
 ID ADF26556 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003199674-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 290  
 ID ADF34345 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003194410-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 291  
 ID ADF46582 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003195344-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 292  
 ID ADE91733 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003199058-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 293  
 ID ADG02312 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207352-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96

Best Local Similarity: 48.08% Mismatches: 96  
 Query Match: 30.61% Indels: 13  
 RESULT 294  
 ID ADG22098 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003207360-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 295  
 ID ADG20168 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207376-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 296  
 ID ADF98074 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207422-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 297  
 ID ADG24291 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003207426-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 298  
 ID ADF98645 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003208055-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 299  
 ID ADG03476 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207351-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 300  
 ID ADF99197 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207353-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 301  
 ID ADG16782 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207359-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13  
 Query Match: 30.61%  
 RESULT 302  
 ID ADG05241 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003207375-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. Mismatches: 96  
 Best Local Similarity: 48.08% Indels: 13

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Query Match: 30.61% Indels: 13
RESULT 303
ID ADG19508 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 304
ID ADG13345 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 305
ID ADG08402 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 306
ID ADG15572 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 307
ID ADF96970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 308
ID ADG06155 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 309
ID ADG23739 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 310
ID ADG04028 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 311
ID ADG24929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 312
ID ADG07226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 313
ID ADG07778 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 314
ID ADG55273 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 315
ID ADG60937 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 316
ID ADG62041 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 317
ID ADG82242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 318
ID ADG57481 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 319
ID ADG56929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 320
ID ADG55825 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 321
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ID ADG58585 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207368-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 322  
ID ADG70951 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207420-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 323  
ID ADG58033 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207363-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 324  
ID ADG53617 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207415-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 325  
ID ADG71503 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207421-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 326  
ID ADG50568 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003207803-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 327  
ID ADG81690 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207805-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 328  
ID ADH30652 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200307723-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 329  
ID ADH12019 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207419-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 330  
ID ADG49944 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.

PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 331  
ID ADG51816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215908-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 332  
ID ADG52441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207414-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 333  
ID ADG54169 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207416-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 334  
ID ADG49320 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216305-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 335  
ID ADG81138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 336  
ID ADG56377 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207366-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 337  
ID ADH12643 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 338  
ID ADG48696 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 30.61% Indels: 13  
RESULT 339  
ID ADG61489 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207429-A1.

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PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 340  
ID ADH25617 standard; protein; 260 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 350  
ID ADG09928 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 351  
ID ADI15399 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 352  
ID ADG09276 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 353  
ID ADI14731 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 354  
ID ADI18326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 355  
ID ADI37154 standard; protein; 260 AA.  
DE Human TADG-14 protein.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 356  
ID ADJ63607 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 357  
ID ADJ77502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 340  
ID ADH28576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 341  
ID ADG54721 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 342  
ID ADG59761 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 343  
ID ADG51192 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 344  
ID ADH43505 standard; protein; 260 AA.  
DE Human PRO polypeptide #36.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 345  
ID ADG59136 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 346  
ID ADG62592 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 347  
ID ADI81185 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.08% Mismatches: 96  
Indels: 13  
Query Match:  
RESULT 348  
ID ADI39730 standard; protein; 260 AA.  
DE Human TADG-14 protein.  
PN US6642013-B1.  
PD 04-NOV-2003.

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Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 358
ID ADK82850 standard; protein; 260 AA.
DE Human PRO polypeptide #36.
PN US2000403927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 359
ID ADJ65624 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2000403835-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 360
ID ADM27760 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US20004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 361
ID ADM17394 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US20004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 362
ID ADL07228 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US20004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 363
ID ADM42484 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US20004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
Query Match: 30.61% Indels: 13
RESULT 364
ID ADN62866 standard; protein; 260 AA.
DE Human NOV11h.
PN US20004038223-A1.
PD 26-FEB-2004.
PA (SMIT ) SMITHSON G.
PA (MILL ) MILLET I.
PA (PEVM ) PEYMAN J. A.
PA (KEKU ) KEKUDA R.
PA (JUJJ ) JU J.
PA (LILL ) LI L.
PA (GUOX ) GUO X.
PA (PATT ) PATTURAJAN M.
PA (SPYT ) SPYTEK K. A.
PA (EDIN ) EDINGER S. R.
PA (ELLE ) ELLERMAN K.
PA (MALY ) MALYANKAR U. M.
PA (ORTT ) ORT T.
PA (GORM ) GORMAN L.
PA (ZERH ) ZERHUSEN B. D.
PA (ANDE ) ANDERSON D. W.
PA (ZHON ) ZHONG M.
PA (CATT ) CATTERTON E.
Mismatches: 95
Indels: 13

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Query Match: 30.42% Indels: 13  
 RESULT 372  
 ID AAY32853 standard; protein; 305 AA.  
 DE Human serine protease protein sequence.  
 PN JP11225765-A.  
 PD 24-AUG-1999.  
 PA (SUNR ) SUNTORY LTD.  
 Best Local Similarity: 50.85% Mismatches: 90  
 Query Match: 30.35% Indels: 2  
 RESULT 373  
 ID AAB37985 standard; protein; 306 AA.  
 DE Human secreted protein encoded by gene 2 clone HWJAE49.  
 PN WO200055371-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 50.85% Mismatches: 90  
 Query Match: 30.35% Indels: 2  
 RESULT 374  
 ID ABP411332 standard; protein; 315 AA.  
 DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 50.85% Mismatches: 90  
 Query Match: 30.35% Indels: 2  
 RESULT 375  
 ID AD117074 standard; protein; 260 AA.  
 DE Rat NOVX protein homologue Seqid 610.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 47.04% Mismatches: 93  
 Query Match: 30.28% Indels: 7  
 RESULT 376  
 ID AAY06438 standard; protein; 260 AA.  
 DE Human protease HUPM-7.  
 PN WO9936550-A2.  
 PD 22-JUL-1999.  
 PA (INCY-) INCYTE PHARM INC.  
 Best Local Similarity: 47.68% Mismatches: 97  
 Query Match: 30.23% Indels: 13  
 RESULT 377  
 ID AAM10694 standard; protein; 260 AA.  
 DE Human recombinant neuropsin, used for antibody production.  
 PN JP08245700-A.  
 PD 24-SEP-1996.  
 PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5  
 RESULT 378  
 ID AAM12393 standard; protein; 260 AA.  
 DE Mouse neuropsin protein.  
 PN JP08311099-A.  
 PD 26-NOV-1996.  
 PA (SHIO/) SHIOZAKA S.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5  
 RESULT 379  
 ID ABB57219 standard; protein; 260 AA.  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.  
 PN WO20018188-A2.  
 PD 22-NOV-2001.  
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5  
 RESULT 380  
 ID AD117073 standard; protein; 260 AA.  
 DE Murine NOVX protein homologue Seqid 609.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5

RESULT 381  
 ID ADI39731 standard; protein; 260 AA.  
 DE Mouse neuropsin protein.  
 PN US6642013-B1.  
 PD 04-NOV-2003.  
 PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5  
 RESULT 382  
 ID ADI37155 standard; protein; 260 AA.  
 DE Mouse neuropsin.  
 PN US2003199010-A1.  
 PD 23-OCT-2003.  
 PA (UYAR-) UNIV ARKANSAS.  
 Best Local Similarity: 48.99% Mismatches: 93  
 Query Match: 30.13% Indels: 5  
 RESULT 383  
 ID AAB21325 standard; protein; 250 AA.  
 DE Human TLSP.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 384  
 ID AAY99390 standard; protein; 250 AA.  
 DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.  
 PN WO20012708-A2.  
 PD 09-MAR-2000.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 385  
 ID AAB61139 standard; protein; 250 AA.  
 DE Protein of the invention #51.  
 PN WO200078961-A1.  
 PD 28-DEC-2000.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 386  
 ID AAU12424 standard; protein; 250 AA.  
 DE Human PRO1279 polypeptide sequence.  
 PN WO200140466-A2.  
 PD 07-JUN-2001.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 387  
 ID ABB50479 standard; protein; 250 AA.  
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
 PN WO200162891-A2.  
 PD 30-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 388  
 ID AAU83684 standard; protein; 250 AA.  
 DE Human PRO protein, Seq ID No 186.  
 PN WO200208288-A2.  
 PD 31-JAN-2002.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 389  
 ID ABG61816 standard; protein; 250 AA.  
 DE Prostate cancer-associated protein #17.  
 PN WO200230288-A2.  
 PD 18-APR-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 390

ID ABB84920 standard; protein; 250 AA.  
DE Human PRO1279 protein sequence SEQ ID NO:208.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 391  
ID ABB95526 standard; protein; 250 AA.  
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERE/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 392  
ID ABO17868 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 393  
ID ABU08031 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 394  
ID ABO33797 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 395  
ID ABU81122 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 396  
ID ABU56739 standard; protein; 250 AA.  
DE Lung cancer-associated polypeptide #332.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 397  
ID ABU66822 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN WO2003049816-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 398  
ID ABUS9903 standard; protein; 250 AA.  
DE Novel secreted and transmembrane protein PRO1279.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 399  
ID ABO25093 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein (PRO) #253.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 400  
ID ABU82140 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003080863-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 401  
ID ABU67098 standard; protein; 250 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 402  
ID ADA46025 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 403  
ID ADA76456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 404  
ID ABU72320 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 405  
ID ADA19106 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 406  
ID ADA61729 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049816-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 407  
ID ADB19514 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 408  
ID ADB28055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 409  
ID ADA86534 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 410  
ID ADB16098 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 411  
ID ADA47884 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 412  
ID ABO44736 standard; protein; 250 AA.  
DE Novel human secreted protein #179.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 413  
ID ABO33632 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 414  
ID ADA67679 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 415  
ID ADB30686 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068794-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 416  
ID ADA85982 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 417  
ID ADA97194 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 418  
ID ADA79498 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 419  
ID ADA87637 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 420  
ID ADB16839 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 421  
ID ADA91931 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 422  
ID ADB14994 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 423  
ID ADB18955 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 424  
ID ADA94170 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US200307722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 425	
ID ADB20066 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003082691-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 426	
ID ADB13378 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003082710-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 427	
ID ABO43401 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US200304945-A1.	
PD 06-MAR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 428	
ID ADA74632 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003068798-A1.	
PD 10-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 429	
ID ADB24865 standard; protein; 250 AA.	
DE Human PRO polypeptide SEQ ID NO 506.	
PN US200307713-A1.	
PD 24-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 430	
ID ADA82389 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003082701-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 431	
ID ADA75352 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003073216-A1.	
PD 17-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 432	
ID ADA85430 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003082695-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 433	
ID ADA84878 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003082708-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 434	
ID ADB30134 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003073214-A1.	
PD 17-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 435	
ID ADA80662 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003082761-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 436	
ID ADA75904 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003082703-A1.	
PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 437	
ID ADA47129 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003073210-A1.	
PD 17-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 438	
ID ADB25425 standard; protein; 250 AA.	
DE Human PRO polypeptide SEQ ID NO 506.	
PN US200307715-A1.	
PD 24-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 439	
ID ADA93601 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US200307721-A1.	
PD 24-APR-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 440	
ID ADB26951 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003092147-A1.	
PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 441	
ID ADB31238 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003096386-A1.	
PD 22-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 442	
ID ABJ72448 standard; protein; 250 AA.	
DE Human PRO1279 protein.	
PN US2003027988-A1.	
PD 06-FEB-2003.	
PA (GETH ) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5

RESULT 443  
ID ADA61166 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 444  
ID ADB24313 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077114-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 445  
ID ADA96642 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 446  
ID ADA81214 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 447  
ID ADA96090 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 448  
ID ADB26399 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 449  
ID ADB21884 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 450  
ID ABO34343 standard; protein; 250 AA.  
DE Human secreted/transmembrane polypeptide PRO 1279.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 451  
ID ADA77663 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 452  
ID ABO33509 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 453  
ID ADA87086 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 454  
ID ABO4485 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 455  
ID ADA8189 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 456  
ID ADA46577 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 457  
ID ADB28607 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 458  
ID ADB29159 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 459  
ID ABO26216 standard; protein; 250 AA.  
DE Human protein from novel secreted protein gene 179.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 460  
ID ADA77111 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 461  
ID ABO33509 standard; protein; 250 AA.



DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 462  
ID ADA88741 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 463  
ID ADA97746 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 464  
ID ADB27503 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 465  
ID ADB22436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 466  
ID ADBJ72150 standard; protein; 250 AA.  
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 467  
ID ADA67127 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 468  
ID ADB22988 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 469  
ID ADB23761 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 470  
ID ADA92483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082712-A1.  
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 471  
ID ADB15546 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 472  
ID ADB83676 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 473  
ID ADB80782 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 474  
ID ADB73323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 475  
ID ADB38798 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 476  
ID ADB78405 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 477  
ID ADB38246 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 478  
ID ADB66718 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 479  
ID ADB85053 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 480
ID ADB89798 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 481
ID ADB90530 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 482
ID ADB80596 standard; protein; 250 AA.
DE Ovarian cancer-associated protein #81.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 483
ID ADB39631 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 484
ID ADB78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 485
ID ADB87225 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 486
ID ADB84807 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 487
ID ADB47254 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 488
ID ADB83922 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 489
ID ADB86861 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 490
ID ADB73077 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 491
ID ADB77466 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 492
ID ADB75388 standard; protein; 250 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 493
ID ADB34623 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 494
ID ADB35727 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 495
ID ADB34071 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 496
ID ADB35175 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 497
ID ADB36279 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
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RESULT 498  
ID ADB46674 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 499  
ID ADC18039 standard; protein; 250 AA.  
DE Human PRO polypeptide #51.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 500  
ID ADC36915 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 501  
ID ADC21905 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 502  
ID ADC50547 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 503  
ID ADC72094 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 504  
ID ADC60073 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 505  
ID ADC49936 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 506  
ID ADC49135 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5

ID ADC49652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 508  
ID ADC47513 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 509  
ID ADC53080 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 510  
ID ADC57434 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 511  
ID ADC60625 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 512  
ID ADC51100 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 513  
ID ADC65627 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 514  
ID ADC54725 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 515  
ID ADC53686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 516  
ID ADC59209 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 517  
ID ADC56087 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 518  
ID ADC58657 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 519  
ID ADC47288 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 520  
ID ADD03331 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 521  
ID ADC90323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 522  
ID ADC69742 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 523  
ID ADC48631 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 524  
ID ADD10160 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 525  
ID ADC78133 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105013-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 526  
ID ADD04735 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 527  
ID ADD06368 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 528  
ID ADC80691 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 529  
ID ADD11198 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 530  
ID ADD10497 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 531  
ID ADC48079 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 532  
ID ADC77887 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 533  
ID ADC80139 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 534  
ID ADD11457 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105013-A1.

PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 535  
ID ADD09608 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 536  
ID ADD50850 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 537  
ID ADD41321 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 538  
ID ADD52460 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 539  
ID ADD51096 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 540  
ID ADD70685 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 541  
ID ADD39762 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 542  
ID ADD53200 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 543  
ID ADD53752 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 544  
ID ADD70208 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 545  
ID ADD37250 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 546  
ID ADD38329 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 547  
ID ADD39285 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 548  
ID ADD51908 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 549  
ID ADD02707 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 550  
ID ADD50577 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 551  
ID ADD02141 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 552  
ID ADD54323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 553
ID AD50331 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US200306970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 554
ID AD38808 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 555
ID AD40239 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 556
ID AD51342 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 557
ID ADE50460 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 558
ID ADD92640 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 559
ID ADD91536 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 560
ID ADE04150 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 561
ID ADE20072 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 562
ID ADE32447 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 563
ID ADE22379 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 564
ID ADD79603 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 565
ID ADE42139 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 566
ID ADE17956 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 567
ID ADD92088 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 568
ID ADE33551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 569
ID ADE34103 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 570
ID ADD80155 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
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RESULT 571
ID ADE49983 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 572
ID ADD93192 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 573
ID ADE19612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 574
ID ADE21541 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 575
ID ADE19060 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 576
ID ADE43256 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 577
ID ADD96045 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 578
ID ADE22931 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199084-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 579
ID ADD79049 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 580
ID ADE32999 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 581
ID ADE42691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 582
ID ADD80707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 583
ID ADD89735 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 584
ID ADE41019 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 585
ID ADE04818 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 587
ID ADF29966 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 588
ID ADF55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches: 89
Query Match: 29.94% Indels: 5
RESULT 589
ID ADG21656 standard; protein; 250 AA.
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DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 590  
ID ADG323297 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 591  
ID ADF97632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 592  
ID ADG80696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 593  
ID ADG80144 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 594  
ID ADH55436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 595  
ID ADH55988 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 596  
ID ADH99363 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 597  
ID ADI64207 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 598  
ID ADI65156 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 599  
ID ADH82069 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 600  
ID ADH81517 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 601  
ID ADM82686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 602  
ID ADN16085 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 603  
ID ADN16714 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 604  
ID ADN39242 standard; protein; 250 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 605  
ID ADN15533 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 606  
ID ADN14981 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 607  
ID ADI63655 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207387-A1.



PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 608  
ID ADC48889 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 609  
ID ADC81243 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 610  
ID ADE21060 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 611  
ID ADR05904 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 612  
ID ADD76691 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 613  
ID ADD75133 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 614  
ID ADR75879 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 615  
ID ADR85111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 616  
ID ADR86937 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100738-A1.  
PD 29-MAY-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 617  
ID ADR20814 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 618  
ID ADR39111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 619  
ID ADR8055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 620  
ID ADR86459 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 621  
ID ADR05658 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 622  
ID ADR73643 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 623  
ID ADR75907 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 624  
ID ADR78483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 625  
ID ADR41458 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 626	
ID ADR23483 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003092108-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 627	
ID ADR21306 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100736-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 628	
ID ADR77421 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100732-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 629	
ID ADR20568 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100733-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 630	
ID ADR75633 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003100064-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 631	
ID ADR74149 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003100708-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 632	
ID ADR74395 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003100709-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 633	
ID ADR76125 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100718-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 634	
ID ADR85617 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100721-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89

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Query Match: 29.94%	Indels: 5
RESULT 635	
ID ADR24035 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003092110-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 636	
ID ADR24678 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003092111-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 637	
ID ADR87503 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003203439-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 638	
ID ADR05166 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003100726-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 639	
ID ADR75379 standard; protein; 250 AA.	
DE Human PRO polypeptide #93.	
PN US2003100714-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 640	
ID ADR76923 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100715-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 641	
ID ADR86691 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100719-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 642	
ID ADR89369 standard; protein; 250 AA.	
DE Human PRO polypeptide #253.	
PN US2003199062-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89
Query Match: 29.94%	Indels: 5
RESULT 643	
ID ADR78159 standard; protein; 250 AA.	
DE Novel human secreted and transmembrane protein PRO1279.	
PN US2003100731-A1.	
PD 29-MAY-2003.	
PA (GETH) GENENTECH INC.	
Best Local Similarity: 48.19%	Mismatches: 89

RESULT 644  
ID ADE18508 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 645  
ID ADE88817 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 646  
ID ADD77667 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 647  
ID ADD77913 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 648  
ID ADD85371 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 649  
ID ADD73903 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 650  
ID ADD74641 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 651  
ID ADD77169 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 652  
ID ADD85863 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 653  
ID ADE29489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 654  
ID ADD74887 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 655  
ID ADE96543 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 656  
ID ADE94837 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 657  
ID ADE91248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 658  
ID ADE25854 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 659  
ID ADE95389 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 660  
ID ADE93499 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 661  
ID ADF24753 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 662  
ID ADE29489 standard; protein; 250 AA.

DE Human secreted/transmembrane protein PRO1279.  
 PN US2003203401-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 663  
 ID ADF35080 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199029-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 664  
 ID ADE97020 standard; protein; 250 AA.  
 DE Human secreted/transmembrane protein PRO1279.  
 PN US2003195334-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 665  
 ID ADE92395 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003199051-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 666  
 ID ADE90696 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199063-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 667  
 ID ADE91843 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003199058-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 668  
 ID ADG05699 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003096959-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 669  
 ID ADG27253 standard; protein; 250 AA.  
 DE Human PRO polypeptide #93.  
 PN US2003096962-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 670  
 ID ADG02422 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207352-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 671  
 ID ADG22208 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.

PN US2003207360-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 672  
 ID ADG20278 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207376-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 673  
 ID ADF98184 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207422-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 674  
 ID ADG24401 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003207426-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 675  
 ID ADF98755 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003208055-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 676  
 ID ADG03586 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207351-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 677  
 ID ADF99307 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207353-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 678  
 ID ADG16892 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207359-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 679  
 ID ADG05351 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207375-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 RESULT 680  
 ID ADG19618 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003207425-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 681  
ID ADG11316 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 682  
ID ADG13455 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 683  
ID ADG08512 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 684  
ID ADG15682 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 685  
ID ADG12095 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 686  
ID ADF97080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 687  
ID ADG06265 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 688  
ID ADG23849 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 689  
ID ADG04138 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 690  
ID ADG25039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 691  
ID ADF94652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 692  
ID ADG07336 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 693  
ID ADG07888 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 694  
ID ADG06748 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 695  
ID ADG55383 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 696  
ID ADG61047 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 697  
ID ADG62151 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 698  
ID ADH03058 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 699  
ID ADG82352 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 700  
ID ADG57591 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 701  
ID ADG57039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 702  
ID ADG55935 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 703  
ID ADG58695 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 704  
ID ADG71061 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 705  
ID ADH04012 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 706  
ID ADH03535 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 707  
ID ADH39092 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 708  
ID ADG58143 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 709  
ID ADG53727 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 710  
ID ADG71613 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 711  
ID ADG81800 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 712  
ID ADH30762 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 713  
ID ADH12129 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 714  
ID ADG52551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 715  
ID ADG54279 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 716  
ID ADG81248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 717

ID ADG56487 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 718  
ID ADH12753 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 719  
ID ADG61599 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 720  
ID ADH28686 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
FN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 721  
ID ADG54831 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 722  
ID ADG59871 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 723  
ID ADH43641 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
FN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 724  
ID ADG34182 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 725  
ID ADH04489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
FN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 726  
ID ADI81295 standard; protein; 250 AA.

DE Human PRO polypeptide #253.  
FN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 727  
ID ADI33652 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
FN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 728  
ID ADH69746 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
FN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 729  
ID ADH61490 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
FN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 730  
ID ADG10038 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 731  
ID ADI15509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 732  
ID ADG09386 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 733  
ID ADI14841 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 734  
ID ADI29907 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 735  
ID ADI18436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003207349-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 736  
ID ADM27304 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US200404179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 737  
ID ADJ63717 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 738  
ID ADJ77612 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 739  
ID ADK62986 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 740  
ID ADK66662 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 741  
ID ADJ65734 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 742  
ID ADM27870 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 743  
ID ADM42594 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 744  
ID ADL94689 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004073015-A1.

PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 745  
ID ADM28456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 746  
ID ADI95938 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 747  
ID ADI96490 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 748  
ID ADR72632 standard; protein; 250 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 749  
ID ADR72890 standard; protein; 250 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 750  
ID ADS34892 standard; protein; 250 AA.  
DE Human autoimmune disease-related protein - SEQ ID 106.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 751  
ID AAY42439 standard; protein; 282 AA.  
DE CASB12 amino acid sequence.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 752  
ID AAB11712 standard; protein; 282 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.  
PN WO20031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 753  
ID AAY43636 standard; protein; 282 AA.  
DE A human prostate-associated serum protease (PRASP).  
PN WO9941387-A2.  
PD 19-AUG-1999.



PA (INCY-) INCYTE PHARM INC.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 754  
ID ADN11325 standard; protein; 282 AA.  
DE Human kallikrein-11, marker for prostate cancer.  
PN WO2004029616-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 755  
ID ADQ17587 standard; protein; 282 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 756  
ID ADR72631 standard; protein; 282 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 757  
ID ADR72889 standard; protein; 282 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein1.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 758  
ID ADS34893 standard; protein; 282 AA.  
DE Human autoimmune disease-related protein - SEQ ID 107.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 48.13% Mismatches: 89  
Query Match: 29.94% Indels: 5  
RESULT 759  
ID AYA42440 standard; protein; 281 AA.  
DE CASB12 polypeptide derived from Expressed Sequence Tag products.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 47.98% Mismatches: 89  
Query Match: 29.65% Indels: 5  
RESULT 760  
ID AAU82732 standard; protein; 320 AA.  
DE Amino acid sequence of novel human protease #31.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 41.90% Mismatches: 100  
Query Match: 29.55% Indels: 51  
RESULT 761  
ID AAEL19166 standard; protein; 320 AA.  
DE Human protease, PRTS-3 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 41.90% Mismatches: 100  
Query Match: 29.55% Indels: 51  
RESULT 762  
ID AAB36482 standard; protein; 288 AA.  
DE Fusion gene with human serine protease catalytic domain protein #13.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.

Best Local Similarity: 51.10% Mismatches: 87  
Query Match: 29.16% Indels: 3  
RESULT 763  
ID AAB67542 standard; protein; 288 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Best Local Similarity: 51.10% Mismatches: 87  
Query Match: 29.16% Indels: 3  
RESULT 764  
ID AAY36093 standard; protein; 250 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 478.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 47.39% Mismatches: 91  
Query Match: 29.11% Indels: 5  
RESULT 765  
ID ADP19401 standard; protein; 250 AA.  
DE Human secreted polypeptide #252.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST) GENSET SA.  
Best Local Similarity: 47.39% Mismatches: 91  
Query Match: 29.11% Indels: 5  
RESULT 766  
ID AAB11714 standard; protein; 275 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO.6.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Best Local Similarity: 44.16% Mismatches: 88  
Query Match: 29.09% Indels: 30  
RESULT 767  
ID ADI17075 standard; protein; 225 AA.  
DE Murine NOVX protein homologue Segid 611.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 49.78% Mismatches: 86  
Query Match: 28.99% Indels: 2  
RESULT 768  
ID AAU79390 standard; protein; 256 AA.  
DE Novel human kallikrein KLK15.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 47.08% Mismatches: 88  
Query Match: 28.99% Indels: 16  
RESULT 769  
ID ADN10932 standard; protein; 256 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 47.08% Mismatches: 88  
Query Match: 28.99% Indels: 16  
RESULT 770  
ID AAB36483 standard; protein; 289 AA.  
DE Fusion gene with human serine protease catalytic domain protein #14.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.  
Best Local Similarity: 49.14% Mismatches: 79  
Query Match: 28.97% Indels: 5  
RESULT 771  
ID AAB67543 standard; protein; 289 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Best Local Similarity: 49.14% Mismatches: 79

Query Match:	28.97%	Indels:	5
RESULT 772			
ID AAE08017 standard; protein; 248 AA.			
DE Human PS133 consensus protein sequence.			
PN US6232456-B1.			
PD 15-MAY-2001.			
PA (ABBOTT ) ABBOTT LAB.			
Best Local Similarity: 47.79%	Mismatches:	87	
Query Match: 28.92%	Indels:	7	
RESULT 773			
ID AAB11713 standard; protein; 276 AA.			
DE Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.			
PN WO200031257-A1.			
PD 02-JUN-2000.			
PA (FUSO ) FUSO PHARM IND LTD.			
Best Local Similarity: 47.01%	Mismatches:	95	
Query Match: 28.92%	Indels:	5	
RESULT 774			
ID ADI117077 standard; protein; 260 AA.			
DE Human NOVX protein homologue SeqID 613.			
PN WO200268649-A2.			
PD 06-SEP-2002.			
PA (CURA-) CURAGEN CORP.			
Best Local Similarity: 46.54%	Mismatches:	100	
Query Match: 28.82%	Indels:	13	
RESULT 775			
ID ADC31389 standard; protein; 298 AA.			
DE Human novel polypeptide sequence, SEQ ID NO:1471.			
PN WO2003029271-A2.			
PD 10-APR-2003.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 48.12%	Mismatches:	79	
Query Match: 28.80%	Indels:	14	
RESULT 776			
ID AAB21312 standard; protein; 228 AA.			
DE Human tLSP.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 49.33%	Mismatches:	77	
Query Match: 28.65%	Indels:	4	
RESULT 777			
ID AAW08475 standard; protein; 247 AA.			
DE Porcine trypsinogen.			
PN WO9700316-A1.			
PD 03-JAN-1997.			
PA (NOVO ) NOVO-NORDISK AS.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 778			
ID ABB98258 standard; protein; 247 AA.			
DE Pig trypsinogen SEQ ID NO 1.			
PN WO200261064-A2.			
PD 08-AUG-2002.			
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.			
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 779			
ID ADJ92132 standard; protein; 247 AA.			
DE Pig pro-trypsin.			
PN US2004043455-A1.			
PD 04-MAR-2004.			
PA (NOVO ) NOVOZYMES BIOTECH INC.			
Best Local Similarity: 45.56%	Mismatches:	83	
Query Match: 27.73%	Indels:	10	
RESULT 780			
ID ABU26666 standard; protein; 267 AA.			
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.			
PN WO2003000844-A2.			
PD 03-JAN-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 44.81%	Mismatches:	88	
Query Match:			
Query Match:	27.66%	Indels:	25
RESULT 781			
ID AAB21306 standard; protein; 251 AA.			
DE Human KLK-L6 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.85%	Mismatches:	87	
Query Match: 27.57%	Indels:	15	
RESULT 782			
ID ADNI0930 standard; protein; 251 AA.			
DE Human Kallikrein 14, marker of endocrine cancer.			
PN WO2004029285-A2.			
PD 08-APR-2004.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.85%	Mismatches:	87	
Query Match: 27.57%	Indels:	15	
RESULT 783			
ID AAB21298 standard; protein; 250 AA.			
DE Human KLK-L3 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 784			
ID ABP64969 standard; protein; 250 AA.			
DE Human protein SEQ ID 629.			
PN WO200259260-A2.			
PD 01-AUG-2002.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 785			
ID ABR55400 standard; protein; 250 AA.			
DE Amino acid sequence of human Kallikrein 9 (hK9).			
PN WO2003033731-A2.			
PD 24-APR-2003.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 786			
ID ADR05516 standard; protein; 250 AA.			
DE Antipsoriatic protein sequence #924.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 46.67%	Mismatches:	89	
Query Match: 27.52%	Indels:	15	
RESULT 787			
ID AAB21300 standard; protein; 277 AA.			
DE Human KLK-L4 protein #2.			
PN WO200053776-A2.			
PD 14-SEP-2000.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	
RESULT 788			
ID ABO00554 standard; protein; 277 AA.			
DE Novel human polypeptide #141.			
PN WO2003023013-A2.			
PD 20-MAR-2003.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	
RESULT 789			
ID ADL71094 standard; protein; 277 AA.			
DE Human Kallikrein 13 protein SEQ ID NO:1.			
PN WO2004021009-A2.			
PD 11-MAR-2004.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 46.77%	Mismatches:	80	
Query Match: 27.44%	Indels:	16	

RESULT 790  
ID ADN04184 standard; protein; 277 AA.  
DE Antipsoriatic protein sequence #287.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 46.77% Mismatches: 80  
Query Match: 27.44% Indels: 16  
RESULT 791  
ID ADRI4575 standard; protein; 277 AA.  
DE Human NF-kappaB pathway-associated protein SeqID576.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Best Local Similarity: 46.77% Mismatches: 80  
Query Match: 27.44% Indels: 16  
RESULT 792  
ID AAU16971 standard; protein; 251 AA.  
DE Human novel secreted protein, SEQ ID 212.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 46.85% Mismatches: 89  
Query Match: 27.42% Indels: 15  
RESULT 793  
ID AAU23217 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #303.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 46.85% Mismatches: 90  
Query Match: 27.32% Indels: 15  
RESULT 794  
ID AAV16777 standard; protein; 293 AA.  
DE Human keratinocyte derived protease (KDP).  
PN WO9918219-A1.  
PD 15-APR-1999.  
PA (PROC ) PROCTER & GAMBLE CO.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 795  
ID AAY30524 standard; protein; 293 AA.  
DE Human PDSP-1 protein.  
PN WO9946391-A2.  
PD 16-SEP-1999.  
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 796  
ID AAY38412 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 797  
ID AAY38426 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 798  
ID AAY66726 standard; protein; 293 AA.  
DE Membrane-bound protein PRO1132.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 799  
ID ADA56974 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.

ID AAB21296 standard; protein; 293 AA.  
DE Human KIK-L2 protein.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 800  
ID AAU12399 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 801  
ID AAB65249 standard; protein; 293 AA.  
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 802  
ID AAU81966 standard; protein; 293 AA.  
DE Human PRO1132.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 803  
ID ABU58064 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 804  
ID ABU59142 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1132.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 805  
ID ABU82654 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 806  
ID AB017843 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 807  
ID ADA57425 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 808  
ID ADA56974 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.

PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 809  
ID ADA57427 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 810  
ID ADA57428 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 811  
ID ABU60573 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 812  
ID ABU13955 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 813  
ID ABU81097 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 814  
ID ABU72540 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 815  
ID ABU66797 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 816  
ID ADA41303 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 817  
ID ADA41305 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 818  
ID ADA40825 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 819  
ID ADA41306 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 820  
ID ABU59878 standard; protein; 293 AA.  
DE Novel secreted and transmembrane protein PRO1132.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 821  
ID ABU59289 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 822  
ID ABO25986 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 823  
ID ABO25068 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein (PRO) #228.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 824  
ID ABU58995 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 825  
ID ABU92373 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 826  
ID ABU59438 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1346.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 827

ID ABU67073 standard; protein; 293 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 456.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 828  
ID ABU92204 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 829  
ID ABU10910 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 830  
ID ABU81662 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002171164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 831  
ID ABU88601 standard; protein; 293 AA.  
DE Human secreted and transmembrane polypeptide PRO1132.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 832  
ID ABO34115 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 833  
ID ADA45975 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 834  
ID ADA76406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 835  
ID ADA19056 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 836  
ID ADA61679 standard; protein; 293 AA.  
DE Homo sapiens.  
PN US2003049816-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 837  
ID ADB19464 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 838  
ID ADB28005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 839  
ID ADA86484 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 840  
ID ADB16048 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 841  
ID ADA37820 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 842  
ID ADA47834 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 843  
ID ADA1506 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 844  
ID ADA10293 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, PRO1132.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 845  
ID ADA67629 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83



PD 01-MAY-2003.	Best Local Similarity: 45.34%	Mismatches: 83	Best Local Similarity: 45.34%	Mismatches: 83
PA (GETH ) GENENTECH INC.	Query Match: 27.32%	Indels: 5	Query Match: 27.32%	Indels: 5
RESULT 865				
ID ADA75302 standard; protein; 293 AA.			ID ADA93551 standard; protein; 293 AA.	
DE Human PRO polypeptide #228.			DE Human PRO polypeptide #228.	
PN US2003073216-A1.			PN US2003077721-A1.	
PD 17-APR-2003.			PD 24-APR-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 866			RESULT 875	
ID ADA85380 standard; protein; 293 AA.			ID ADB26901 standard; protein; 293 AA.	
DE Novel human secreted and transmembrane protein PRO1132.			DE Human PRO polypeptide #228.	
PN US2003082695-A1.			PN US2003092147-A1.	
PD 01-MAY-2003.			PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 867			RESULT 876	
ID ADA84828 standard; protein; 293 AA.			ID ADB31188 standard; protein; 293 AA.	
DE Novel human secreted and transmembrane protein PRO1132.			DE Human PRO polypeptide #228.	
PN US2003082708-A1.			PN US2003096386-A1.	
PD 01-MAY-2003.			PD 22-MAY-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 868			RESULT 877	
ID ADB30084 standard; protein; 293 AA.			ID ADA92871 standard; protein; 293 AA.	
DE Human PRO polypeptide #228.			DE Human secreted/transmembrane protein PRO1132.	
PN US2003073214-A1.			PN US2003060407-A1.	
PD 17-APR-2003.			PD 27-MAR-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 869			RESULT 878	
ID ADA80612 standard; protein; 293 AA.			ID ADA61116 standard; protein; 293 AA.	
DE Human PRO polypeptide #228.			DE Homo sapiens.	
PN US2003082761-A1.			PN US2003049817-A1.	
PD 01-MAY-2003.			PD 13-MAR-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 870			RESULT 879	
ID ADA75854 standard; protein; 293 AA.			ID ADB24263 standard; protein; 293 AA.	
DE Human PRO polypeptide #228.			DE Human PRO polypeptide SEQ ID NO 456.	
PN US2003082703-A1.			PN US2003077714-A1.	
PD 01-MAY-2003.			PD 24-APR-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 871			RESULT 880	
ID ADA38750 standard; protein; 293 AA.			ID ADA96592 standard; protein; 293 AA.	
DE Human secreted/transmembrane protein PRO1132.			DE Human PRO polypeptide #228.	
PN US2003059780-A1.			PN US2003082690-A1.	
PD 27-MAR-2003.			PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 872			RESULT 881	
ID ADA47079 standard; protein; 293 AA.			ID ADA81164 standard; protein; 293 AA.	
DE Human PRO polypeptide #228.			DE Human PRO polypeptide #228.	
PN US2003073210-A1.			PN US2003082702-A1.	
PD 17-APR-2003.			PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	
RESULT 873			RESULT 882	
ID ADB25375 standard; protein; 293 AA.			ID ADA96040 standard; protein; 293 AA.	
DE Human PRO polypeptide SEQ ID NO 456.			DE Human PRO polypeptide #228.	
PN US2003077715-A1.			PN US2003082759-A1.	
PD 24-APR-2003.			PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 45.34%			Best Local Similarity: 45.34%	
Query Match: 27.32%			Query Match: 27.32%	

RESULT 883  
ID ADB26349 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 884  
ID ADB21834 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 885  
ID ADA77613 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 886  
ID ADB18353 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US200307710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 887  
ID ADA87036 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 888  
ID ADA88139 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 889  
ID ADA46527 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 890  
ID ADB28557 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 891  
ID ADB29109 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 892  
ID ABO53201 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 893  
ID ADA77061 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 894  
ID ADA22432 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 895  
ID ADA88691 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 896  
ID ADA97696 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 897  
ID ADB27453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022339-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 898  
ID ADB22386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 899  
ID ABO22571 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 900  
ID ADA06598 standard; protein; 293 AA.  
DE Human secreted/transmembrane PRO polypeptide #96.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 901  
ID ADA39291 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5



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ID ADA67077 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068793-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 903
ID ADB22938 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077711-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 904
ID ADB23711 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077712-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 905
ID ADA92433 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082712-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 906
ID ADB15496 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087352-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 907
ID ADB38748 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082766-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 908
ID ADB96317 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003054403-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 909
ID ADB38196 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087347-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 910
ID ADB66668 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082689-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 911
ID ADB99748 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077716-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 912
ID ADB90480 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082762-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 913
ID ADB80490 standard; protein; 293 AA.
DE Ovarian cancer-associated protein #27.
PN WO2002102235-A2.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 914
ID ADB39581 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 915
ID ADB47204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082687-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 916
ID ADB86811 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082697-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 917
ID ADB77416 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082696-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 918
ID ADB34573 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077717-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 919
ID ADB35677 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077719-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 920
ID ADB34021 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077716-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
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PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 921  
ID ADB35125 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US200307718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 922  
ID ADB36229 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 923  
ID ADB46624 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 924  
ID ADC57789 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 925  
ID ADC55153 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 926  
ID ADC12020 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 927  
ID ADC56442 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003064375-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 928  
ID ADC07497 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003068647-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 929  
ID ADC11487 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 930  
ID ADC50497 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.

PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 931  
ID ADC72044 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 932  
ID ADC60023 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 933  
ID ADC57384 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 934  
ID ADC57384 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 935  
ID ADC60575 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 936  
ID ADC51050 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 937  
ID ADC65577 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 938  
ID ADC54675 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 939  
ID ADC53636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087364-A1.

PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 940  
ID ADC59159 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 941  
ID ADC56037 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 942  
ID ADC58607 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 943  
ID ADC14609 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 944  
ID ADD08141 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068623-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 945  
ID ADD03281 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 946  
ID ADC90273 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 947  
ID ADC81966 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 948  
ID ADCG9692 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5

RESULT 949  
ID ADC48581 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 950  
ID ADD10110 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 951  
ID ADD07608 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 952  
ID ADD04685 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 953  
ID ADC82499 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 954  
ID ADC80641 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 955  
ID ADD11148 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 956  
ID ADC48029 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 957  
ID ADD08679 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 958  
ID ADC80089 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.

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PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 959
ID ADD06928 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 960
ID ADD09558 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 961
ID ADC83175 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 962
ID ADD41271 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 963
ID ADD52410 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 964
ID ADD53150 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194782-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 965
ID ADD53702 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 966
ID ADD55282 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 967
ID ADD56240 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 968
ID ADD51858 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 969
ID ADD02657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 970
ID ADD02091 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 971
ID ADD54273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 972
ID ADD54678 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 973
ID ADD92590 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 974
ID ADD91486 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 975
ID AD804100 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 976
ID ADE26832 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mismatches: 83
Query Match: 27.32% Indels: 5
RESULT 977
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ID ADE32397 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 978  
ID ADE22329 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 979  
ID ADD79553 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 980  
ID ADE42089 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 981  
ID ADE17906 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 982  
ID ADD92038 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 983  
ID ADE33501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 984  
ID ADE34053 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 985  
ID ADD80105 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 986  
ID ADD93142 standard; protein; 293 AA.

DE Human PRO polypeptide #228.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 987  
ID ADE19562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 988  
ID ADE19010 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 989  
ID ADE43206 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 990  
ID ADD95995 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 991  
ID ADE22881 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 992  
ID ADD78999 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 993  
ID ADE26299 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 994  
ID ADE32949 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 995  
ID ADE42641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199032-A1.

PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 996  
 ID AD80657 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207418-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 997  
 ID AD89685 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003199028-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 998  
 ID ADE04768 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003199034-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 999  
 ID ADE04768 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003199034-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1000  
 ID ADE2897 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003194777-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1001  
 ID ADE67236 standard; protein; 293 AA.  
 DE Human PRO1132 amino acid sequence SEQ ID NO:309.  
 PN US2002198148-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1002  
 ID ADG21606 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207355-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1003  
 ID ADG23247 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207384-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1004  
 ID ADF97582 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207370-A1.  
 PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1005  
 ID ADG80646 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207373-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1006  
 ID ADG8094 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207372-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1007  
 ID ADH55386 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207381-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1008  
 ID ADH55938 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207379-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1009  
 ID ADI35490 standard; protein; 293 AA.  
 DE Human PRO polypeptide #96.  
 PN US2003050457-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1010  
 ID ADI64157 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207385-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1011  
 ID ADI65106 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207386-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1012  
 ID ADI63605 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207387-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1013  
 ID ADH82019 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207388-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1014  
 ID ADF97582 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207370-A1.  
 PD 06-NOV-2003.

Query Match: 27.32% Indels: 5  
RESULT 1014  
ID ADH99982 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1015  
ID ADH81467 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1016  
ID ADM82636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1017  
ID ADN16035 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1018  
ID ADN16664 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1019  
ID ADN39198 standard; protein; 293 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1020  
ID ADN15483 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1021  
ID ADN14931 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1022  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1023  
ID ADE18458 standard; protein; 293 AA.

ID ADD76641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1024  
ID ADH88005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1025  
ID ADH86409 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1026  
ID ADE75857 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1027  
ID ADE23433 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1028  
ID ADE23985 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1029  
ID ADE24628 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1030  
ID ADH87453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1031  
ID ADH89319 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1032  
ID ADE18458 standard; protein; 293 AA.

DE Human PRO polypeptide #228.  
PD US2003194794-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1033  
ID ADE98767 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1034  
ID ADE94787 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1035  
ID ADE91198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1036  
ID ADF35435 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1037  
ID ADE95339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1038  
ID ADE93449 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1039  
ID ADF5030 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1040  
ID ADE92345 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1041  
ID ADE90646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199063-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1042  
ID ADE91793 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1043  
ID ADG11685 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1044  
ID ADG02372 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1045  
ID ADG22158 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1046  
ID ADG20228 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1047  
ID ADF98134 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1048  
ID ADG24351 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1049  
ID ADF98705 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1050  
ID ADG03536 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207351-A1.  
PD 06-NOV-2003.



PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1051  
ID ADF9257 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1052  
ID ADG16842 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1053  
ID ADG05301 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1054  
ID ADG19568 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1055  
ID ADG13405 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1056  
ID ADG08462 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1057  
ID ADG15632 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1058  
ID ADF97030 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1059  
ID ADG06215 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1060  
ID ADG23799 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1061  
ID ADG04088 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1062  
ID ADG24989 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1063  
ID ADG07286 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1064  
ID ADG07838 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1065  
ID ADG55333 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1066  
ID ADG60997 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1067  
ID ADG62101 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1068  
ID ADG82302 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5

Query Match: 27.32% Indels: 5  
RESULT 1069  
ID ADG57541 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207362-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1070  
ID ADG56989 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207364-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1071  
ID ADG55885 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207365-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1072  
ID ADG58645 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207368-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1073  
ID ADG71011 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207420-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1074  
ID ADG58093 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207363-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1075  
ID ADG53677 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207415-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1076  
ID ADG71563 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207421-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1077  
ID ADG81750 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207805-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1078  
ID ADG61549 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.

ID ADH19555 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1079  
ID ADH30712 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1080  
ID ADH12079 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1081  
ID ADG52501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1082  
ID ADG54229 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1083  
ID ADG81198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1084  
ID ADG56437 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1085  
ID ADH12703 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1086  
ID ADH21048 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1087  
ID ADG61549 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.

PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1088  
ID ADH20088 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1089  
ID ADH28636 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1090  
ID ADG54781 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1091  
ID ADG59821 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1092  
ID ADI81245 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1093  
ID ADG09988 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1094  
ID ADI15459 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1095  
ID ADG09336 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1096  
ID ADI14791 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207383-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1097  
ID ADI18386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1098  
ID ADJ63667 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1099  
ID ADJ77562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1100  
ID ADJ5684 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1101  
ID ADM27820 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1102  
ID ADK52481 standard; protein; 293 AA.  
DE Human kallikrein 5 protein.  
PN WO2004021008-A2.  
PD 11-MAR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
PA (YOUS/) YOUSEF G.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1103  
ID ADM42544 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1104  
ID ADM28406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.34% Mismatches: 83  
Query Match: 27.32% Indels: 5  
RESULT 1105  
ID ADI95888 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077659-A1.

PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1106  
 ID AD196440 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1107  
 ID ADR72621 standard; protein; 293 AA.  
 DE Human renal cell carcinoma-related kallikrein 5 (hK5) protein.  
 PN WO2004077060-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1108  
 ID ADR72873 standard; protein; 293 AA.  
 DE Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein.  
 PN WO2004075713-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1109  
 ID AAY14072 standard; protein; 322 AA.  
 DE Human BS247 specific epitope.  
 PN WO9220227-A1.  
 PD 06-MAY-1999.  
 PA (ABBO ) ABBOTT LAB.  
 Best Local Similarity: 45.34% Mismatches: 83  
 Query Match: 27.32% Indels: 5  
 RESULT 1110  
 ID AAW07620 standard; protein; 276 AA.  
 DE Human NES1 polypeptide.  
 PN WO9639175-A1.  
 PD 12-DEC-1996.  
 PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1111  
 ID AAB21327 standard; protein; 276 AA.  
 DE Human NES1.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1112  
 ID ABG96356 standard; protein; 276 AA.  
 DE Human ovarian cancer marker OV32.  
 PN WO200271928-A2.  
 PD 19-SEP-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1113  
 ID AAU82729 standard; protein; 276 AA.  
 DE Amino acid sequence of novel human protease #28.  
 PN WO200200860-A2.  
 PD 03-JAN-2002.  
 PA (SUGE-) SUGEN INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1114  
 ID ADB80527 standard; protein; 276 AA.  
 DE Ovarian cancer-associated protein #46.  
 PN WO2002102235-A2.  
 PD 27-DEC-2002.

PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1115  
 ID ADE40473 standard; protein; 276 AA.  
 DE Human kallikrein 10 (gene ID 2045) protein.  
 PN WO2003070883-A2.  
 PD 28-AUG-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1116  
 ID ADN39880 standard; protein; 276 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1117  
 ID ADN04446 standard; protein; 276 AA.  
 DE Antipsoriatic protein sequence #416.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1118  
 ID ADQ89070 standard; protein; 276 AA.  
 DE Human urological disorder related protein 2045 SEQ:22.  
 PN WO2004065576-A2.  
 PD 05-AUG-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1119  
 ID ADR72628 standard; protein; 276 AA.  
 DE Human renal cell carcinoma-related kallikrein 10 (hK10) protein.  
 PN WO2004077060-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1120  
 ID ADR72886 standard; protein; 276 AA.  
 DE Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.  
 PN WO2004075713-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 45.91% Mismatches: 92  
 Query Match: 27.30% Indels: 18  
 RESULT 1121  
 ID AAB21305 standard; protein; 237 AA.  
 DE Human K1K-L6 protein #1.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 48.10% Mismatches: 84  
 Query Match: 27.20% Indels: 8  
 RESULT 1122  
 ID AAB21299 standard; protein; 256 AA.  
 DE Human K1K-L4 protein #1.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 49.12% Mismatches: 78  
 Query Match: 27.18% Indels: 5  
 RESULT 1123  
 ID AAB21309 standard; protein; 287 AA.  
 DE Human K1K-L2.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.

Best Local Similarity: 46.0% Mismatches: 80  
Query Match: 27.1% Indels: 5  
RESULT 1124  
ID ABB98259 standard; protein; 228 AA.  
DE Synthetic shortened trypsinogen SEQ ID NO 23.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 46.7% Mismatches: 77  
Query Match: 27.1% Indels: 6  
RESULT 1125  
ID AAB21310 standard; protein; 239 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1126  
ID AAR44532 standard; protein; 244 AA.  
DE Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL) LILLY & CO ELI.  
Best Local Similarity: 46.7% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1127  
ID AAW22985 standard; protein; 244 AA.  
DE Human serine protease 59 (SP59).  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR) SUNTORY LTD.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1128  
ID AAW51006 standard; protein; 244 AA.  
DE Protease M, a novel serine protease.  
PN WO9811238-A2.  
PD 19-MAR-1998.  
PA (DAND) DANA FARBEN CANCER INST INC.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1129  
ID AAB21323 standard; protein; 244 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1130  
ID AAE37572 standard; protein; 244 AA.  
DE Human 2047 protein.  
PN WO2003037258-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1131  
ID ADB80567 standard; protein; 244 AA.  
DE Ovarian cancer-associated protein #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 46.6% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1132  
ID ADN39212 standard; protein; 244 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1133  
ID ADN04074 standard; protein; 244 AA.  
DE Antipsoriatic protein sequence #232.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1134  
ID ADN29289 standard; protein; 244 AA.  
DE Human kallikrein 6 associated protein.  
PN US2004097452-A1.  
PD 20-MAY-2004.  
PA (IGIS-) IGIS PHARM INC.  
Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1135  
ID ADQ89076 standard; protein; 244 AA.  
DE Human urological disorder related protein 2047 SEQ:28.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1136  
ID ADR72624 standard; protein; 244 AA.  
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1137  
ID ADR72876 standard; protein; 244 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 46.67% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1138  
ID ABG96357 standard; protein; 244 AA.  
DE Human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 46.86% Mismatches: 83  
Query Match: 27.1% Indels: 10  
RESULT 1139  
ID AAB21297 standard; protein; 296 AA.  
DE Human KLK-L3 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 46.12% Mismatches: 79  
Query Match: 26.96% Indels: 30  
RESULT 1140  
ID ADA05734 standard; protein; 252 AA.  
DE Human NOV18b protein SEQ ID NO:94.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 44.66% Mismatches: 88  
Query Match: 26.89% Indels: 19  
RESULT 1141  
ID ADN62898 standard; protein; 252 AA.  
DE Human NOV18b.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.  
 PA (KEKU/) KEKUDA R.  
 PA (JUGJ/) JU J.  
 PA (LILL/) LI L.  
 PA (GUOX/) GUO X.  
 PA (PATT/) PATTURAJAN M.  
 PA (SPYT/) SPYTEK K A.  
 PA (EDIN/) EDINGER S R.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ORTT/) ORT T.  
 PA (GORM/) GORMAN L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (ANDE/) ANDERSON D W.  
 PA (ZHON/) ZHONG M.  
 PA (CATT/) CATTERTON E.  
 PA (JIWW/) JI W.  
 PA (MILL/) MILLER C E.  
 PA (RAST/) RASTELLI L.  
 PA (STON/) STONE D J.  
 PA (PENA/) PENA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LEAC/) LEACH M D.  
 PA (AGEE/) AGEE M L.  
 PA (BERG/) BERGHS C.  
 PA (DIPI/) DIPIPO V A.  
 PA (EISE/) EISEN A.  
 PA (GANG/) GANGOLLI E A.  
 PA (RIEG/) RIEGER D K.  
 PA (SPAD/) SPADERNA S K.  
 Best Local Similarity: 44.66% Mismatches: 88  
 Query Match: 26.86% Indels: 19  
 RESULT 1142  
 ID AAB21302 standard; protein; 111 AA.  
 DE Human KLK-L5 protein #2.  
 PN WO200053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 55.78% Mismatches: 0  
 Query Match: 26.86% Indels: 89  
 RESULT 1143  
 ID ADN10928 standard; protein; 111 AA.  
 DE Human kallikrein 12, marker of endocrine cancer.  
 PN WO2004029285-A2.  
 PD 08-APR-2004.  
 PA (MOUN) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 55.78% Mismatches: 0  
 Query Match: 26.86% Indels: 88  
 RESULT 1144  
 ID AAR67888 standard; protein; 253 AA.  
 DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).  
 PN WO9500651-A1.  
 PD 05-JAN-1995.  
 PA (SYMB-) SYMBICOM AB.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1145  
 ID AAW05383 standard; protein; 253 AA.  
 DE Human amyloid precursor protein protease.  
 PN WO9631122-A1.  
 PD 10-OCT-1996.  
 PA (ELIL) LILLY & CO ELI.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1146  
 ID AAY08025 standard; protein; 253 AA.  
 DE Mouse protease-related protein (PVP).  
 PN DE19736198-C1.  
 PD 24-DEC-1998.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 Best Local Similarity: 42.52% Mismatches: 89

Query Match: 26.86% Indels: 10  
 RESULT 1147  
 ID ABB84421 standard; peptide; 253 AA.  
 DE Human SCCE protein N-terminal fragment SEQ ID 48.  
 PN WO200262135-A2.  
 PD 15-AUG-2002.  
 PA (EGEL/) EGELRUD T.  
 PA (HANS/) HANSSON L.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1148  
 ID ABB84406 standard; protein; 253 AA.  
 DE Human SCCE protein.  
 PN WO200262135-A2.  
 PD 15-AUG-2002.  
 PA (EGEL/) EGELRUD T.  
 PA (HANS/) HANSSON L.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1149  
 ID AAU82740 standard; protein; 253 AA.  
 DE Amino acid sequence of novel human protease #39.  
 PN WO200200860-A2.  
 PD 03-JAN-2002.  
 PA (SUGE-) SUGEN INC.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1150  
 ID ABU07440 standard; protein; 253 AA.  
 DE Protein differentially regulated in prostate cancer #43.  
 PN WO200281638-A2.  
 PD 17-OCT-2002.  
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1151  
 ID ABU07471 standard; protein; 253 AA.  
 DE Protein differentially regulated in prostate cancer #74.  
 PN WO200281638-A2.  
 PD 17-OCT-2002.  
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1152  
 ID ABR58471 standard; protein; 253 AA.  
 DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.  
 PN WO2003029468-A1.  
 PD 10-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1153  
 ID AD880484 standard; protein; 253 AA.  
 DE Ovarian cancer-associated protein #24.  
 PN WO2002102235-A2.  
 PD 27-DEC-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1154  
 ID ADJ68833 standard; protein; 253 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SegID639.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Best Local Similarity: 44.57% Mismatches: 90  
 Query Match: 26.86% Indels: 16  
 RESULT 1155  
 ID ADN31980 standard; protein; 253 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.  
 PN WO2003042861-A2.  
 PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.	90	Mismatches:	77
Best Local Similarity: 44.57%	16	Indels:	6
Query Match: 26.86%			
RESULT 1156			
ID ADL06515 standard; protein; 253 AA.			
DE Human tumour-associated antigenic target (TAT) polypeptide #14.			
PN WO2004016225-A2.			
PD 26-FEB-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 44.57%	90	Mismatches:	73
Query Match: 26.86%	16	Indels:	6
RESULT 1157			
ID ADN04182 standard; protein; 253 AA.			
DE Antipsoariatic protein sequence #286.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 44.57%	90	Mismatches:	77
Query Match: 26.86%	16	Indels:	6
RESULT 1158			
ID ADNR72880 standard; protein; 253 AA.			
DE Human ovarian cancer-related tumour marker kallikrein 7 (HK7) protein.			
PN WO2004075713-A2.			
PD 10-SEP-2004.			
PA (MOUN ) MOUNT SINAI HOSPITAL.			
Best Local Similarity: 44.57%	90	Mismatches:	77
Query Match: 26.86%	16	Indels:	6
RESULT 1159			
ID ADN62896 standard; protein; 250 AA.			
DE Human NOV18a.			
PN US2004038223-A1.			
PD 26-FEB-2004.			
PA (SMIT/) SMITHSON G.			
PA (MILL/) MILLET I.			
PA (PEYM/) PEYMAN J. A.			
PA (KEKU/) KEKUDA R.			
PA (JUJ/) JU J.			
PA (LIL/) LI L.			
PA (GUOX/) GUO X.			
PA (PATT/) PATTURAJAN M.			
PA (SPYT/) SPYTEK K. A.			
PA (EDIN/) EDINGER S. R.			
PA (ELLE/) ELLERMAN K.			
PA (MALY/) MALYANKAR U. M.			
PA (ORTT/) ORT T.			
PA (GORM/) GORMAN L.			
PA (ZERH/) ZERHUSEN B. D.			
PA (ANDE/) ANDERSON D. W.			
PA (ZHON/) ZHONG M.			
PA (CATT/) CATTERTON E.			
PA (JIW/) JI W.			
PA (MILL/) MILLER C. E.			
PA (RST/) RASTELLI L.			
PA (STON/) STONE D. J.			
PA (PENA/) PENA C. E. A.			
PA (SHEN/) SHENOY S. G.			
PA (SHIM/) SHIMKETS R. A.			
PA (ROTH/) ROTHENBERG M. E.			
PA (LEAC/) LEACH M. D.			
PA (AGEE/) AGEE M. L.			
PA (BERG/) BERGHS C.			
PA (DIPI/) DIPIPO V. A.			
PA (EISE/) EISEN A.			
PA (GANG/) GANGOLLI E. A.			
PA (RIEG/) RIEGER D. K.			
PA (SPAD/) SPADERNA S. K.			
Best Local Similarity: 44.84%	90	Mismatches:	92
Query Match: 26.77%	12	Indels:	15
RESULT 1160			
ID AAY77494 standard; protein; 229 AA.			
DE Bovine trypsinogen.			
PN WO200005384-A1.			
PD 03-FEB-2000.			





PD 26-APR-2001.	PA (COLM/) COLMAN S D.		
PA (UYAR-) UNIV ARKANSAS.	PA (WOLE/) WOLENC A R.		
Best Local Similarity: 46.52%	PA (PENA/) PENAC E A.		
Query Match: 26.38%	PA (FURT/) FURTAK K.		
RESULT 1184	PA (GROS/) GROSSE W M.		
ID AAY78975 standard; protein; 246 AA.	PA (ALSO/) ALSOBROOK J P.		
DE Canine anionic trypsinogen amino acid sequence.	PA (LEFL/) LEFLEY D M.		
PD WO200009739-A1.	PA (RIEG/) RIEGER D K.		
PD 24-FEB-2000.	PA (BURG/) BURGESS C E.		
Best Local Similarity: 44.22%	Best Local Similarity: 44.35%	Mismatches: 103	
Query Match: 26.38%	Query Match: 26.11%	Indels: 5	
RESULT 1185	RESULT 1191		
ID AAB21326 standard; protein; 257 AA.	ID ABB78122 standard; peptide; 223 AA.		
DE Human HSCER.	DE Amino acid sequence of trypsin.		
PD WO200053776-A2.	PN US2002072863-A1.		
PD 14-SEP-2000.	PD 13-JUN-2002.		
PA (MOUN) MOUNT SINAI HOSPITAL.	PA (FUJIT) FUJITSU LTD.		
Best Local Similarity: 44.11%	Best Local Similarity: 45.61%	Mismatches: 78	
Query Match: 26.33%	Query Match: 26.04%	Indels: 6	
RESULT 1186	RESULT 1192		
ID AAW64260 standard; protein; 246 AA.	ID ABB83322 standard; protein; 223 AA.		
DE Human amyloid beta-protein precursor inhibitor.	DE Partial trypsin sequence.		
PD WO9824886-A1.	PN US2002035434-A1.		
PD 11-JUN-1998.	PD 21-MAR-2002.		
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.	PA (FUJIT) FUJITSU LTD.		
Best Local Similarity: 44.53%	Best Local Similarity: 45.61%	Mismatches: 78	
Query Match: 26.28%	Query Match: 26.04%	Indels: 6	
RESULT 1187	RESULT 1193		
ID ADC73299 standard; protein; 220 AA.	ID ABB94419 standard; peptide; 243 AA.		
DE Stereostereorelated 2PTC_E protein.	DE Bovine SCCE protein N-terminal fragment SEQ ID 46.		
PD WO2003060765-A1.	PN WO200262135-A2.		
PD 24-JUL-2003.	PD 15-AUG-2002.		
PA (AJIN) AJINOMOTO CO INC.	PA (EGEL/) EGELRUD T.		
PA (UMEY/) UMEYAMA H.	PA (HANS/) HANSSON L.		
Best Local Similarity: 46.85%	Best Local Similarity: 43.70%	Mismatches: 83	
Query Match: 26.19%	Query Match: 25.82%	Indels: 23	
RESULT 1188	RESULT 1194		
ID ADC73301 standard; protein; 279 AA.	ID ABB04644 standard; protein; 240 AA.		
DE Stereostereorelated 2PTC protein.	DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.		
PD WO2003060765-A1.	PN JP2001269173-A.		
PD 24-JUL-2003.	PD 02-OCT-2001.		
PA (AJIN) AJINOMOTO CO INC.	PA (NISE) JAPAN TOBACCO INC.		
PA (UMEY/) UMEYAMA H.	Best Local Similarity: 45.71%	Mismatches: 87	
Best Local Similarity: 46.85%	Query Match: 25.41%	Indels: 10	
Query Match: 26.19%	RESULT 1195		
RESULT 1189	ID AAW64261 standard; protein; 232 AA.		
ID ADL16686 standard; protein; 259 AA.	DE Kallikrein substrate binding site.		
DE Human NOVX protein to treat human pathological conditions SeqID222.	PN WO9824886-A1.		
PD WO200268649-A2.	PD 11-JUN-1998.		
PD 06-SEP-2002.	PA (BGHM) BRIGHAM & WOMENS HOSPITAL.		
PA (CURA-) CURAGEN CORP.	Best Local Similarity: 43.64%	Mismatches: 79	
Best Local Similarity: 44.35%	Query Match: 25.36%	Indels: 14	
Query Match: 26.11%	RESULT 1196		
RESULT 1190	ID ABB94423 standard; peptide; 249 AA.		
ID ADN42340 standard; protein; 259 AA.	DE Murine SCCE protein N-terminal fragment SEQ ID 50.		
DE Human novel protein NOV 62.	PN WO200262135-A2.		
PD US2004033493-A1.	PD 15-AUG-2002.		
PD 19-FEB-2004.	PA (EGEL/) EGELRUD T.		
PA (TCHE/) TCHERNEV V T.	PA (HANS/) HANSSON L.		
PA (SPYT/) SPYTEK K A.	Best Local Similarity: 42.97%	Mismatches: 97	
PA (ZERR/) ZERRHUSEN B D.	Query Match: 25.24%	Indels: 9	
PA (PATT/) PATTURAJAN M.	RESULT 1197		
PA (SHIM/) SHIMKETS R A.	ID ABR96164 standard; protein; 261 AA.		
PA (LILL/) LI L.	DE Human NOV13a protein SEQ ID NO:70.		
PA (GANG/) GANGOLLI E A.	PN WO200290568-A2.		
PA (PADI/) PADIGARU M.	PD 14-NOV-2002.		
PA (ANDE/) ANDERSON D W.	PA (CURA-) CURAGEN CORP.		
PA (RAST/) RASTELLI L.	Best Local Similarity: 40.00%	Mismatches: 91	
PA (MILL/) MILLER C E.	Query Match: 25.15%	Indels: 17	
PA (GERL/) GERLACH V.	RESULT 1198		
PA (TAUP/) TAUFIER R J.	ID ADL15205 standard; protein; 232 AA.		
PA (GUSE/) GUSEV V Y.	DE Pancreatic kallikrein #1.		
	PN CN1384199-A.		

PD 11-DEC-2002.  
 PA (REMI-) REMIN HOSPITAL SHENZHEN CITY. 73  
 Best Local Similarity: 44.54% Mismatches: 14  
 Query Match: 25.12% Indels:  
 RESULT 1199  
 ID AAW94493 standard; protein; 268 AA.  
 DE Human kallikrein.  
 PN WO9842849-A1.  
 PD 01-OCT-1998.  
 PA (INCY-) INCYTE PHARM INC. 95  
 Best Local Similarity: 42.42% Mismatches: 20  
 Query Match: 25.10% Indels:  
 RESULT 1200  
 ID ABG70276 standard; protein; 247 AA.  
 DE Human Serine Protease TLSP-like protein.  
 PN WO200255702-A2.  
 PD 18-JUL-2002.  
 PA (CURA-) CURAGEN CORP. 77  
 Best Local Similarity: 42.51% Mismatches: 36  
 Query Match: 24.98% Indels:  
 RESULT 1201  
 ID ADL27347 standard; peptide; 464 AA.  
 DE Amino acid sequence of trypsinogen-3aa-sp55.  
 PN WO2004019878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC. 114  
 Best Local Similarity: 38.56% Mismatches: 34  
 Query Match: 24.54% Indels:  
 RESULT 1202  
 ID ABB04645 standard; protein; 241 AA.  
 DE Engraulis japonicus trypsinogen (stry II) SEQ ID NO:2.  
 PN JP2001269173-A.  
 PD 02-OCT-2001.  
 PA (NISB) JAPAN TOBACCO INC. 92  
 Best Local Similarity: 45.87% Mismatches: 10  
 Query Match: 24.39% Indels:  
 RESULT 1203  
 ID AAU87693 standard; protein; 247 AA.  
 DE Human pancreatic tumour protein #5.  
 PN WO200212331-A2.  
 PD 14-FEB-2002.  
 PA (CORI-) CORIXA CORP. 91  
 Best Local Similarity: 43.27% Mismatches: 10  
 Query Match: 24.25% Indels:  
 RESULT 1204  
 ID ADN04140 standard; protein; 247 AA.  
 DE Antipsoriatic protein sequence #265.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH) GENENTECH INC. 91  
 Best Local Similarity: 43.27% Mismatches: 10  
 Query Match: 24.25% Indels:  
 RESULT 1205  
 ID ADN99594 standard; protein; 247 AA.  
 DE Novel human protein sequence #410.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 91  
 Best Local Similarity: 43.27% Mismatches: 10  
 Query Match: 24.25% Indels:  
 RESULT 1206  
 ID ADQ30589 standard; protein; 247 AA.  
 DE Pancreas cancer marker - trypsin II precursor.  
 PN WO2004055519-A2.  
 PD 01-JUL-2004.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN. 91  
 Best Local Similarity: 43.27% Mismatches: 10  
 Query Match: 24.25% Indels:  
 RESULT 1207  
 ID ABR41530 standard; protein; 261 AA.  
 DE Human DITHP protein modification/maintenance protein.

PN WO200297031-A2.  
 PD 05-DEC-2002.  
 PA (INCY-) INCYTE GENOMICS INC. 91  
 Best Local Similarity: 43.27% Mismatches: 10  
 Query Match: 24.25% Indels:  
 RESULT 1208  
 ID ADL27346 standard; peptide; 461 AA.  
 DE Amino acid sequence of trypsinogen-0aa-sp55.  
 PN WO2004019878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC. 112  
 Best Local Similarity: 38.24% Mismatches: 37  
 Query Match: 24.23% Indels:  
 RESULT 1209  
 ID AAB03862 standard; protein; 223 AA.  
 DE Human neurosin amino acid sequence.  
 PN WO2000031284-A1.  
 PD 02-JUN-2000.  
 PA (FUSO) FUSO PHARM IND LTD. 69  
 Best Local Similarity: 43.46% Mismatches: 36  
 Query Match: 24.20% Indels:  
 RESULT 1210  
 ID ADL27345 standard; peptide; 280 AA.  
 DE Amino acid sequence of trypsinogen.  
 PN WO2004019878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC. 101  
 Best Local Similarity: 41.03% Mismatches: 24  
 Query Match: 24.15% Indels:  
 RESULT 1211  
 ID AAB21294 standard; protein; 254 AA.  
 DE Human KIK-L1 protein #2.  
 PN WO2000053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN) MOUNT SINAI HOSPITAL. 87  
 Best Local Similarity: 43.10% Mismatches: 8  
 Query Match: 24.10% Indels:  
 RESULT 1212  
 ID AAU01174 standard; protein; 254 AA.  
 DE Human prostate-specific amino acid sequence P703P.  
 PN WO200151633-A2.  
 PD 19-JUL-2001.  
 PA (CORI-) CORIXA CORP. 87  
 Best Local Similarity: 43.10% Mismatches: 8  
 Query Match: 24.10% Indels:  
 RESULT 1213  
 ID AAU69819 standard; protein; 254 AA.  
 DE Human prostate cDNA encoded protein #27.  
 PN WO200173032-A2.  
 PD 04-OCT-2001.  
 PA (CORI-) CORIXA CORP. 87  
 Best Local Similarity: 43.10% Mismatches: 8  
 Query Match: 24.10% Indels:  
 RESULT 1214  
 ID AAG99059 standard; protein; 254 AA.  
 DE Human prostate-specific amino acid of P703P.  
 PN WO200134802-A2.  
 PD 17-MAY-2001.  
 PA (CORI-) CORIXA CORP. 87  
 Best Local Similarity: 43.10% Mismatches: 8  
 Query Match: 24.10% Indels:  
 RESULT 1215  
 ID ABU71710 standard; protein; 254 AA.  
 DE Prostate cancer specific antigen P703P #7.  
 PN US2002192763-A1.  
 PD 19-DEC-2002.  
 PA (XUJ) XU J. 87  
 PA (DILL) DILLON D C. 8  
 PA (MITC) MITCHAM J L.  
 PA (HARL) HARLOCKER S L.  
 PA (JTIAN) JTIAN Y.

PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1216  
ID ABB95279 standard; protein; 254 AA.  
DE Human P703P putative full length protein SEQ ID NO 525.  
PN US200202248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1217  
ID ABP54360 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:13.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1218  
ID ABP54357 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:6.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1219  
ID ABR54391 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 525.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1220  
ID ADB13975 standard; protein; 254 AA.  
DE Human prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1221  
ID ADG26391 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #60.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1222  
ID BAB74830 standard; protein; 1079 AA.  
DE Prostate tumour antigen amino acid sequence for a fusion protein.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1223  
ID ABU71860 standard; protein; 1079 AA.  
DE Prostate specific antigen fusion protein #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Best Local Similarity: 43.10% Mismatches: 87  
Query Match: 24.10% Indels: 8  
RESULT 1224  
ID ADI17268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 47.44% Mismatches: 73  
Query Match: 24.08% Indels: 17  
RESULT 1225  
ID ADI17276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 47.44% Mismatches: 73  
Query Match: 24.08% Indels: 17  
RESULT 1226  
ID ADJ83075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.

PA (PATT/) PATTURAJAN M.  
 PA (LEPL/) LEFLEY D M.  
 PA (BURG/) BURGESS C E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (GROS/) GROSSE W M.  
 PA (SZEK/) SZEKERES E S.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (CASW/) CASMAN S J.  
 PA (BOLD/) BOLDOG F L.  
 PA (GORM/) GORMAN L.  
 PA (GANG/) GANGOLLI E A.  
 PA (FERN/) FERNANDES E R.  
 PA (RIEG/) RIEGER D K.  
 PA (EDIN/) EDINGER S R.  
 PA (GUNT/) GUNTHER E.  
 PA (MILL/) MILLET I.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MACD/) MACDOUGALL J R.  
 PA (SMIT/) SMITHSON G.  
 Best Local Similarity: 47.44% Mismatches: 73  
 Query Match: 24.08% Indels: 17  
 RESULT 1227  
 ID ADL27348 standard; peptide; 485 AA.  
 DE Amino acid sequence of trypsinogen-20aa-sp55.  
 PN WO2004019878-A2.  
 PD 11-WAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC.  
 PA (AFEY/) AFEYAN N B.  
 Best Local Similarity: 42.74% Mismatches: 96  
 Query Match: 24.08% Indels: 11  
 RESULT 1228  
 ID AAB21307 standard; protein; 249 AA.  
 DE Human prostatic.  
 PN WO2000053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 43.10% Mismatches: 87  
 Query Match: 24.08% Indels: 8  
 RESULT 1229  
 ID AAB21320 standard; protein; 254 AA.  
 DE Human prostatic.  
 PN WO2000053776-A2.  
 PD 14-SEP-2000.  
 PA (MOUN) MOUNT SINAI HOSPITAL.  
 Best Local Similarity: 43.10% Mismatches: 87  
 Query Match: 24.06% Indels: 8  
 RESULT 1230  
 ID AAV72525 standard; protein; 254 AA.  
 DE Human prostatic antigen #3.  
 PN WO200104143-A2.  
 PD 18-JAN-2001.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.10% Mismatches: 87  
 Query Match: 24.06% Indels: 8  
 RESULT 1231  
 ID AAU74901 standard; protein; 254 AA.  
 DE Protein sequence of prostate homologue #3.  
 PN WO200200708-A2.  
 PD 03-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.10% Mismatches: 87  
 Query Match: 24.06% Indels: 8  
 RESULT 1232  
 ID AAU74932 standard; protein; 254 AA.  
 DE Amino acid sequence of prostate protein fragment #3.  
 PN WO200200867-A1.  
 PD 03-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.10% Mismatches: 87  
 Query Match: 24.06% Indels: 8  
 RESULT 1233  
 ID AAW60592 standard; protein; 248 AA.  
 DE Human prostate-specific kallikrein (HPSK) protein.  
 PN WO9820117-A1.  
 PD 14-MAY-1998.  
 PA (INCY-) INCYTE PHARM INC.  
 Best Local Similarity: 43.44% Mismatches: 84  
 Query Match: 24.03% Indels: 13  
 RESULT 1234  
 ID AAY72524 standard; protein; 248 AA.  
 DE Human prostatic antigen #2.  
 PN WO200104143-A2.  
 PD 18-JAN-2001.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.44% Mismatches: 84  
 Query Match: 24.03% Indels: 13  
 RESULT 1235  
 ID AAU74770 standard; protein; 248 AA.  
 DE Protein sequence of prostate homologue #2.  
 PN WO200200708-A2.  
 PD 03-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.44% Mismatches: 84  
 Query Match: 24.03% Indels: 13  
 RESULT 1236  
 ID AAU74931 standard; protein; 248 AA.  
 DE Amino acid sequence of prostate protein fragment #2.  
 PN WO200200867-A1.  
 PD 03-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.44% Mismatches: 84  
 Query Match: 24.03% Indels: 13  
 RESULT 1237  
 ID ABU71889 standard; protein; 585 AA.  
 DE Prostatic cancer specific antigen fusion protein #3.  
 PN US2002192763-A1.  
 PD 19-DEC-2002.  
 PA (XUJJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T M.  
 Best Local Similarity: 40.14% Mismatches: 110  
 Query Match: 24.03% Indels: 17  
 RESULT 1238  
 ID ABR54580 standard; protein; 585 AA.  
 DE Prostatic tumour-related protein SEQ ID 1020.  
 PN WO200289747-A2.  
 PD 14-NOV-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 40.14% Mismatches: 110  
 Query Match: 24.03% Indels: 17  
 RESULT 1239  
 ID ADB14470 standard; protein; 585 AA.  
 DE FOPF/hFAP fusion protein, FOPF3.

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PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1240
ID ADG26993 standard; protein; 585 AA.
DE Human prostate-specific polypeptide #249.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14% Mismatches: 110
Query Match: 24.03% Indels: 17
RESULT 1241
ID ABG76997 standard; protein; 262 AA.
DE Human kallikrein protein variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC) Tsuchihashi Z.
PA (HUIL) HUI L.
Best Local Similarity: 40.38% Mismatches: 99
Query Match: 23.96% Indels: 18
RESULT 1242
ID ADR90673 standard; protein; 246 AA.
DE Human trypsinogen partial protein.
PN WO2004078777-A2.
PD 16-SEP-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1243
ID AAB21321 standard; protein; 247 AA.
DE Human trypsinogen.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1244
ID ABR54239 standard; protein; 247 AA.
DE Human NOV35a protein SEQ ID NO:146.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1245
ID ABR54241 standard; protein; 247 AA.
DE Human NOV35c protein SEQ ID NO:150.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1246
ID ADQ30588 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin I precursor.
PN WO200405519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Best Local Similarity: 41.94% Mismatches: 97
Query Match: 23.94% Indels: 11
RESULT 1247
ID AAM01173 standard; protein; 254 AA.
DE Human prostate-specific amino acid mature form of P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1248
ID ABR34390 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 523.
PN WO200289747-A2.
PD 14-NOV-2002.

12 ID AAG9818 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #26.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1249
ID AAG99058 standard; protein; 254 AA.
DE Human prostate-specific mature protein of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1250
ID ABU71709 standard; protein; 254 AA.
DE Prostate cancer associated protein #12.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIAN) JIANG Y.
PA (KALO) KALOS M D.
PA (FANG) FANGER G R.
PA (RETT) RETTER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CART) CARTER D.
PA (LISK) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.
PA (HEND) HENDERSON R A.
PA (HURA) HURAL J.
PA (MCNE) MCNEILL P D.
PA (HOUG) HOUGHTON R L.
PA (DBAS) Y DE BASSOLS C V.
PA (FOYT) FOY T M.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1251
ID ABB95278 standard; protein; 254 AA.
DE Human P703P mature protein SEQ ID NO 523.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ) XU J.
PA (DILL) DILLON D C.
PA (MITC) MITCHAM J L.
PA (HARL) HARLOCKER S L.
PA (JIAN) JIANG Y.
PA (KALO) KALOS M D.
PA (FANG) FANGER G R.
PA (RETT) RETTER M W.
PA (STOL) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDV) VEDVICK T S.
PA (CART) CARTER D.
PA (LISK) LI S X.
PA (WANG) WANG A.
PA (SKEI) SKEIKY Y A W.
PA (HEPL) HEPLER W T.
PA (HEND) HENDERSON R A.
Best Local Similarity: 42.68% Mismatches: 88
Query Match: 23.91% Indels: 8
RESULT 1252
ID ABR34390 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 523.
PN WO200289747-A2.
PD 14-NOV-2002.
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PA (CORI-) CORIXA CORP.  
Best Local Similarity: 42.68% Mismatches: 88  
Query Match: 23.91% Indels: 8  
RESULT 1253  
ID ADB13973 standard; protein; 254 AA.  
DE Human mature prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 42.68% Mismatches: 88  
Query Match: 23.91% Indels: 8  
RESULT 1254  
ID ADG26389 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #59.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 42.68% Mismatches: 88  
Query Match: 23.91% Indels: 8  
RESULT 1255  
ID AAB21319 standard; protein; 262 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1256  
ID ABG76996 standard; protein; 262 AA.  
DE Human kallikrein protein.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1257  
ID ADL15197 standard; protein; 262 AA.  
DE Human pancreatic kallikrein.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1258  
ID ADL64969 standard; protein; 262 AA.  
DE Human kallikrein protein (KLK1).  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUIL/) HUI L.  
PA (PERR/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAWA/) RAWANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERR/) ZERBA K.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1259  
ID ADQ39654 standard; protein; 262 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1260  
ID ADS34891 standard; protein; 262 AA.  
DE Human autoimmune disease-related protein - SEQ ID 105.  
PN WO2004093403-A2.  
PD 30-SEP-2004.

PA (APPL-) APPLERA CORP.  
Best Local Similarity: 40.38% Mismatches: 99  
Query Match: 23.91% Indels: 18  
RESULT 1261  
ID ABR54277 standard; protein; 240 AA.  
DE Human trypsinogen protein SEQ ID NO:341.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 42.56% Mismatches: 93  
Query Match: 23.89% Indels: 11  
RESULT 1262  
ID AAB21316 standard; protein; 241 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 42.56% Mismatches: 93  
Query Match: 23.89% Indels: 11  
RESULT 1263  
ID ADN04297 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #343.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 42.15% Mismatches: 89  
Query Match: 23.86% Indels: 10  
RESULT 1264  
ID AAB21308 standard; protein; 253 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 42.80% Mismatches: 85  
Query Match: 23.86% Indels: 12  
RESULT 1265  
ID AAB21324 standard; protein; 258 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 42.80% Mismatches: 85  
Query Match: 23.86% Indels: 12  
RESULT 1266  
ID AAW71005 standard; protein; 262 AA.  
DE Human prostate-associated kallikrein designated HPAK.  
PN WO9832865-A1.  
PD 30-JUL-1998.  
PA (INCY-) INCYTE PHARM INC.  
Best Local Similarity: 40.38% Mismatches: 100  
Query Match: 23.86% Indels: 18  
RESULT 1267  
ID ABP74711 standard; protein; 262 AA.  
DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.  
PN WO200281646-A2.  
PD 17-OCT-2002.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Best Local Similarity: 40.38% Mismatches: 100  
Query Match: 23.86% Indels: 18  
RESULT 1268  
ID ADL15204 standard; protein; 262 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Best Local Similarity: 40.38% Mismatches: 100  
Query Match: 23.86% Indels: 18  
RESULT 1269  
ID ADM72846 standard; protein; 263 AA.  
DE Human glandular kallikrein 1 protein SEQ ID NO:105.  
PN WO2004022709-A2.  
PD 18-NAR-2004.  
PA (MANN-) MANNKIND CORP.

Best Local Similarity: 40.38%	Mismatches: 100	
Query Match: 23.86%	Indels: 18	
RESULT 1270		
ID AAB99503 standard; protein; 225 AA.		
DE Human trypsin serine protease catalytic domain.		
PN WO200129056-A1.		
PD 26-APR-2001.		
PA (UYAR-) UNIV ARKANSAS.		
Best Local Similarity: 43.67%	Mismatches: 89	
Query Match: 23.81%	Indels: 6	
RESULT 1271		
ID AAW93488 standard; protein; 230 AA.		
DE Human TRYI trypsinogen variant protein.		
PN WO9910503-A1.		
PD 04-MAR-1999.		
PA (HOFF) ROCHE DIAGNOSTICS GMBH.		
Best Local Similarity: 43.67%	Mismatches: 89	
Query Match: 23.81%	Indels: 6	
RESULT 1272		
ID AAB21315 standard; protein; 256 AA.		
DE Human KUKI.		
PN WO200053776-A2.		
PD 14-SEP-2000.		
PA (MOUN) MOUNT SINAI HOSPITAL.		
Best Local Similarity: 41.11%	Mismatches: 94	
Query Match: 23.81%	Indels: 18	
RESULT 1273		
ID AAP95121 standard; protein; 262 AA.		
DE Kallikrein encoded by clone lambda HK65a.		
PN EP297913-A.		
PD 04-JAN-1989.		
PA (AMGE-) AMGEN.		
Best Local Similarity: 40.38%	Mismatches: 100	
Query Match: 23.81%	Indels: 18	
RESULT 1274		
ID ABG76998 standard; protein; 262 AA.		
DE Human kallikrein protein variant #2.		
PN WO200261131-A2.		
PD 08-AUG-2002.		
PA (BRIM) BRISTOL-MYERS SQUIBB CO.		
PA (TSUC/) TSUCHIHASHI Z.		
PA (HUIL/) HUI L.		
Best Local Similarity: 40.38%	Mismatches: 100	
Query Match: 23.81%	Indels: 18	
RESULT 1275		
ID AAB54293 standard; protein; 267 AA.		
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.		
PN WO200055320-A1.		
PD 21-SEP-2000.		
PA (HUNA-) HUMAN GENOME SCI INC.		
Best Local Similarity: 40.38%	Mismatches: 100	
Query Match: 23.81%	Indels: 18	
RESULT 1276		
ID ABG77002 standard; protein; 262 AA.		
DE Human kallikrein 1 polymorphic sequence.		
PN WO200261131-A2.		
PD 08-AUG-2002.		
PA (BRIM) BRISTOL-MYERS SQUIBB CO.		
PA (TSUC/) TSUCHIHASHI Z.		
PA (HUIL/) HUI L.		
Best Local Similarity: 40.38%	Mismatches: 100	
Query Match: 23.77%	Indels: 18	
RESULT 1277		
ID ADA05744 standard; protein; 224 AA.		
DE Human NOV18g; protein SEQ ID NO:104.		
PN WO2003029424-A2.		
PD 10-APR-2003.		
PA (CURA-) CURAGEN CORP.		
Best Local Similarity: 45.29%	Mismatches: 75	
Query Match: 23.72%	Indels: 16	
RESULT 1278		
ID ADN62908 standard; protein; 224 AA.		
DE Human NOV18g.		

  

PN	US2004038223-A1.		
PD	26-FEB-2004.		
PA	(SMIT/) SMITHSON G.		
PA	(MILL/) MILLET I.		
PA	(PEYM/) PEYMAN J A.		
PA	(KEKU/) KEKUDA R.		
PA	(JUJ/) JU J.		
PA	(LILL/) LI L.		
PA	(GUOX/) GUO X.		
PA	(PATT/) PATTURAJAN M.		
PA	(SPVT/) SPYTEK K A.		
PA	(EDIN/) EDINGER S R.		
PA	(ELLE/) ELLERMAN K.		
PA	(MAY/) MALYANKAR U M.		
PA	(ORTT/) ORT T.		
PA	(GORM/) GORMAN L.		
PA	(ZERR/) ZERHUSEN B D.		
PA	(ANDE/) ANDERSON D W.		
PA	(ZHON/) ZHONG M.		
PA	(CATI/) CATTERTON E.		
PA	(JIW/) JI W.		
PA	(MILL/) MILLER C E.		
PA	(ASTO/) RASTELLI L.		
PA	(STON/) STONE D J.		
PA	(PENA/) PENA C E A.		
PA	(SHEN/) SHENOY S G.		
PA	(ROTH/) ROTHENBERG M E.		
PA	(LEAC/) LEACH M D.		
PA	(AGEE/) AGEE M L.		
PA	(BERG/) BERGHS C.		
PA	(DIFI/) DIPPO V A.		
PA	(EISE/) EISEN A.		
PA	(GANG/) GANGOLLI E A.		
PA	(RIEG/) RIEGER D K.		
PA	(SPAD/) SPADERNA S K.		
Best Local Similarity: 45.29%	Mismatches: 75		
Query Match: 23.72%	Indels: 16		
RESULT 1279			
ID AAE00397 standard; protein; 234 AA.			
DE Human serine protease, PROST 07.			
PN WO200125446-A1.			
PD 12-APR-2001.			
PA (SCHD) SCHERING AG.			
Best Local Similarity: 43.04%	Mismatches: 85		
Query Match: 23.69%	Indels: 7		
RESULT 1280			
ID ABM3250 standard; protein; 333 AA.			
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.			
PN WO2004023973-A2.			
PD 25-MAR-2004.			
PA (INCY-) INCYTE CORP.			
Best Local Similarity: 40.00%	Mismatches: 106		
Query Match: 23.67%	Indels: 19		
RESULT 1281			
ID ABU71888 standard; protein; 585 AA.			
DE Prostate cancer associated protein #72.			
PN US2002192763-A1.			
PD 19-DEC-2002.			
PA (XUJ/) XU J.			
PA (DILL/) DILLON D C.			
PA (MITC/) MITCHAM J L.			
PA (HARL/) HARLOCKER S L.			
PA (JIAN/) JIANG Y.			
PA (KALO/) KALOS M D.			
PA (FANG/) FANGER G R.			
PA (RETT/) RETTER M W.			
PA (STOL/) STOLK J A.			
PA (DAYC/) DAY C H.			
PA (VEDV/) VEDVICK T S.			
PA (CART/) CARTER D.			
PA (LISX/) LI S X.			
PA (WANG/) WANG A.			

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PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J. P D.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOVT/) FOY T M.
Best Local Similarity: 37.24% Mismatches: 96
Query Match: 23.67% Indels: 44
RESULT 1282
ID AAU25510 standard; protein; 231 AA.
DE Human prostate serine protease protein.
PN EP936270-A2.
PD 18-AUG-1999.
PA (BADI) BASF AG.
Best Local Similarity: 43.95% Mismatches: 80
Query Match: 23.64% Indels: 7
RESULT 1283
ID ABR96163 standard; protein; 274 AA.
DE Human NOVI2a protein SEQ ID NO:68.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 40.82% Mismatches: 101
Query Match: 23.64% Indels: 18
RESULT 1284
ID ADN04726 standard; protein; 247 AA.
DE Antipsoriatic protein sequence #544.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 42.32% Mismatches: 92
Query Match: 23.62% Indels: 10
RESULT 1285
ID ADN99593 standard; protein; 247 AA.
DE Novel human protein sequence #409.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Best Local Similarity: 42.32% Mismatches: 92
Query Match: 23.62% Indels: 10
RESULT 1286
ID AAM01227 standard; protein; 449 AA.
DE P703P and PSA fusion amino acid sequence.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1287
ID AAU69872 standard; protein; 449 AA.
DE Human prostate serum antigen/P703P fusion protein.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1288
ID ABU71763 standard; protein; 449 AA.
DE Prostate cancer specific antigen fusion protein #1.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOVT/) FOY T M.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1289
ID ABR95332 standard; protein; 449 AA.
DE Human P703P/PSA fusion protein SEQ ID NO 617.
PN US2002022448-A1.
PD 21-FEB-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1290
ID ABR54444 standard; protein; 449 AA.
DE Prostate tumour specific protein sequence SEQ ID 617.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1291
ID ADB14067 standard; protein; 449 AA.
DE Human prostate specific protein P703P/PSA fusion protein.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1292
ID ADG26483 standard; protein; 449 AA.
DE Human prostate-specific polypeptide #113.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14% Mismatches: 80
Query Match: 23.60% Indels: 7
RESULT 1293
ID ABU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.

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PA (FANG/) FANGER G R.	Query Match:	23.28%	Indels:	18
PA (RETT/) RETTER M W.	RESULT 1301			
PA (STOL/) STOLK J A.	ID AAY72522 standard; protein; 312 AA.			
PA (DAYC/) DAY C H.	DE NS1-P703P-His fusion protein.			
PA (VEDV/) VEDVICK T S.	PN WO200104143-A2.			
PA (CART/) CARTER D.	PD 18-JAN-2001.			
PA (LISX/) LI S X.	PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.			
PA (WANG/) WANG A.	PA (CORI-) CORIXA CORP.			
PA (SKEI/) SKEIKY Y A W.	Best Local Similarity: 42.49%	Mismatches:	82	
PA (HEPL/) HEPLER W T.	Query Match:	23.18%	Indels:	12
PA (HEND/) HENDERSON R A.	RESULT 1302			
PA (HURA/) HURAL J. P D.	ID AAU74768 standard; protein; 312 AA.			
PA (MCNE/) MCNEILL P D.	DE Amino acid sequence of wild-type NS1-p703-His fusion protein.			
PA (HOUG/) HOUGHTON R L.	PN WO200200708-A2.			
PA (DBAS/) Y DE BASSOLS C V.	PD 03-JAN-2002.			
PA (FOYT/) FOY T M.	PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.			
Best Local Similarity: 44.14%	Best Local Similarity: 42.49%	Mismatches:	82	
Query Match:	Query Match:	23.60%	Indels:	12
RESULT 1294				
ID AAY31160 standard; protein; 224 AA.				
DE Human trypsin serine protease protein domain.				
PN US5948892-A.				
PD 07-SEP-1999.				
PA (AMGE-) AMGEN INC.				
Best Local Similarity: 43.42%	Mismatches:	89		
Query Match:	Query Match:	23.57%	Indels:	6
RESULT 1295				
ID ADL15207 standard; protein; 261 AA.				
DE Pancreatic kallikrein #3.				
PN CN1384199-A.				
PD 11-DEC-2002.				
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.				
Best Local Similarity: 40.23%	Mismatches:	96		
Query Match:	Query Match:	23.45%	Indels:	19
RESULT 1296				
ID ABM83249 standard; protein; 261 AA.				
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.				
PN WO2004023973-A2.				
PD 25-MAR-2004.				
PA (INCY-) INCYTE CORP.				
Best Local Similarity: 43.50%	Mismatches:	82		
Query Match:	Query Match:	23.43%	Indels:	6
RESULT 1297				
ID AAW57740 standard; protein; 240 AA.				
DE Trypsinogen-like protein.				
PN JP10099080-A.				
PD 21-APR-1998.				
PA (SHIS ) SHISEIDO CO LTD.				
Best Local Similarity: 42.49%	Mismatches:	84		
Query Match:	Query Match:	23.40%	Indels:	11
RESULT 1298				
ID ADL15206 standard; protein; 260 AA.				
DE Pancreatic kallikrein #2.				
PN CN1384199-A.				
PD 11-DEC-2002.				
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.				
Best Local Similarity: 39.77%	Mismatches:	98		
Query Match:	Query Match:	23.38%	Indels:	16
RESULT 1299				
ID AAB21293 standard; protein; 237 AA.				
DE Human KUK-L1 protein #1.				
PN WO200053776-A2.				
PD 14-SEP-2000.				
PA (MOUN ) MOUNT SINAI HOSPITAL.				
Best Local Similarity: 42.24%	Mismatches:	89		
Query Match:	Query Match:	23.35%	Indels:	7
RESULT 1300				
ID AAP70568 standard; protein; 262 AA.				
DE Human kallikrein-like substance has hypotensive activity.				
PN JP62126980-A.				
PD 09-JUN-1987.				
PA (NAXA/) NAKANISHI S.				
Best Local Similarity: 40.00%	Mismatches:	101		
Query Match:	Query Match:	23.11%	Indels:	7
RESULT 1301				
ID AAY72522 standard; protein; 312 AA.				
DE NS1-P703P-His fusion protein.				
PN WO200104143-A2.				
PD 18-JAN-2001.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
PA (CORI-) CORIXA CORP.				
Best Local Similarity: 42.49%	Mismatches:	82		
Query Match:	Query Match:	23.18%	Indels:	12
RESULT 1302				
ID AAU74768 standard; protein; 312 AA.				
DE Amino acid sequence of wild-type NS1-p703-His fusion protein.				
PN WO200200708-A2.				
PD 03-JAN-2002.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 42.49%	Mismatches:	82		
Query Match:	Query Match:	23.18%	Indels:	12
RESULT 1303				
ID AAU74929 standard; protein; 312 AA.				
DE Amino acid sequence of wild-type NS1-p703P-His fusion protein.				
PN WO200200867-A1.				
PD 03-JAN-2002.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 42.49%	Mismatches:	82		
Query Match:	Query Match:	23.18%	Indels:	12
RESULT 1304				
ID AAB08449 standard; protein; 375 AA.				
DE A human prostate specific antigen variant polypeptide.				
PN WO200049158-A2.				
PD 24-AUG-2000.				
PA (COMP-) COMPUGEN LTD.				
Best Local Similarity: 37.42%	Mismatches:	111		
Query Match:	Query Match:	23.16%	Indels:	46
RESULT 1305				
ID AAU01290 standard; protein; 216 AA.				
DE Human serine protease HETAA37p.				
PN WO200123587-A2.				
PD 05-APR-2001.				
PA (SMIK ) SMITHKLINE BEECHAM PLC.				
Best Local Similarity: 44.34%	Mismatches:	82		
Query Match:	Query Match:	23.11%	Indels:	7
RESULT 1306				
ID AAY72526 standard; protein; 226 AA.				
DE Human prostate antigen P703PDE5 sequence.				
PN WO200104143-A2.				
PD 18-JAN-2001.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
PA (CORI-) CORIXA CORP.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Query Match:	23.11%	Indels:	7
RESULT 1307				
ID AAU74902 standard; protein; 226 AA.				
DE Protein sequence of prostate homologue #4.				
PN WO200200708-A2.				
PD 03-JAN-2002.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Query Match:	23.11%	Indels:	7
RESULT 1308				
ID AAU74933 standard; protein; 226 AA.				
DE Amino acid sequence of prostate protein fragment #4.				
PN WO200200867-A1.				
PD 03-JAN-2002.				
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.				
Best Local Similarity: 43.84%	Mismatches:	79		
Query Match:	Query Match:	23.11%	Indels:	7
RESULT 1309				
ID ABU71866 standard; protein; 344 AA.				
DE Human prostate specific antigen (PSA) epitope #26.				
PN US2002192763-A1.				
PD 19-DEC-2002.				
PA (XUJ/) XU J.				

PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T M.  
 Best Local Similarity: 43.84%  
 Query Match: 23.11%  
 Mismatches: 79  
 Indels: 7  
 RESULT 1310  
 ID ABM2601 standard; protein; 239 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 40.08%  
 Query Match: 23.02%  
 Mismatches: 72  
 Indels: 55  
 RESULT 1311  
 ID ABM2602 standard; protein; 239 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2851.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 40.08%  
 Query Match: 23.02%  
 Mismatches: 72  
 Indels: 55  
 RESULT 1312  
 ID ABM2603 standard; protein; 239 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:2852.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 40.08%  
 Query Match: 23.02%  
 Mismatches: 72  
 Indels: 55  
 RESULT 1313  
 ID ADN99649 standard; protein; 280 AA.  
 DE Novel human protein sequence #465.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 37.72%  
 Query Match: 22.89%  
 Mismatches: 96  
 Indels: 44  
 RESULT 1314  
 ID RAY82008 standard; protein; 220 AA.  
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.  
 PN WO200004149-A2.  
 PD 27-JAN-2000.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1315  
 ID AAW01123 standard; protein; 220 AA.  
 DE Human prostate-specific amino acid sequence P703PDE6.  
 PN WO200151633-A2.  
 PD 19-JUL-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1316  
 ID AAU69768 standard; protein; 220 AA.

DE Human prostate cDNA encoded protein #8.  
 PN WO200173032-A2.  
 PD 04-OCT-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1317  
 ID AAB74806 standard; protein; 220 AA.  
 DE Prostate tumour antigen predicted amino acid sequence for P703PDE5.  
 PN WO200125272-A2.  
 PD 12-APR-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1318  
 ID AAG99008 standard; protein; 220 AA.  
 DE Human prostate-specific amino acid sequence P703PDE5.  
 PN WO200134802-A2.  
 PD 17-MAY-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1319  
 ID AAG62147 standard; protein; 220 AA.  
 DE Human P703P inventive antigen SEQ ID NO: 330.  
 PN WO200125273-A2.  
 PD 12-APR-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1320  
 ID ABU71659 standard; protein; 220 AA.  
 DE Prostate cancer specific antigen P703P #4.  
 PN US2002192763-A1.  
 PD 19-DEC-2002.  
 PA (XUJU/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T M.  
 Best Local Similarity: 43.78%  
 Query Match: 22.87%  
 Mismatches: 78  
 Indels: 7  
 RESULT 1321  
 ID ABB95228 standard; protein; 220 AA.  
 DE Human P703PDE5 protein SEQ ID NO 327.  
 PN US2002022448-A1.  
 PD 21-FEB-2002.  
 PA (XUJU/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.	Query Match:	22.77%	Indels:	13
PA (VEDV/) VEDVICK T S.	RESULT 1330			
PA (CART/) CARTER D.	ID AAW13649 standard; protein; 261 AA.			
PA (LISK/) LI S X.	DE Human prostate specific antigen.			
PA (WANG/) WANG A.	PN WO9711172-A1.			
PA (SKEI/) SKEIKY Y A W.	PD 27-MAR-1997.			
PA (HEPL/) HEPLER W T.	PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.			
PA (HEND/) HENDERSON R A.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 43.78%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1331			
RESULT 1322	ID AAY56048 standard; protein; 261 AA.			
ID ABR54340 standard; protein; 220 AA.	DE Human prostate-specific antigen.			
DE Prostate tumour specific protein sequence SEQ ID 327.	PN WO9961088-A1.			
PN WO200289747-A2.	PD 02-DEC-1999.			
PA (CORI-) CORIXA CORP.	PA (UYPE-) UNIV PENNSYLVANIA.			
Best Local Similarity: 43.78%	Best Local Similarity: 40.40%	Mismatches:	103	
Query Match:	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1323			
RESULT 1323	ID AAY77842 standard; protein; 261 AA.			
ID ADB13777 standard; protein; 220 AA.	DE Human prostate-specific antigen (PSA) sequence.			
DE Human prostate specific protein P703PDE5.	PN WO9960984-A2.			
PN US2003185830-A1.	PD 02-DEC-1999.			
PA (CORI-) CORIXA CORP.	PA (ENTR-) ENTREMED INC.			
Best Local Similarity: 43.78%	Best Local Similarity: 40.40%	Mismatches:	103	
Query Match:	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1324			
RESULT 1324	ID AAB21317 standard; protein; 261 AA.			
ID ADG26193 standard; protein; 220 AA.	DE Human PSA.			
DE Human prostate-specific polypeptide #9.	PN WO200053776-A2.			
PN US2003157089-A1.	PD 14-SEP-2000.			
PD 21-AUG-2003.	PA (MOUN) MOUNT SINAI HOSPITAL.			
PA (CORI-) CORIXA CORP.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 43.78%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1325			
RESULT 1325	ID AAB74821 standard; protein; 261 AA.			
ID ADI3732 standard; protein; 262 AA.	DE Prostate tumour antigen amino acid sequence for PSA.			
DE Human glandular kallikrein (HK2) protein.	PN WO200125272-A2.			
PN US6642013-B1.	PD 12-APR-2001.			
PD 04-NOV-2003.	PA (CORI-) CORIXA CORP.			
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 38.93%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1326			
RESULT 1326	ID AAG62144 standard; protein; 261 AA.			
ID ADI37156 standard; protein; 262 AA.	DE Human prostate specific membrane antigen SEQ ID NO: 327.			
DE Human glandular kallikrein (hHK2) protein.	PN WO200125273-A2.			
PN US2003199010-A1.	PD 12-APR-2001.			
PD 23-OCT-2003.	PA (CORI-) CORIXA CORP.			
PA (UYAR-) UNIV ARKANSAS.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 38.93%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1327			
RESULT 1327	ID AAP92314 standard; protein; 245 AA.			
ID AAP92314 standard; protein; 245 AA.	DE Human recombinant kallikrein gene.			
DE Human recombinant kallikrein gene.	PN EP297913-A.			
PN EP297913-A.	PD 04-JAN-1989.			
PD 04-JAN-1989.	PA (AMGE-) AMGEN.			
PA (AMGE-) AMGEN.	Best Local Similarity: 40.17%	Mismatches:	97	
Best Local Similarity: 40.17%	Query Match:	22.80%	Indels:	12
Query Match:	RESULT 1328			
RESULT 1328	ID AAB21313 standard; protein; 255 AA.			
ID AAB21313 standard; protein; 255 AA.	DE Human PSA.			
DE Human PSA.	PN WO200053776-A2.			
PN WO200053776-A2.	PD 14-SEP-2000.			
PD 14-SEP-2000.	PA (MOUN) MOUNT SINAI HOSPITAL.			
PA (MOUN) MOUNT SINAI HOSPITAL.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 40.40%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1329			
RESULT 1329	ID AAU06276 standard; protein; 257 AA.			
ID AAU06276 standard; protein; 257 AA.	DE Prostate specific Antigen (PSA) polypeptide.			
DE Prostate specific Antigen (PSA) polypeptide.	PN WO200145728-A2.			
PN WO200145728-A2.	PD 28-JUN-2001.			
PD 28-JUN-2001.	PA (EPIM-) EPIMUNE INC.			
PA (EPIM-) EPIMUNE INC.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 40.40%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1336			
RESULT 1336	ID AAG62146 standard; protein; 261 AA.			
ID AAG62146 standard; protein; 261 AA.	DE Human prostate specific antigen SEQ ID NO: 329.			
DE Human prostate specific antigen SEQ ID NO: 329.	PN WO200125273-A2.			
PN WO200125273-A2.	PD 12-APR-2001.			
PD 12-APR-2001.	PA (CORI-) CORIXA CORP.			
PA (CORI-) CORIXA CORP.	Best Local Similarity: 40.40%	Mismatches:	103	
Best Local Similarity: 40.40%	Query Match:	22.77%	Indels:	13
Query Match:	RESULT 1337			
RESULT 1337	ID ABU71859 standard; protein; 261 AA.			
ID ABU71859 standard; protein; 261 AA.	DE Human prostatic specific membrane antigen (PSMA).			
DE Human prostatic specific membrane antigen (PSMA).	PN US2002192763-A1.			
PN US2002192763-A1.	PD 19-DEC-2002.			
PD 19-DEC-2002.	PA (XUGJ/) XU J.			
PA (XUGJ/) XU J.	PA (DILL/) DILLON D C.			
PA (DILL/) DILLON D C.	PA (MITC/) MITCHAM J L.			
PA (MITC/) MITCHAM J L.	PA (HARL/) HARLOCKER S L.			
PA (HARL/) HARLOCKER S L.	PA (JIAN/) JIANG Y.			
PA (JIAN/) JIANG Y.	PA (KALO/) KALOS M D.			
PA (KALO/) KALOS M D.	PA (FANG/) FANGER G R.			
PA (FANG/) FANGER G R.	PA (RETT/) RETTER M W.			
PA (RETT/) RETTER M W.	PA (STOL/) STOLK J A.			
PA (STOL/) STOLK J A.	PA (DAYC/) DAY C H.			
PA (DAYC/) DAY C H.	PA (VEDV/) VEDVICK T S.			
PA (VEDV/) VEDVICK T S.				

PA (CART/) CARTER D.  
PA (LISK/) LJ S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1338  
ID ABP74202 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO200281646-A2.  
PD 17-OCT-2002.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1339  
ID ADB82777 standard; protein; 261 AA.  
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1340  
ID ADC09580 standard; protein; 261 AA.  
DE PSA protein #SEQ ID 78.  
PN WO2003008537-A2.  
PD 30-JAN-2003.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1341  
ID ADJ59022 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1342  
ID ADI39733 standard; protein; 261 AA.  
DE Human prostate specific antigen (PSA) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1343  
ID ADI37157 standard; protein; 261 AA.  
DE Human prostate specific antigen (hPSA).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1344  
ID ADM72819 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1345  
ID ABM82166 standard; protein; 261 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.

PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1346  
ID AAG62154 standard; protein; 692 AA.  
DE Human WT1/PSA fusion protein SEQ ID NO: 357.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.77% Indels: 13  
RESULT 1347  
ID AAB67545 standard; protein; 284 AA.  
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Best Local Similarity: 43.75% Mismatches: 82  
Query Match: 22.70% Indels: 8  
RESULT 1348  
ID AAY72521 standard; protein; 312 AA.  
DE NS1-p703P mutated-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 42.06% Mismatches: 83  
Query Match: 22.70% Indels: 12  
RESULT 1349  
ID AAU74767 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 42.06% Mismatches: 83  
Query Match: 22.70% Indels: 12  
RESULT 1350  
ID AAU74928 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-p703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 42.06% Mismatches: 83  
Query Match: 22.70% Indels: 12  
RESULT 1351  
ID ADJ59024 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 40.40% Mismatches: 103  
Query Match: 22.68% Indels: 13  
RESULT 1352  
ID AAU74903 standard; protein; 231 AA.  
DE Amino acid sequence of p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 43.38% Mismatches: 80  
Query Match: 22.63% Indels: 7  
RESULT 1353  
ID AAU74934 standard; protein; 231 AA.  
DE Amino acid sequence of P703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Best Local Similarity: 43.38% Mismatches: 80  
Query Match: 22.63% Indels: 7  
RESULT 1354  
ID AAP81243 standard; protein; 247 AA.  
DE Human spleen trypsin III (trypsinogen III).

PN JP63160582-A.  
PD 04-JUL-1988.  
PA (SANY ) SANKYO CO LTD.  
Best Local Similarity: 40.91% Mismatches: 92  
Query Match: 22.60% Indels: 10  
RESULT 1355  
ID AAR82703 standard; protein; 247 AA.  
DE Human pancreatic trypsin III.  
PN JP07184655-A.  
PD 25-JUL-1995.  
PA (SANY ) SANKYO CO LTD.  
Best Local Similarity: 40.91% Mismatches: 92  
Query Match: 22.60% Indels: 10  
RESULT 1356  
ID ADJ59026 standard; protein; 261 AA.  
DE Human PSA analogue (Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 40.40% Mismatches: 104  
Query Match: 22.58% Indels: 13  
RESULT 1357  
ID AB884422 standard; peptide; 226 AA.  
DE Rat SCE protein N-terminal fragment SEQ ID 48.  
PN WO2002621135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Best Local Similarity: 42.67% Mismatches: 87  
Query Match: 22.48% Indels: 9  
RESULT 1358  
ID ADJ59028 standard; protein; 261 AA.  
DE Human PSA analogue (L155/Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 40.40% Mismatches: 104  
Query Match: 22.48% Indels: 13  
RESULT 1359  
ID ADP27546 standard; protein; 281 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Best Local Similarity: 39.70% Mismatches: 105  
Query Match: 22.48% Indels: 23  
RESULT 1360  
ID ADP27545 standard; protein; 297 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Best Local Similarity: 39.70% Mismatches: 105  
Query Match: 22.48% Indels: 23  
RESULT 1361  
ID ADA50549 standard; protein; 237 AA.  
DE Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Best Local Similarity: 42.62% Mismatches: 96  
Query Match: 22.46% Indels: 12  
RESULT 1362  
ID ADM12395 standard; protein; 261 AA.  
DE Human prostate-specific antigen protein.  
PN US2003235594-A1.  
PD 25-DEC-2003.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Best Local Similarity: 40.00% Mismatches: 104  
Query Match: 22.43% Indels: 13  
RESULT 1363  
ID ADR66838 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.25% Mismatches: 101  
Query Match: 22.39% Indels: 11  
RESULT 1364  
ID ADR66277 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.25% Mismatches: 101  
Query Match: 22.39% Indels: 11  
RESULT 1365  
ID ADR66934 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.25% Mismatches: 101  
Query Match: 22.39% Indels: 11  
RESULT 1366  
ID ADR66036 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.25% Mismatches: 101  
Query Match: 22.39% Indels: 11  
RESULT 1367  
ID AAR84668 standard; protein; 261 AA.  
DE Prepro-hk2 kallikrein.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Best Local Similarity: 40.23% Mismatches: 112  
Query Match: 22.29% Indels: 11  
RESULT 1368  
ID AAW10600 standard; protein; 261 AA.  
DE Human prepro-Trip226-glandular kallikrein-2.  
PN WO9701630-A1.  
PD 16-JAN-1997.  
PA (ORIN ) ORION YHTYMAE OY.  
Best Local Similarity: 40.23% Mismatches: 112  
Query Match: 22.29% Indels: 11  
RESULT 1369  
ID AAU98921 standard; protein; 245 AA.  
DE Human prostate specific antigen (PSA) variant.  
PN WO200240059-A2.  
PD 23-MAY-2002.  
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.  
PA (MINC/) MINCHEFF M S.  
PA (LOUK/) LOUKINOV D I.  
PA (ZOUB/) ZOUBAK S.  
Best Local Similarity: 41.38% Mismatches: 95  
Query Match: 22.24% Indels: 11

RESULT 1370  
ID AAY0894 standard; protein; 238 AA.  
DE Chimeric serine protease FXT protein.  
PN EP927764-A2.  
PA (HOF) ROCHE DIAGNOSTICS GMBH. Mismatches: 95  
Best Local Similarity: 40.52% Indels: 8  
Query Match: 22.22%  
RESULT 1371  
ID AAB21314 standard; protein; 255 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1372  
ID AAW06971 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein prepro-hk2.  
PN WO9634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITECH INC. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1373  
ID AAW83203 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein protein pphk2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1374  
ID AAW49085 standard; protein; 261 AA.  
DE Wild-type human Kallikrein 2 (hk2).  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1375  
ID AAW45397 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein precursor prepro-hk2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1376  
ID AAW96189 standard; protein; 261 AA.  
DE Prepro human Kallikrein 2 (preprohk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1377  
ID AAB21318 standard; protein; 261 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1378  
ID AAU06279 standard; protein; 261 AA.

DE Human Kallikrein2 polypeptide.  
PN WO200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMUNE INC. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1379  
ID ADB75390 standard; protein; 261 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 108  
Best Local Similarity: 40.80% Indels: 11  
Query Match: 22.19%  
RESULT 1380  
ID AAW83213 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hk3.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1381  
ID AAW56086 standard; protein; 237 AA.  
DE Human prostate specific antigen protein.  
PN WO9810292-A1.  
PD 12-MAR-1998.  
PA (CENZ) CENTOCOR INC. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1382  
ID AAW96187 standard; protein; 237 AA.  
DE Human prostate specific antigen (psa).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1383  
ID AAB11041 standard; peptide; 237 AA.  
DE Human prostate-specific antigen N-terminal fragment #2.  
PN EP1043394-A2.  
PD 11-OCT-2000.  
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1384  
ID AAB19819 standard; protein; 237 AA.  
DE Prostate specific antigen specific to benign prostatic hyperplasia.  
PN WO200067030-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITECH INC. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1385  
ID AAB19818 standard; protein; 237 AA.  
DE Prostate specific antigen elevated in benign prostatic hyperplasia.  
PN WO20006718-A1.  
PD 09-NOV-2000.  
PA (BAYU) BAYLOR COLLEGE MEDICINE. Mismatches: 95  
Best Local Similarity: 41.56% Indels: 11  
Query Match: 22.14%  
RESULT 1386  
ID ADA50546 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.  
PN WO2003031569-A2.  
PD 17-APR-2003.

PA (CENZ ) CENTOCOR INC. Mismatches: 95  
 Best Local Similarity: 41.56% Indels: 11  
 Query Match: 22.14%  
 RESULT 1387  
 ID ADA09840 standard; protein; 237 AA.  
 DE Human mature prostate specific antigen (PSA).  
 PN US2003059864-A1.  
 PD 27-MAR-2003.  
 PA (MIKO/) MIKOLAJCZYK S D.  
 PA (RITT/) RITTENHOUSE H G.  
 Best Local Similarity: 41.56% Mismatches: 95  
 Query Match: 22.14% Indels: 11  
 RESULT 1388  
 ID ADJ59023 standard; protein; 237 AA.  
 DE Human PSA mature protein sequence.  
 PN WO2003047506-A2.  
 PD 12-JUN-2003.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 41.56% Mismatches: 95  
 Query Match: 22.14% Indels: 11  
 RESULT 1389  
 ID ADF60980 standard; protein; 237 AA.  
 DE Human prostate specific antigen (PSA).  
 PN US2003166036-A1.  
 PD 04-SEP-2003.  
 PA (MIKO/) MIKOLAJCZYK S D.  
 PA (RITT/) RITTENHOUSE H G.  
 Best Local Similarity: 41.56% Mismatches: 95  
 Query Match: 22.14% Indels: 11  
 RESULT 1390  
 ID AAP70677 standard; protein; 245 AA.  
 DE Human kallikrein gene product.  
 PN WO8702709-A.  
 PD 07-MAY-1987.  
 PA (BIOT-) BIOTECHN RES PARTN.  
 PA (CALB-) CALIF BIOTECHNOL INC.  
 Best Local Similarity: 39.73% Mismatches: 99  
 Query Match: 22.07% Indels: 12  
 RESULT 1391  
 ID AAW45398 standard; protein; 237 AA.  
 DE Prostate-specific antigen protein hK3 (PSA).  
 PN WO9802748-A1.  
 PD 22-JAN-1998.  
 PA (MAYO-) MAYO FOUNDATION.  
 PA (HYBR-) HYBRITECH INC.  
 Best Local Similarity: 41.56% Mismatches: 96  
 Query Match: 22.05% Indels: 11  
 RESULT 1392  
 ID ADJ59025 standard; protein; 237 AA.  
 DE Human PSA mature protein sequence.  
 PN WO2003047506-A2.  
 PD 12-JUN-2003.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 41.56% Mismatches: 95  
 Query Match: 22.05% Indels: 11  
 RESULT 1393  
 ID AAW06972 standard; protein; 261 AA.  
 DE Kallikrein prepro-hK2v217 variant.  
 PN WO9634964-A2.  
 PD 07-NOV-1996.  
 PA (HYBR-) HYBRITECH INC.  
 PA (MAYO-) MAYO FOUNDATION.  
 Best Local Similarity: 40.80% Mismatches: 108  
 Query Match: 22.05% Indels: 11  
 RESULT 1394  
 ID AAW45400 standard; protein; 261 AA.  
 DE Prostate-specific glandular kallikrein hK2v217.  
 PN WO9802748-A1.  
 PD 22-JAN-1998.  
 PA (MAYO-) MAYO FOUNDATION.  
 PA (HYBR-) HYBRITECH INC.  
 Best Local Similarity: 40.80% Mismatches: 108  
 Query Match: 22.05% Indels: 11

RESULT 1395  
 ID AAW59129 standard; protein; 232 AA.  
 DE Homo sapiens Tub Interactor (HTI-1) protein.  
 PN WO9812302-A1.  
 PD 26-MAR-1998.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 43.78% Mismatches: 76  
 Query Match: 22.00% Indels: 11  
 RESULT 1396  
 ID AAY72523 standard; protein; 232 AA.  
 DE Human prostate antigen #1.  
 PN WO200104143-A2.  
 PD 18-JAN-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 43.78% Mismatches: 76  
 Query Match: 22.00% Indels: 11  
 RESULT 1397  
 ID AAU74769 standard; protein; 232 AA.  
 DE Protein sequence of prostate homologue #1.  
 PN WO200200708-A2.  
 PD 03-JAN-2002.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.78% Mismatches: 76  
 Query Match: 22.00% Indels: 11  
 RESULT 1398  
 ID AAU74930 standard; protein; 232 AA.  
 DE Amino acid sequence of prostate protein fragment #1.  
 PN WO200200867-A1.  
 PD 03-JAN-2002.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 Best Local Similarity: 43.78% Mismatches: 76  
 Query Match: 22.00% Indels: 11  
 RESULT 1399  
 ID AAR84669 standard; protein; 244 AA.  
 DE Pro-hK2 kallikrein.  
 PN WO9530758-A1.  
 PD 16-NOV-1995.  
 PA (MAYO-) MAYO FOUNDATION.  
 PA (HYBR-) HYBRITECH INC.  
 Best Local Similarity: 41.18% Mismatches: 100  
 Query Match: 22.00% Indels: 11  
 RESULT 1400  
 ID ADO38617 standard; protein; 261 AA.  
 DE Prostate Specific Antigen (PSA).  
 PN US2004058881-A1.  
 PD 25-MAR-2004.  
 PA (ANTL-) ANTIGEN EXPRESS INC.  
 Best Local Similarity: 39.60% Mismatches: 105  
 Query Match: 22.00% Indels: 13  
 RESULT 1401  
 ID ADJ59027 standard; protein; 237 AA.  
 DE Human PSA analogue (Y154) mature protein sequence.  
 PN WO2003047506-A2.  
 PD 12-JUN-2003.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 41.56% Mismatches: 96  
 Query Match: 21.95% Indels: 11  
 RESULT 1402  
 ID AAW83204 standard; protein; 244 AA.  
 DE Prostate-specific glandular kallikrein protein phK2.  
 PN WO9846795-A1.  
 PD 22-OCT-1998.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA (MAYO-) MAYO FOUNDATION.  
 Best Local Similarity: 41.81% Mismatches: 96  
 Query Match: 21.90% Indels: 11  
 RESULT 1403  
 ID AAW45396 standard; protein; 244 AA.  
 DE Prostate-specific glandular kallikrein precursor pro-hK2.  
 PN WO9802748-A1.  
 PD 22-JAN-1998.  
 PA (MAYO-) MAYO FOUNDATION.

PA (HYBR-) HYBRITECH INC.  
Best Local Similarity: 41.81% Mismatches: 96  
Query Match: 21.90% Indels: 11  
RESULT 1404  
ID AAW96188 standard; protein; 244 AA.  
DE Pro human kallikrein 2 (prohK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Best Local Similarity: 41.81% Mismatches: 96  
Query Match: 21.90% Indels: 11  
RESULT 1405  
ID AAW03130 standard; protein; 250 AA.  
DE Prostate-specific antigen.  
PN WO9621042-A2.  
PD 11-JUL-1996.  
PA (UYBO-) UNIV BOSTON.  
Best Local Similarity: 40.52% Mismatches: 96  
Query Match: 21.90% Indels: 11  
RESULT 1406  
ID ADP27538 standard; protein; 281 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Best Local Similarity: 41.81% Mismatches: 96  
Query Match: 21.90% Indels: 11  
RESULT 1407  
ID ADP27537 standard; protein; 297 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Best Local Similarity: 41.81% Mismatches: 96  
Query Match: 21.90% Indels: 11  
RESULT 1408  
ID ADJ59029 standard; protein; 236 AA.  
DE Human PSA analogue (U155/Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 41.52% Mismatches: 96  
Query Match: 21.88% Indels: 11  
RESULT 1409  
ID AAR77098 standard; protein; 237 AA.  
DE Prostate-specific antigen.  
PN WO9528498-A1.  
PD 26-OCT-1995.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Best Local Similarity: 40.69% Mismatches: 96  
Query Match: 21.81% Indels: 11  
RESULT 1410  
ID AAW63202 standard; protein; 237 AA.  
DE Prostate-specific glandular kallikrein protein hk2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Best Local Similarity: 41.93% Mismatches: 96  
Query Match: 21.81% Indels: 11  
RESULT 1411  
ID AAW45395 standard; protein; 237 AA.  
DE Mature prostate-specific glandular kallikrein hk2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Best Local Similarity: 41.99% Mismatches: 96  
Query Match: 21.81% Indels: 11  
RESULT 1412

ID AAW96186 standard; protein; 237 AA.  
DE Mature human kallikrein 2 (hk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Best Local Similarity: 41.99% Mismatches: 96  
Query Match: 21.81% Indels: 11  
RESULT 1413  
ID ADA50561 standard; protein; 237 AA.  
DE Kallikrein KLK2, SEQ ID NO:16.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Best Local Similarity: 41.99% Mismatches: 96  
Query Match: 21.81% Indels: 11  
RESULT 1414  
ID AAR84667 standard; protein; 237 AA.  
DE Mature kallikrein hk2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Best Local Similarity: 41.99% Mismatches: 96  
Query Match: 21.71% Indels: 11  
RESULT 1415  
ID ADI17277 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 813.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 44.44% Mismatches: 87  
Query Match: 21.66% Indels: 13  
RESULT 1416  
ID ADI17269 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 805.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 44.44% Mismatches: 87  
Query Match: 21.66% Indels: 13  
RESULT 1417  
ID ADJ83076 standard; protein; 217 AA.  
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.  
PN US2003170830-A1.  
PD 11-SEP-2003.  
PA (ALSO) ALSOBROOK J P.  
PA (TCH) TCHERNEV V T.  
PA (LIUX) LIU X.  
PA (SPYT) SPYTEK K A.  
PA (ZERH) ZERHUSEN B D.  
PA (PAT) PATURAJAN M.  
PA (LEPL) LEPL D M.  
PA (BURG) BURGESS C E.  
PA (SHIM) SHIMKETS R A.  
PA (GROS) GROSSE W M.  
PA (SZEK) SZEKERES E S.  
PA (VERN) VERNET C A M.  
PA (LILL) LI L.  
PA (CASM) CASMAN S J.  
PA (BOLD) BOLDOG F L.  
PA (GORM) GORMAN L.  
PA (GANG) GANGOLLI E A.  
PA (FERN) FERNANDES E R.  
PA (RIEG) RIEGER D K.  
PA (EDIN) EDINGER S R.  
PA (GUNT) GUNTHER E.  
PA (MILL) MILLET I.  
PA (SCIO) SCIORE P.  
PA (ELLE) ELLERMAN K.  
PA (MACD) MACDOUGALL J R.



PA (SMIT/) SMITHSON G. 87  
Query Match: 44.44% Mismatches: 13  
Indels: 13  
RESULT 1418  
ID AAW83212 standard; protein; 237 AA.  
DE HK2 variant A217V.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match: 41.99% Mismatches: 96  
Indels: 11  
RESULT 1419  
ID AAW9087 standard; protein; 237 AA.  
DE Mutant human Kallikrein 2 (HK2) A217V.  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match: 41.99% Mismatches: 96  
Indels: 11  
RESULT 1420  
ID AAW96190 standard; protein; 237 AA.  
DE Variant human Kallikrein 2 (HK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match: 41.99% Mismatches: 96  
Indels: 11  
RESULT 1421  
ID AAW11023 standard; protein; 240 AA.  
DE Human prostate specific antigen.  
PN WO9640754-A1.  
PD 19-DEC-1996.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match: 41.03% Mismatches: 96  
Indels: 14  
RESULT 1422  
ID AAR84671 standard; protein; 237 AA.  
DE Mature kallikrein HK3.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match: 41.13% Mismatches: 97  
Indels: 11  
RESULT 1423  
ID ABM82643 standard; protein; 227 AA.  
DE Human diagnostic and therapeutic pproteain SEQ ID NO:2892.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match: 39.59% Mismatches: 82  
Indels: 30  
RESULT 1424  
ID AAR84670 standard; protein; 238 AA.  
DE Mature kallikrein HK2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match: 40.93% Mismatches: 101  
Indels: 11  
RESULT 1425  
ID AAR94526 standard; protein; 279 AA.  
DE Korean Viper Salmoisa thrombin-like protease, Halybin.  
PN EP707067-A2.  
PD 17-APR-1996.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match: 37.66% Mismatches: 110  
Indels: 110

Query Match: 21.25% Indels: 4  
RESULT 1426  
ID AAG79000 standard; protein; 233 AA.  
DE Mamushi fibrinolytic enzyme, brevinase.  
PN KR2001045716-A.  
PD 05-JUN-2001.  
PA (LEEU/) LEE J W.  
PA (PARK/) PARK W.  
Query Match: 37.93% Mismatches: 92  
Indels: 11  
RESULT 1427  
ID AAM52944 standard; protein; 260 AA.  
DE Agkistrodon halys brevicaudus thrombin-like protease, salmobin.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match: 36.14% Mismatches: 106  
Indels: 12  
RESULT 1428  
ID AAB50447 standard; protein; 205 AA.  
DE Human prostate cancer-related intracellular protein #1.  
PN WO200071711-A2.  
PD 30-NOV-2000.  
PA (SAAT/) SAATCIOGLU F.  
Query Match: 44.22% Mismatches: 69  
Indels: 7  
RESULT 1429  
ID ADE78966 standard; protein; 227 AA.  
DE Human protein modification and maintenance molecule (PMMM)-4.  
PN WO2003063888-A2.  
PD 07-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match: 39.18% Mismatches: 84  
Indels: 30  
RESULT 1430  
ID ABR09589 standard; protein; 234 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match: 37.65% Mismatches: 100  
Indels: 11  
RESULT 1431  
ID AAM69388 standard; protein; 205 AA.  
DE Prostate tumour specific gene clone DE13 protein.  
PN WO9837418-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match: 43.72% Mismatches: 70  
Indels: 7  
RESULT 1432  
ID AAW71872 standard; protein; 205 AA.  
DE Protein encoded by prostate tumour clone P703 splice variant DE13.  
PN WO9837093-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match: 43.72% Mismatches: 70  
Indels: 7  
RESULT 1433  
ID AAY82005 standard; protein; 205 AA.  
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.  
PN WO200004149-A2.  
PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match: 43.72% Mismatches: 70  
Indels: 7  
RESULT 1434  
ID ABG94414 standard; protein; 205 AA.  
DE Human prostate tumour protein partial variant sequence #2.  
PN US2002090372-A1.  
PD 11-JUL-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.

Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1435  
ID AAM01120 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1436  
ID AAU69766 standard; protein; 205 AA.  
DE Human prostate cDNA encoded protein #6.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1437  
ID AAB74803 standard; protein; 205 AA.  
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1438  
ID AAG99005 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1439  
ID ABU71656 standard; protein; 205 AA.  
DE Prostate cancer specific antigen P703P #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1440  
ID AAU04964 standard; protein; 205 AA.  
DE Human prostate tumour protein DE13.  
PN US6262245-B1.  
PD 17-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1441  
ID ABB95225 standard; protein; 205 AA.

Human P703P-DE13 protein SEQ ID NO 176.  
US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1442  
ID ABG76668 standard; protein; 205 AA.  
DE Prostate tumour protein #6.  
PN US2002081580-A1.  
PD 27-JUN-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1443  
ID ABR54337 standard; protein; 205 AA.  
DE Prostate tumour specific protein sequence SEQ ID 176.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1444  
ID ADB13626 standard; protein; 205 AA.  
DE Human prostate specific protein P703P-DE13.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1445  
ID ADG26042 standard; protein; 205 AA.  
DE Human prostate-specific polypeptide #6.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 43.72% Mismatches: 70  
Query Match: 20.64% Indels: 7  
RESULT 1446  
ID ADK36957 standard; protein; 281 AA.  
DE Novel human polypeptide SeqID9039.  
PN WO200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 39.26% Mismatches: 91  
Query Match: 20.45% Indels: 19  
RESULT 1447  
ID ABU92024 standard; protein; 218 AA.  
DE Human protein modification and maintenance molecule-4 (PMM-4).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 37.76% Mismatches: 83  
Query Match: 20.43% Indels: 38  
RESULT 1448  
ID AAB31579 standard; peptide; 225 AA.

DE Amino acid sequence of cod trypsin isozymes.  
PN WO200078332-A2.  
PD 28-DEC-2000.  
PA (BJAR/) BJARNASON J B. Mismatches: 92  
Best Local Similarity: 44.30% Indels: 10  
Query Match: 20.38%  
RESULT 1449  
ID ADE15982 standard; protein; 218 AA.  
DE G-coupled protein receptor related polypeptide, SEQ ID NO 12.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP. Mismatches: 83  
Best Local Similarity: 37.76% Indels: 38  
Query Match: 20.33%  
RESULT 1450  
ID ADL93921 standard; protein; 218 AA.  
DE Human G-coupled protein receptor-related protein #6.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL/) LI L.  
PA (GERL/) GERLACH V.  
PA (LIUX/) LIU X.  
PA (MILL/) MILLER C E.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERHUSEN B D.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (ZHON/) ZHONG H.  
PA (SMIT/) SMITHSON G.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOGF L.  
PA (VOSS/) VOSS E Z.  
PA (VERN/) VERNET C A.  
PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (MALY/) MALYANKAR U M.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
Best Local Similarity: 37.76% Mismatches: 83  
Query Match: 20.33% Indels: 38  
RESULT 1451  
ID AAY28641 standard; protein; 207 AA.  
DE Human secreted protein from cDNA clone HKAET41.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 69  
Best Local Similarity: 50.28% Indels: 4  
Query Match: 20.23%  
RESULT 1452  
ID AA46773 standard; protein; 233 AA.  
DE Amino acid sequence of Salmonase.  
PN EP814164-A2.  
PD 29-DEC-1997.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST. Mismatches: 95  
Best Local Similarity: 36.64% Indels: 11  
Query Match: 20.21%  
RESULT 1453  
ID AA21442 standard; protein; 226 AA.  
DE Human trypsin domain consensus protein #2.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 56  
Best Local Similarity: 42.58% Indels: 65  
Query Match: 20.16%  
RESULT 1454

ID ABG75786 standard; protein; 226 AA.  
DE Trypsin domain consensus sequence, SMART.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R. Mismatches: 56  
Best Local Similarity: 42.58% Indels: 65  
Query Match: 20.16%  
RESULT 1455  
ID ABM83248 standard; protein; 299 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3497.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP. Mismatches: 91  
Best Local Similarity: 36.07% Indels: 53  
Query Match: 20.04%  
RESULT 1456  
ID ADA05736 standard; protein; 198 AA.  
DE Human NOVI8c protein SEQ ID NO:96.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP. Mismatches: 65  
Best Local Similarity: 36.82% Indels: 71  
Query Match: 19.97%  
RESULT 1457  
ID ADN62900 standard; protein; 198 AA.  
DE Human NOVI8c.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Best Local Similarity: 36.82% Mismatches: 65  
Query Match: 19.97% Indels: 71  
RESULT 1458  
ID ADA50560 standard; protein; 194 AA.  
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ-) CENTOCOR INC. Mismatches: 75  
Best Local Similarity: 38.74% Indels: 36  
Query Match: 19.80%  
RESULT 1459

ID AAG75694 standard; protein; 215 AA.  
DE Human protein modification and maintenance molecule polypeptide SeqID8.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 37.14% Mismatches: 77  
Query Match: 19.80% Indels: 42  
RESULT 1460

ID ABM92829 standard; protein; 215 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3078.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 37.14% Mismatches: 77  
Query Match: 19.80% Indels: 42  
RESULT 1461

ID ADA05738 standard; protein; 181 AA.  
DE Human NOVI8d protein SEQ ID NO:98.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 37.39% Mismatches: 61  
Query Match: 19.77% Indels: 63  
RESULT 1462

ID ADNG2902 standard; protein; 181 AA.  
DE Human NOVI8d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATI/) PATURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIP/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Best Local Similarity: 37.39% Mismatches: 61  
Query Match: 19.77% Indels: 63  
RESULT 1463

ID ABM82641 standard; protein; 222 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 36.69% Mismatches: 88  
Query Match: 19.70% Indels: 36  
RESULT 1464

ID AAB08510 standard; protein; 230 AA.  
DE A recombinant protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI) INSTRUMENTATION LAB.  
Best Local Similarity: 36.21% Mismatches: 94  
Query Match: 19.68% Indels: 13  
RESULT 1465

ID AAW76538 standard; protein; 231 AA.  
DE A. concortrix protein C activator protein fragment.  
PN WO9842850-A1.  
PD 01-OCT-1998.  
PA (RPMS-) RPMS TECHNOLOGY LTD.  
Best Local Similarity: 36.21% Mismatches: 94  
Query Match: 19.68% Indels: 13  
RESULT 1466

ID AAW69041 standard; protein; 246 AA.  
DE Polypeptide fragment encoded by gene 179.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 41.56% Mismatches: 110  
Query Match: 19.68% Indels: 6  
RESULT 1467

ID ABB51196 standard; protein; 246 AA.  
DE Human secreted protein encoded by gene 179 SEQ ID NO:1149.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 41.56% Mismatches: 110  
Query Match: 19.68% Indels: 6  
RESULT 1468

ID ABO45453 standard; protein; 246 AA.  
DE Novel human secreted protein #179 fragment #1.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 41.56% Mismatches: 110  
Query Match: 19.68% Indels: 6  
RESULT 1469

ID ABO26933 standard; protein; 246 AA.  
DE Protein associated with novel secreted protein gene 179 #1.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 41.56% Mismatches: 110  
Query Match: 19.68% Indels: 6  
RESULT 1470

ID ABB09590 standard; protein; 218 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Best Local Similarity: 36.49% Mismatches: 94  
Query Match: 19.63% Indels: 9  
RESULT 1471

ID ABM84665 standard; protein; 220 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 36.65% Mismatches: 82  
Query Match: 19.60% Indels: 42  
RESULT 1472

ID AAB08511 standard; protein; 230 AA.  
DE Biosynthetic variant of protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI) INSTRUMENTATION LAB.  
Best Local Similarity: 36.96% Mismatches: 97  
Query Match: 19.53% Indels: 9  
RESULT 1473

ID AAR20557 standard; protein; 234 AA.

DE Fibrinogenolytic protein #4 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (BADI ) BASF AG. Mismatches: 105  
Best Local Similarity: 36.68% Indels: 4  
Query Match: 19.51%  
RESULT 1474  
ID AAP81333 standard; protein; 255 AA.  
DE Batroxobin.  
PN JP63049084-A.  
PD 01-MAR-1988.  
PA (YAMA/) YAMASHINA I. Mismatches: 109  
Best Local Similarity: 32.92% Indels: 4  
Query Match: 19.46%  
RESULT 1475  
ID AAR05436 standard; protein; 255 AA.  
DE Batroxobin gene product.  
PN JP02124092-A.  
PD 11-MAY-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD. Mismatches: 109  
Best Local Similarity: 32.92% Indels: 4  
Query Match: 19.46%  
RESULT 1476  
ID AAV17869 standard; protein; 255 AA.  
DE Araraca batroxobin.  
PN WO9929838-A1.  
PD 17-JUN-1999.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO. Mismatches: 109  
Best Local Similarity: 32.92% Indels: 4  
Query Match: 19.46%  
RESULT 1477  
ID AAE21441 standard; protein; 249 AA.  
DE Human trypsin domain consensus protein #1.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 65  
Best Local Similarity: 40.32% Indels: 53  
Query Match: 19.43%  
RESULT 1478  
ID AAM52946 standard; protein; 231 AA.  
DE Batroxobin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST. Mismatches: 101  
Best Local Similarity: 34.21% Indels: 4  
Query Match: 19.36%  
RESULT 1479  
ID AAW89042 standard; protein; 228 AA.  
DE Polypeptide fragment encoded by gene 179.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 100  
Best Local Similarity: 42.22% Indels: 5  
Query Match: 19.17%  
RESULT 1480  
ID ABB51197 standard; protein; 228 AA.  
DE Human secreted protein encoded by gene 179 SEQ ID NO:1150.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 100  
Best Local Similarity: 42.22% Indels: 5  
Query Match: 19.17%  
RESULT 1481  
ID ABO45454 standard; protein; 228 AA.  
DE Novel human secreted protein #179 fragment #2.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 100  
Best Local Similarity: 42.22% Indels: 5  
Query Match: 19.17%  
RESULT 1482  
ID ABO26934 standard; protein; 228 AA.  
DE Protein associated with novel secreted protein gene 179 #2.

PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 100  
Best Local Similarity: 42.22% Indels: 5  
Query Match: 19.17%  
RESULT 1483  
ID AAB11711 standard; protein; 264 AA.  
DE Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD. Mismatches: 102  
Best Local Similarity: 39.10% Indels: 25  
Query Match: 19.14%  
RESULT 1484  
ID AAM52945 standard; protein; 236 AA.  
DE Flabobobin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST. Mismatches: 109  
Best Local Similarity: 36.25% Indels: 8  
Query Match: 19.12%  
RESULT 1485  
ID AAR20556 standard; protein; 236 AA.  
DE Fibrinogenolytic protein #3 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (BADI ) BASF AG. Mismatches: 92  
Best Local Similarity: 37.28% Indels: 14  
Query Match: 19.02%  
RESULT 1486  
ID ABM82831 standard; protein; 233 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP. Mismatches: 77  
Best Local Similarity: 36.78% Indels: 42  
Query Match: 18.97%  
RESULT 1487  
ID AAE39993 standard; protein; 253 AA.  
DE Human adipin protein #2.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA. Mismatches: 91  
Best Local Similarity: 38.00% Indels: 18  
Query Match: 18.93%  
RESULT 1488  
ID ABG75785 standard; protein; 227 AA.  
DE Trypsin domain consensus sequence, PFAM.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R. Mismatches: 60  
Best Local Similarity: 40.43% Indels: 48  
Query Match: 18.83%  
RESULT 1489  
ID ADE58223 standard; protein; 253 AA.  
DE Human Protein P00746, SEQ ID NO 4094.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP. Mismatches: 91  
Best Local Similarity: 38.49% Indels: 18  
Query Match: 18.83%  
RESULT 1490  
ID AAP70758 standard; protein; 269 AA.  
DE Pig pancreas elastase-2.  
PN JP62000276-A.  
PD 06-JAN-1987.  
PA (SANY ) SANKYO CO LTD. Mismatches: 100  
Best Local Similarity: 38.55% Indels: 28  
Query Match: 18.78%  
RESULT 1491  
ID AAE39992 standard; protein; 253 AA.  
DE Human adipin protein #1.

PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA.  
Best Local Similarity: 38.49% Mismatches: 92  
Query Match: 18.73% Indels: 18  
RESULT 1492  
ID AAB11710 standard; protein; 264 AA.  
DE Human serine protease BSSP5 (hbssps) SEQ ID NO:2.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Best Local Similarity: 36.84% Mismatches: 105  
Query Match: 18.71% Indels: 25  
RESULT 1493  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSET polypeptide clone name vCTRL-1.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST ) GENSET SA.  
Best Local Similarity: 36.84% Mismatches: 105  
Query Match: 18.71% Indels: 25  
RESULT 1494  
ID ABU09382 standard; protein; 271 AA.  
DE Consensus sequence of trypsin-like domain.  
PN WO2003031463-A2.  
PD 17-APR-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 39.05% Mismatches: 86  
Query Match: 18.68% Indels: 56  
RESULT 1495  
ID ABM82830 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 36.33% Mismatches: 79  
Query Match: 18.66% Indels: 45  
RESULT 1496  
ID ABM82644 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 36.33% Mismatches: 79  
Query Match: 18.66% Indels: 45  
RESULT 1497  
ID ABM81778 standard; protein; 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 36.84% Mismatches: 105  
Query Match: 18.66% Indels: 25  
RESULT 1498  
ID ADR66037 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.19% Mismatches: 85  
Query Match: 18.64% Indels: 14  
RESULT 1499  
ID ADR66935 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 40.19% Mismatches: 85  
Query Match: 18.64% Indels: 14  
RESULT 1500  
ID ADE58221 standard; protein; 263 AA.  
DE Rat Protein AAB31922, SEQ ID NO 4092.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 37.41% Mismatches: 106  
Query Match: 18.64% Indels: 22

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 5, 2005, 22:38:43 ; Search time 40 Seconds  
(without alignments)  
4072.106 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 2066  
Sequence: 1 caagcaggtcatcccttg.....aggggcaaaaaa 1091

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.epool\_p/US10015385/runat\_05032005\_173552\_17285/app\_query\_fasta\_1.1287  
-DB=Issued\_Patents\_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowum62 -TRANS=human40.cdi  
-LIST=1500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10015385@cgn1.1.46 @runat\_05032005\_173552\_17285 -NCPUS=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1372.5	66.4	254	4	US-09-949-016-6948
2	1371.5	66.4	249	4	US-09-949-016-8151
3	811	39.3	162	4	US-09-244-111-6
4	632.5	30.6	260	4	US-09-618-259-7
5	628.5	30.4	260	3	US-09-070-526-2
6	624.5	30.2	260	3	US-09-008-271A-7
7	622.5	30.1	260	3	US-09-025-059-3
8	622.5	30.1	260	4	US-09-618-259-8
9	618.5	29.9	250	4	US-09-205-238-427
10	618.5	29.9	282	3	US-09-025-059-1
11	602.5	29.2	288	4	US-09-386-642-13
12	598.5	29.0	289	4	US-09-386-642-14

13	597.5	28.9	248	3	US-08-944-483-24	Sequence 24, Appl
14	573	27.7	247	2	US-08-956-267A-2	Sequence 2, Appl
15	569	27.5	325	4	US-09-949-016-7713	Sequence 7113, Ap
16	568	27.5	290	4	US-09-949-016-8166	Sequence 8166, Ap
17	564.5	27.3	270	4	US-09-949-016-7712	Sequence 7712, Ap
18	564.5	27.3	293	4	US-09-509-908-2	Sequence 2, Appl
19	564	27.3	276	1	US-08-467-155A-1	Sequence 1, Appl
20	564	27.3	276	2	US-08-628-198-1	Sequence 1, Appl
21	564	27.3	276	3	US-09-201-038-1	Sequence 1, Appl
22	564	27.3	276	5	PCT-US96-07343-1	Sequence 1, Appl
23	561	27.2	244	1	US-08-361-395-1	Sequence 1, Appl
24	560	27.1	265	4	US-09-949-016-7716	Sequence 7716, Ap
25	555	26.9	253	2	US-08-557-146-2	Sequence 2, Appl
26	555	26.9	253	2	US-08-824-874-3	Sequence 3, Appl
27	555	26.9	253	2	US-09-154-344-2	Sequence 2, Appl
28	555	26.9	253	3	US-08-930-188-2	Sequence 2, Appl
29	555	26.9	253	3	US-09-210-084-3	Sequence 3, Appl
30	555	26.9	253	4	US-09-764-762-3	Sequence 3, Appl
31	555	26.9	253	5	PCT-US96-04294-2	Sequence 2, Appl
32	552	26.7	229	3	US-09-120-582-2	Sequence 2, Appl
33	547	26.5	223	1	US-08-278-091-9	Sequence 9, Appl
34	547	26.5	223	1	US-08-483-859-9	Sequence 9, Appl
35	547	26.5	223	1	US-08-472-173-9	Sequence 9, Appl
36	547	26.5	223	2	US-08-487-167-9	Sequence 9, Appl
37	547	26.5	223	2	US-08-482-816-9	Sequence 9, Appl
38	547	26.5	223	2	US-08-296-149-9	Sequence 9, Appl
39	547	26.5	223	2	US-08-801-499-9	Sequence 9, Appl
40	547	26.5	223	2	US-08-615-271-9	Sequence 9, Appl
41	547	26.5	223	3	US-09-074-660-9	Sequence 9, Appl
42	547	26.5	223	3	US-09-074-659-9	Sequence 9, Appl
43	547	26.5	223	3	US-09-106-468-9	Sequence 9, Appl
44	547	26.5	223	3	US-09-106-466A-9	Sequence 9, Appl
45	547	26.5	223	3	US-09-106-467-9	Sequence 9, Appl
46	547	26.5	223	4	US-09-601-318-2	Sequence 2, Appl
47	546	26.4	244	4	US-09-618-259-11	Sequence 11, Appl
48	545	26.4	225	4	US-09-027-337-4	Sequence 4, Appl
49	545	26.4	225	4	US-09-654-600A-4	Sequence 4, Appl
50	545	26.4	225	4	US-09-654-600A-4	Sequence 4, Appl
51	544.5	26.4	291	1	US-08-467-155A-11	Sequence 11, Appl
52	544.5	26.4	291	2	US-08-628-198-11	Sequence 11, Appl
53	544.5	26.4	291	3	US-09-201-038-11	Sequence 11, Appl
54	544.5	26.4	291	5	PCT-US96-07343-11	Sequence 11, Appl
55	543	26.3	246	2	US-08-978-404B-44	Sequence 44, Appl
56	540	26.1	224	3	US-08-944-483-33	Sequence 33, Appl
57	539.5	25.6	225	2	US-08-557-146-12	Sequence 12, Appl
58	539.5	25.6	225	2	US-09-154-344-12	Sequence 12, Appl
59	524	25.4	232	2	US-08-978-404B-45	Sequence 45, Appl
60	520	25.2	232	1	US-08-278-091-8	Sequence 8, Appl
61	520	25.2	232	1	US-08-483-859-8	Sequence 8, Appl
62	520	25.2	232	2	US-08-472-173-8	Sequence 8, Appl
63	520	25.2	232	2	US-08-487-167-8	Sequence 8, Appl
64	520	25.2	232	2	US-08-482-816-8	Sequence 8, Appl
65	520	25.2	232	2	US-08-296-149-8	Sequence 8, Appl
66	520	25.2	232	2	US-08-801-499-8	Sequence 8, Appl
67	520	25.2	232	2	US-08-615-271-8	Sequence 8, Appl
68	520	25.2	232	3	US-09-074-660-8	Sequence 8, Appl
69	520	25.2	232	3	US-09-074-659-8	Sequence 8, Appl
70	520	25.2	232	3	US-09-106-468-8	Sequence 8, Appl
71	520	25.2	232	3	US-09-106-466A-8	Sequence 8, Appl
72	520	25.2	232	3	US-09-106-467-8	Sequence 8, Appl
73	518.5	25.1	268	2	US-08-824-874-1	Sequence 1, Appl
74	518.5	25.1	268	3	US-09-210-084-1	Sequence 1, Appl
75	518.5	25.1	268	4	US-09-764-762-1	Sequence 1, Appl
76	503	24.3	263	2	US-08-790-137-4	Sequence 4, Appl
77	503	24.3	263	2	US-08-824-874-5	Sequence 5, Appl
78	503	24.3	263	3	US-08-807-151-5	Sequence 5, Appl
79	503	24.3	263	3	US-09-210-084-5	Sequence 5, Appl
80	503	24.3	263	3	US-09-478-957-5	Sequence 5, Appl
81	503	24.3	263	4	US-09-764-762-5	Sequence 5, Appl
82	501	24.2	249	4	US-09-949-016-8770	Sequence 8770, Ap
83	498	24.1	254	3	US-09-439-313-525	Sequence 525, App
84	498	24.1	254	4	US-09-636-215-525	Sequence 525, App
85	498	24.1	254	4	US-09-685-166A-525	Sequence 525, App

86	498	24.1	254	4	US-09-679-426-525	Sequence 525, App	159	459	22.2	238	4	US-09-664-595A-15	Sequence 15, Appl
87	498	24.1	254	4	US-09-759-143-525	Sequence 525, App	160	459	22.2	262	3	US-09-025-059-4	Sequence 4, Appl
88	498	24.1	254	4	US-09-651-236-525	Sequence 525, App	161	459	22.2	262	4	US-09-755-100A-14	Sequence 14, Appl
89	497.5	24.1	281	1	US-08-467-155A-7	Sequence 7, Appl	162	458.5	22.2	261	3	US-08-768-859A-6	Sequence 6, Appl
90	497.5	24.1	281	2	US-08-628-198-7	Sequence 7, Appl	163	458.5	22.2	261	3	US-08-767-820A-6	Sequence 6, Appl
91	497.5	24.1	281	3	US-09-201-038-7	Sequence 7, Appl	164	458.5	22.2	261	3	US-08-622-046B-14	Sequence 14, Appl
92	497.5	24.1	281	5	PCT-US96-07343-7	Sequence 7, Appl	165	458.5	22.2	261	3	US-09-100-264-7	Sequence 7, Appl
93	497	24.1	258	1	US-08-744-026-3	Sequence 3, Appl	166	458.5	22.2	261	3	US-08-983-075D-7	Sequence 7, Appl
94	497	24.1	258	2	US-09-102-732-3	Sequence 3, Appl	167	458.5	22.2	261	3	US-08-843-076D-3	Sequence 3, Appl
95	497	24.1	258	3	US-09-261-767-3	Sequence 3, Appl	168	458.5	22.2	278	4	US-09-949-016-7711	Sequence 7711, Ap
96	496.5	24.0	248	1	US-08-744-026-1	Sequence 1, Appl	169	458	22.2	228	1	US-08-278-091-7	Sequence 7, Appl
97	496.5	24.0	248	2	US-09-102-732-1	Sequence 1, Appl	170	458	22.2	228	1	US-08-483-859-7	Sequence 7, Appl
98	496.5	24.0	248	3	US-09-261-767-1	Sequence 1, Appl	171	458	22.2	228	1	US-08-472-173-7	Sequence 7, Appl
99	494	23.9	254	3	US-09-439-315-523	Sequence 523, App	172	458	22.2	228	2	US-08-487-167-7	Sequence 7, Appl
100	494	23.9	254	4	US-09-636-215-523	Sequence 523, App	173	458	22.2	228	2	US-08-482-816-7	Sequence 7, Appl
101	494	23.9	254	4	US-09-685-166A-523	Sequence 523, App	174	458	22.2	228	2	US-08-296-149-7	Sequence 7, Appl
102	494	23.9	254	4	US-09-679-426-523	Sequence 523, App	175	458	22.2	228	2	US-08-801-439-7	Sequence 7, Appl
103	494	23.9	254	4	US-09-759-143-523	Sequence 523, App	176	458	22.2	228	2	US-08-615-271-7	Sequence 7, Appl
104	494	23.9	254	4	US-09-651-236-523	Sequence 523, App	177	458	22.2	228	3	US-09-074-660-7	Sequence 7, Appl
105	493	23.9	262	2	US-08-790-137-1	Sequence 1, Appl	178	458	22.2	228	3	US-09-074-659-7	Sequence 7, Appl
106	493	23.9	262	2	US-08-790-137-3	Sequence 3, Appl	179	458	22.2	228	3	US-09-106-468-7	Sequence 7, Appl
107	493	23.9	262	2	US-08-681-151-4	Sequence 4, Appl	180	458	22.2	228	3	US-09-106-466A-7	Sequence 7, Appl
108	493	23.9	262	2	US-08-824-874-4	Sequence 4, Appl	181	458	22.2	228	3	US-03-106-467-7	Sequence 7, Appl
109	493	23.9	262	3	US-08-807-151-4	Sequence 4, Appl	182	457.5	22.1	237	3	US-08-768-859A-1	Sequence 1, Appl
110	493	23.9	262	3	US-09-210-084-4	Sequence 4, Appl	183	457.5	22.1	237	3	US-08-767-820A-1	Sequence 1, Appl
111	493	23.9	262	3	US-09-478-957-4	Sequence 4, Appl	184	457.5	22.1	237	3	US-08-622-046B-7	Sequence 7, Appl
112	493	23.9	262	4	US-09-764-762-4	Sequence 4, Appl	185	457.5	22.1	237	3	US-08-944-483-38	Sequence 38, Appl
113	492	23.8	225	2	US-09-027-337-5	Sequence 5, Appl	186	457.5	22.1	237	3	US-09-100-264-3	Sequence 3, Appl
114	492	23.8	225	4	US-09-644-600-5	Sequence 5, Appl	187	457.5	22.1	237	4	US-03-303-339-2	Sequence 2, Appl
115	492	23.8	225	4	US-09-654-600A-5	Sequence 5, Appl	188	457.5	22.1	237	4	US-08-843-076D-7	Sequence 7, Appl
116	492	23.8	262	1	US-08-744-026-4	Sequence 4, Appl	189	457.5	22.1	237	4	US-09-303-208-1	Sequence 1, Appl
117	492	23.8	262	1	US-09-102-732-4	Sequence 4, Appl	190	455.5	22.0	237	1	US-08-096-946-11	Sequence 11, Appl
118	492	23.8	262	3	US-09-261-767-4	Sequence 4, Appl	191	455.5	22.0	237	5	PCT-US94-07329-11	Sequence 11, Appl
119	491	23.8	221	4	US-09-959-392-33	Sequence 33, Appl	192	455.5	22.0	237	5	PCT-US95-06157-1	Sequence 1, Appl
120	490	23.7	224	3	US-08-944-483-34	Sequence 34, Appl	193	455.5	22.0	261	3	US-08-768-859A-19	Sequence 19, Appl
121	487.5	23.6	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	22.0	261	3	US-08-767-820A-19	Sequence 19, Appl
122	487.5	23.6	449	4	US-09-685-166A-617	Sequence 617, App	195	455.5	22.0	261	3	US-08-622-046B-3	Sequence 3, Appl
123	487.5	23.6	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	22.0	232	2	US-08-897-340-31	Sequence 31, Appl
124	487.5	23.6	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	22.0	232	2	US-09-252-329-31	Sequence 31, Appl
125	487.5	23.6	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	22.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
126	487	23.6	224	2	US-08-766-982-13	Sequence 13, Appl	199	452.5	21.9	238	5	PCT-US95-06157-8	Sequence 8, Appl
127	487	23.6	224	3	US-08-944-483-36	Sequence 36, Appl	200	452.5	21.9	244	3	US-08-768-859A-10	Sequence 10, Appl
128	487	23.6	224	3	US-09-296-219-13	Sequence 13, Appl	201	452.5	21.9	244	3	US-08-767-820A-10	Sequence 10, Appl
129	478.5	23.2	375	4	US-09-755-100A-11	Sequence 11, Appl	202	452.5	21.9	244	3	US-08-622-046B-16	Sequence 16, Appl
130	478	23.1	224	3	US-08-944-483-35	Sequence 35, Appl	203	452.5	21.9	244	3	US-09-100-264-5	Sequence 5, Appl
131	472.5	22.9	220	3	US-09-439-313-327	Sequence 327, App	204	452.5	21.9	244	4	US-08-843-076D-5	Sequence 5, Appl
132	472.5	22.9	220	3	US-09-352-616A-327	Sequence 327, App	205	450.5	21.8	237	2	US-08-844-024-2	Sequence 2, Appl
133	472.5	22.9	220	4	US-09-232-149A-327	Sequence 327, App	206	450.5	21.8	237	2	US-08-718-547-2	Sequence 2, Appl
134	472.5	22.9	220	4	US-09-636-215-327	Sequence 327, App	207	450.5	21.8	237	3	US-08-768-859A-16	Sequence 16, Appl
135	472.5	22.9	220	4	US-09-685-166A-327	Sequence 327, App	208	450.5	21.8	237	3	US-08-767-820A-16	Sequence 16, Appl
136	472.5	22.9	220	4	US-09-688-489-327	Sequence 327, App	209	450.5	21.8	237	3	US-08-622-046B-12	Sequence 12, Appl
137	472.5	22.9	220	4	US-09-679-426-327	Sequence 327, App	210	450.5	21.8	237	3	US-08-944-483-37	Sequence 37, Appl
138	472.5	22.9	220	4	US-09-759-143-327	Sequence 327, App	211	450.5	21.8	237	3	US-09-100-264-1	Sequence 1, Appl
139	472.5	22.9	220	4	US-09-651-236-327	Sequence 327, App	212	450.5	21.8	237	4	US-08-843-076D-1	Sequence 1, Appl
140	470.5	22.8	262	1	US-08-744-026-5	Sequence 5, Appl	213	450.5	21.8	238	3	US-08-768-859A-8	Sequence 8, Appl
141	470.5	22.8	261	2	US-09-102-732-5	Sequence 5, Appl	214	450.5	21.8	238	3	US-08-767-820A-8	Sequence 8, Appl
142	470.5	22.8	261	3	US-09-083-521-6	Sequence 6, Appl	215	450	21.8	260	3	US-08-983-075D-9	Sequence 9, Appl
143	470.5	22.8	261	3	US-09-261-767-5	Sequence 5, Appl	216	449.5	21.8	244	3	US-08-622-046B-5	Sequence 5, Appl
144	470.5	22.8	261	4	US-09-410-049-1	Sequence 1, Appl	217	448.5	21.7	237	1	US-08-096-946-10	Sequence 10, Appl
145	470.5	22.8	261	4	US-09-907-402-1	Sequence 1, Appl	218	448.5	21.7	237	5	PCT-US94-07329-10	Sequence 10, Appl
146	470.5	22.8	261	4	US-09-618-259-10	Sequence 10, Appl	219	448.5	21.7	237	5	PCT-US95-06157-16	Sequence 16, Appl
147	470.5	22.8	261	4	US-08-944-483-39	Sequence 39, Appl	220	447.5	21.7	237	3	US-08-768-859A-21	Sequence 21, Appl
148	470	22.7	238	3	US-08-944-483-39	Sequence 39, Appl	221	447.5	21.7	237	3	US-08-767-820A-21	Sequence 21, Appl
149	469.5	22.7	271	1	US-08-467-155A-10	Sequence 10, Appl	222	447.5	21.7	237	3	US-08-622-046B-1	Sequence 1, Appl
150	469.5	22.7	271	2	US-08-628-198-10	Sequence 10, Appl	223	447.5	21.7	237	3	US-09-100-264-12	Sequence 12, Appl
151	469.5	22.7	271	3	US-09-201-038-10	Sequence 10, Appl	224	447.5	21.7	237	4	US-08-843-076D-8	Sequence 8, Appl
152	469.5	22.7	271	5	PCT-US96-07343-10	Sequence 10, Appl	225	445	21.5	240	1	US-08-472-228A-1	Sequence 1, Appl
153	469	22.7	284	4	US-09-386-642-54	Sequence 54, Appl	226	445	21.5	240	3	US-09-146-831-1	Sequence 1, Appl
154	464.5	22.5	286	1	US-08-467-155A-9	Sequence 9, Appl	227	445	21.5	240	5	PCT-US96-09303-1	Sequence 1, Appl
155	464.5	22.5	286	2	US-08-628-198-9	Sequence 9, Appl	228	430	20.8	299	1	US-08-467-155A-8	Sequence 8, Appl
156	464.5	22.5	286	3	US-09-201-038-9	Sequence 9, Appl	229	430	20.8	299	2	US-08-628-198-8	Sequence 8, Appl
157	464.5	22.5	286	5	PCT-US96-07343-9	Sequence 9, Appl	230	430	20.8	299	3	US-03-201-038-8	Sequence 8, Appl
158	460.5	22.3	261	5	PCT-US95-06157-6	Sequence 6, Appl	231	430	20.8	299	5	PCT-US96-07343-8	Sequence 8, Appl



232	426.5	20.6	205	3	US-09-020-956-176	Sequence 176, App	Sequence 176, App	305	362.5	17.5	242	3	US-09-004-731-36	Sequence 36, Appl
233	426.5	20.6	205	3	US-09-030-607-176	Sequence 176, App	Sequence 176, App	306	362.5	17.5	242	3	US-08-749-699-36	Sequence 36, Appl
234	426.5	20.6	205	3	US-09-439-313-176	Sequence 176, App	Sequence 176, App	307	362.5	17.5	242	4	US-09-004-729-36	Sequence 36, Appl
235	426.5	20.6	205	3	US-09-352-616A-176	Sequence 176, App	Sequence 176, App	308	362.5	17.5	319	4	US-09-386-642-11	Sequence 11, Appl
236	426.5	20.6	205	4	US-09-232-149A-176	Sequence 176, App	Sequence 176, App	309	362.5	17.5	328	4	US-09-386-642-11	Sequence 12, Appl
237	426.5	20.6	205	4	US-09-159-812-176	Sequence 176, App	Sequence 176, App	310	358.5	17.4	232	4	US-09-959-392-31	Sequence 31, Appl
238	426.5	20.6	205	4	US-09-636-215-176	Sequence 176, App	Sequence 176, App	311	358	17.3	812	4	US-08-991-761A-7	Sequence 7, Appl
239	426.5	20.6	205	4	US-09-683-166A-176	Sequence 176, App	Sequence 176, App	312	357.5	17.3	232	3	US-08-906-769-81	Sequence 81, Appl
240	426.5	20.6	205	4	US-09-115-453-176	Sequence 176, App	Sequence 176, App	313	357.5	17.3	232	3	US-08-906-616-81	Sequence 81, Appl
241	426.5	20.6	205	4	US-09-688-489-176	Sequence 176, App	Sequence 176, App	314	357.5	17.3	232	3	US-08-817-795-81	Sequence 81, Appl
242	426.5	20.6	205	4	US-09-679-436-176	Sequence 176, App	Sequence 176, App	315	357.5	17.3	232	3	US-08-639-075A-81	Sequence 81, Appl
243	426.5	20.6	205	4	US-09-759-143-176	Sequence 176, App	Sequence 176, App	316	357.5	17.3	232	3	US-09-012-431-81	Sequence 81, Appl
244	426.5	20.6	205	4	US-09-651-236-176	Sequence 176, App	Sequence 176, App	317	357.5	17.3	232	3	US-09-012-692-81	Sequence 81, Appl
245	418	20.2	207	4	US-09-244-111-4	Sequence 4, Appl	Sequence 9, Appl	318	357.5	17.3	232	3	US-08-906-613-81	Sequence 81, Appl
246	417.5	20.2	233	2	US-08-738-413B-9	Sequence 16, Appl	Sequence 16, Appl	319	357.5	17.3	232	5	PCT-US95-144A2A-81	Sequence 10712, A
247	406.5	19.7	231	4	US-09-402-515A-16	Sequence 1149, Ap	Sequence 1149, Ap	320	357	17.3	268	4	US-09-949-016-10712	Sequence 63, Appl
248	406.5	19.7	246	4	US-09-205-258-1149	Sequence 6, Appl	Sequence 6, Appl	321	356.5	17.3	248	4	US-08-944-483-63	Sequence 2, Appl
249	404	19.6	234	1	US-08-684-862-6	Sequence 1150, Ap	Sequence 1150, Ap	322	355.5	17.2	148	4	US-09-618-259-2	Sequence 6, Appl
250	396	19.2	228	4	US-09-205-258-1150	Sequence 5, Appl	Sequence 5, Appl	323	355.5	17.2	231	2	US-09-644-600-6	Sequence 6, Appl
251	393	19.0	236	1	US-08-684-862-5	Sequence 11, Appl	Sequence 11, Appl	324	355.5	17.2	231	4	US-09-016-366A-6	Sequence 15, Appl
252	390	18.9	236	2	US-08-738-413B-10	Patent No. 5223425	Patent No. 5223425	325	355.5	17.2	231	4	US-09-016-366A-15	Sequence 21, Appl
253	387	18.7	232	2	US-08-738-413B-11	Patent No. 5223425	Patent No. 5223425	326	355.5	17.2	276	2	US-08-978-404B-21	Patent No. 5270178
254	387	18.7	253	6	5223425-8	Sequence 9575, Ap	Sequence 9575, Ap	327	355.5	17.2	276	2	5270178-2	Patent No. 5270178
255	387	18.7	253	6	5223425-8	Patent No. 5223425	Patent No. 5223425	328	354.5	17.2	461	6	5270178-2	Patent No. 5270178
256	385.5	18.7	267	4	US-09-949-016-9575	Patent No. 5223425	Patent No. 5223425	329	354.5	17.2	461	6	5270178-2	Patent No. 5270178
257	385	18.6	250	6	5223425-4	Sequence 62, Appl	Sequence 62, Appl	330	354	17.1	229	2	US-08-557-146-13	Sequence 13, Appl
258	385	18.6	250	6	5223425-4	Sequence 66, Appl	Sequence 66, Appl	331	354	17.1	229	2	US-09-154-344-13	Sequence 13, Appl
259	377.5	18.3	154	3	US-09-261-416-5	Sequence 5, Appl	Sequence 5, Appl	332	354	17.1	461	6	5270178-17	Patent No. 5270178
260	374.5	18.1	238	6	5223425-5	Patent No. 5223425	Patent No. 5223425	333	354	17.1	461	6	5270178-18	Patent No. 5270178
261	374.5	18.1	238	6	5223425-5	Patent No. 5223425	Patent No. 5223425	334	354	17.1	461	6	5270178-17	Patent No. 5270178
262	374.5	18.1	259	6	5223425-2	Patent No. 5223425	Patent No. 5223425	335	354	17.1	461	6	5270178-18	Patent No. 5270178
263	374.5	18.1	259	6	5223425-2	Patent No. 5223425	Patent No. 5223425	336	353.5	17.1	230	3	US-08-944-483-62	Sequence 62, Appl
264	374	18.1	260	6	5223425-10	Patent No. 5223425	Patent No. 5223425	337	353.5	17.1	270	2	US-08-978-404B-8	Sequence 8, Appl
265	374	18.1	260	6	5223425-10	Patent No. 5223425	Patent No. 5223425	338	353.5	17.1	460	6	5270178-15	Patent No. 5270178
266	370.5	17.9	218	3	US-08-944-483-44	Sequence 44, Appl	Sequence 44, Appl	339	353.5	17.1	460	6	5270178-15	Patent No. 5270178
267	370	17.9	418	4	US-09-370-838-62	Sequence 62, Appl	Sequence 62, Appl	340	353	17.1	274	2	US-08-978-404B-5	Sequence 5, Appl
268	370	17.9	418	4	US-09-854-133-62	Sequence 66, Appl	Sequence 66, Appl	341	351.5	17.0	814	1	US-08-750-711-1	Sequence 1, Appl
269	368	17.8	299	3	US-08-944-483-66	Sequence 25, Appl	Sequence 25, Appl	342	351.5	17.0	1019	1	US-08-296-014A-4	Sequence 4, Appl
270	368	17.8	418	1	US-08-508-448C-25	Sequence 82, Appl	Sequence 82, Appl	343	351.5	17.0	1019	2	US-08-596-405-4	Sequence 4, Appl
271	368	17.8	418	4	US-09-370-838-83	Sequence 83, Appl	Sequence 83, Appl	344	351.5	17.0	1019	2	US-08-877-620-4	Sequence 4, Appl
272	368	17.8	418	4	US-09-370-838-83	Sequence 82, Appl	Sequence 82, Appl	345	351.5	17.0	1019	4	US-09-287-368-4	Sequence 4, Appl
273	368	17.8	418	4	US-09-854-133-82	Sequence 82, Appl	Sequence 82, Appl	346	351.5	17.0	1019	4	US-09-626-795-4	Sequence 4, Appl
274	368	17.8	418	4	US-09-854-133-82	Sequence 83, Appl	Sequence 83, Appl	347	351.5	17.0	1083	1	US-08-296-014A-2	Sequence 2, Appl
275	367	17.8	234	2	US-08-738-413B-12	Sequence 12, Appl	Sequence 12, Appl	348	351.5	17.0	1083	2	US-08-596-405-2	Sequence 2, Appl
276	366.5	17.7	400	3	US-09-518-046-20	Sequence 20, Appl	Sequence 20, Appl	349	351.5	17.0	1083	2	US-08-877-620-2	Sequence 2, Appl
277	366.5	17.7	400	3	US-09-004-731-30	Sequence 30, Appl	Sequence 30, Appl	350	351.5	17.0	1083	4	US-09-287-368-2	Sequence 2, Appl
278	366.5	17.7	400	3	US-09-004-731-33	Sequence 33, Appl	Sequence 33, Appl	351	351.5	17.0	1083	4	US-09-626-795-2	Sequence 2, Appl
279	366.5	17.7	400	3	US-08-749-699-33	Sequence 30, Appl	Sequence 30, Appl	352	349.5	16.9	166	4	US-03-636-215-838	Sequence 838, App
280	366.5	17.7	400	3	US-08-749-699-33	Sequence 33, Appl	Sequence 33, Appl	353	349.5	16.9	166	4	US-09-685-166A-838	Sequence 838, App
281	366.5	17.7	400	4	US-09-004-729-30	Sequence 30, Appl	Sequence 30, Appl	354	349.5	16.9	166	4	US-09-679-426-838	Sequence 838, App
282	366.5	17.7	400	4	US-09-004-729-30	Sequence 33, Appl	Sequence 33, Appl	355	349.5	16.9	166	4	US-09-759-143-838	Sequence 838, App
283	366	17.7	232	1	US-08-508-448C-19	Sequence 19, Appl	Sequence 19, Appl	356	349.5	16.9	166	4	US-09-651-236-838	Sequence 838, App
284	365.5	17.7	245	3	US-08-906-769-121	Sequence 121, App	Sequence 121, App	357	349	16.9	159	3	US-09-020-956-172	Sequence 172, App
285	365.5	17.7	245	3	US-08-906-616-121	Sequence 121, App	Sequence 121, App	358	349	16.9	159	3	US-09-030-607-172	Sequence 172, App
286	365.5	17.7	245	3	US-08-639-075A-121	Sequence 121, App	Sequence 121, App	359	349	16.9	159	3	US-09-439-313-172	Sequence 172, App
287	365.5	17.7	245	3	US-09-012-692-121	Sequence 121, App	Sequence 121, App	360	349	16.9	159	3	US-09-352-616A-172	Sequence 172, App
288	365.5	17.7	245	3	US-09-012-692-121	Sequence 121, App	Sequence 121, App	361	349	16.9	159	4	US-09-232-149A-172	Sequence 172, App
289	365.5	17.7	245	3	US-08-906-613-121	Sequence 121, App	Sequence 121, App	362	349	16.9	159	4	US-09-159-812-172	Sequence 172, App
290	364.5	17.6	312	4	US-09-023-942A-4	Sequence 4, Appl	Sequence 4, Appl	363	349	16.9	159	4	US-09-636-215-172	Sequence 172, App
291	363.5	17.6	314	3	US-09-008-271A-3	Sequence 3, Appl	Sequence 3, Appl	364	349	16.9	159	4	US-03-685-166A-172	Sequence 172, App
292	363.5	17.6	314	4	US-09-023-942A-6	Sequence 6, Appl	Sequence 6, Appl	365	349	16.9	159	4	US-09-115-453-172	Sequence 172, App
293	363.5	17.6	314	4	US-09-007-794A-257	Sequence 257, App	Sequence 257, App	366	349	16.9	159	4	US-09-688-489-172	Sequence 172, App
294	363.5	17.6	314	4	US-09-905-125A-257	Sequence 257, App	Sequence 257, App	367	349	16.9	159	4	US-09-679-426-172	Sequence 172, App
295	363.5	17.6	314	4	US-09-905-125A-257	Sequence 257, App	Sequence 257, App	368	349	16.9	159	4	US-09-759-143-172	Sequence 172, App
296	363.5	17.6	314	4	US-09-906-770A-257	Sequence 257, App	Sequence 257, App	369	349	16.9	159	4	US-09-651-236-172	Sequence 172, App
297	363.5	17.6	314	4	US-09-906-770A-257	Sequence 257, App	Sequence 257, App	370	348	16.8	461	6	5460953-3	Patent No. 5460953
298	363.5	17.6	314	4	US-09-903-603A-257	Sequence 257, App	Sequence 257, App	371	348	16.8	461	6	5460953-3	Patent No. 5460953
299	363.5	17.6	314	4	US-09-904-920A-257	Sequence 257, App	Sequence 257, App	372	348	16.8	262	1	US-07-720-189-1	Sequence 1, Appl
300	363.5	17.6	314	4	US-09-909-064A-257	Sequence 257, App	Sequence 257, App	373	347	16.8	284	4	US-09-387-375-7	Sequence 7, Appl
301	363.5	17.6	314	4	US-09-905-381A-257	Sequence 257, App	Sequence 257, App	374	347	16.8	284	4	US-10-041-400A-7	Sequence 7, Appl
302	363.5	17.6	314	4	US-09-906-618A-257	Sequence 257, App	Sequence 257, App	375	347	16.8	284	4	US-10-042-091A-7	Sequence 7, Appl
303	363.5	17.6	387	3	US-09-032-215-3	Sequence 8, Appl	Sequence 8, Appl	376	347	16.8	306	4	US-10-042-091A-7	Sequence 53, Appl
304	363	17.6	236	1	US-08-684-862-4	Sequence 13, Appl	Sequence 13, Appl	377	347	16.8	356	4	US-09-054-272-18	Sequence 18, Appl

378	347	16.8	409	3	US-09-065-872-2	Sequence 2, Appli	451	340.5	16.5	230	1	US-08-266-407A-47	Sequence 47, Appl
379	347	16.8	409	4	US-09-667-570A-2	Sequence 2, Appli	452	340.5	16.5	230	2	US-08-892-544-47	Sequence 47, Appl
380	347	16.8	410	3	US-09-065-872-1	Sequence 1, Appli	453	340.5	16.5	230	2	US-08-766-982-12	Sequence 12, Appl
381	347	16.8	410	4	US-09-667-570A-1	Sequence 1, Appli	454	340.5	16.5	230	3	US-08-944-483-53	Sequence 53, Appl
382	347	16.8	419	1	US-08-295-411-1	Sequence 1, Appli	455	340.5	16.5	230	3	US-09-296-219-12	Sequence 12, Appl
383	347	16.8	419	2	US-08-955-471-1	Sequence 1, Appli	456	340.5	16.5	244	4	US-09-601-318-4	Sequence 4, Appli
384	347	16.8	419	4	US-09-667-570A-3	Sequence 3, Appli	457	340.5	16.5	244	4	US-09-601-318-6	Sequence 6, Appli
385	347	16.8	419	4	US-10-182-263-1	Sequence 1, Appli	458	340.5	16.5	244	4	US-09-601-318-7	Sequence 7, Appli
386	347	16.8	419	5	PCT-US92-1042-1	Sequence 1, Appli	459	340.5	16.5	244	4	US-09-601-318-7	Sequence 7, Appli
387	347	16.8	460	2	US-08-756-506-2	Sequence 2, Appli	460	340.5	16.5	245	4	US-09-079-970A-6	Sequence 6, Appli
388	347	16.8	460	2	US-08-756-506-4	Sequence 4, Appli	461	340.5	16.5	245	4	US-09-601-318-1	Sequence 1, Appli
389	347	16.8	461	4	US-10-182-263-2	Sequence 2, Appli	462	340.5	16.5	267	2	US-09-016-366A-23	Sequence 23, Appl
390	347	16.8	461	4	US-09-054-272-32	Sequence 32, Appl	463	340.5	16.5	267	2	US-08-978-404B-18	Sequence 18, Appl
391	347	16.8	461	4	US-09-949-016-5921	Sequence 5921, Ap	464	340.5	16.5	267	4	US-09-917-254-101	Sequence 101, App
392	347	16.8	461	6	5225337-2	Sequence 5921, Ap	465	340.5	16.5	300	3	US-08-705-875A-6	Sequence 6, Appli
393	347	16.8	461	6	5225337-2	Sequence 5921, Ap	466	340.5	16.5	300	4	US-09-242-999-6	Sequence 6, Appli
394	347	16.8	485	4	US-09-949-016-10882	Sequence 10882, A	467	340.5	16.5	406	4	US-09-851-588-6	Sequence 6, Appli
395	346.5	16.8	791	1	US-08-643-219-1	Sequence 1, Appli	468	340.5	16.5	423	4	US-09-856-002-2	Sequence 2, Appli
396	346.5	16.8	791	3	US-08-851-350-1	Sequence 1, Appli	469	340.5	16.5	435	3	US-09-008-271A-6	Sequence 6, Appli
397	346	16.7	234	3	US-08-944-483-46	Sequence 46, Appl	470	340.5	16.5	435	4	US-09-607-745-2	Sequence 8, Appli
398	346	16.7	241	3	US-08-944-483-59	Sequence 59, Appl	471	340.5	16.5	437	4	US-09-851-588-8	Sequence 8, Appli
399	346	16.7	419	4	US-10-182-263-5	Sequence 5, Appli	472	340.5	16.5	419	4	US-10-182-263-3	Sequence 3, Appli
400	346	16.7	419	4	US-10-182-263-6	Sequence 6, Appli	473	339.5	16.4	253	3	US-09-578-303-4	Sequence 4, Appli
401	345.5	16.7	248	3	US-08-906-769-111	Sequence 111, App	474	339.5	16.4	258	1	US-07-990-301A-2	Sequence 2, Appli
402	345.5	16.7	248	3	US-08-906-616-111	Sequence 111, App	475	339.5	16.4	333	4	US-08-991-761A-8	Sequence 8, Appli
403	345.5	16.7	248	3	US-08-817-795-111	Sequence 111, App	476	339	16.4	419	4	US-10-182-263-4	Sequence 4, Appli
404	345.5	16.7	248	3	US-08-633-075A-111	Sequence 111, App	477	339	16.4	461	3	US-08-742-877-2	Sequence 2, Appli
405	345.5	16.7	248	3	US-09-012-431-111	Sequence 111, App	478	339	16.4	461	3	US-09-053-871A-21	Sequence 21, Appl
406	345.5	16.7	248	3	US-09-012-692-111	Sequence 111, App	479	339	16.4	461	6	US-10-133-907-5	Sequence 5, Appli
407	345.5	16.7	248	3	US-08-613-111	Sequence 111, App	480	339	16.4	461	6	5521070-2	Patent No. 5521070
408	345.5	16.7	248	5	PCT-US95-14442A-111	Sequence 111, App	481	339	16.4	461	6	5521070-2	Patent No. 5521070
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410	344	16.7	274	2	US-08-978-404B-16	Sequence 16, Appl	483	339	16.4	481	4	US-09-949-016-9238	Sequence 9238, Ap
411	343.5	16.6	273	2	US-08-978-404B-3	Sequence 3, Appli	484	339	16.4	481	4	US-09-949-016-9239	Sequence 9239, Ap
412	343.5	16.6	460	6	5270178-13	Sequence 3, Appli	485	339	16.4	637	4	US-09-949-016-11538	Sequence 11538, A
413	343.5	16.6	460	6	5270178-14	Sequence 3, Appli	486	339	16.4	637	4	US-09-949-016-11539	Sequence 11539, A
414	343.5	16.6	460	6	5270178-16	Sequence 3, Appli	487	338.5	16.4	230	1	US-08-379-621-2	Sequence 2, Appli
415	343.5	16.6	460	6	5270178-13	Sequence 3, Appli	488	338.5	16.4	230	1	US-08-147-000B-2	Sequence 2, Appli
416	343.5	16.6	460	6	5270178-14	Sequence 3, Appli	489	338.5	16.4	230	1	US-08-889-078-2	Sequence 2, Appli
417	343.5	16.6	460	6	5270178-16	Sequence 3, Appli	490	338.5	16.4	261	6	5270178-5	Patent No. 5270178
418	342.5	16.6	248	3	US-09-032-215-37	Sequence 37, Appl	491	338.5	16.4	261	6	5270178-5	Patent No. 5270178
419	342.5	16.6	249	3	US-09-079-970A-5	Sequence 5, Appli	492	338.5	16.4	308	3	US-08-705-875A-10	Sequence 10, Appl
420	342.5	16.6	273	2	US-08-978-404B-6	Sequence 6, Appli	493	338.5	16.4	308	4	US-08-242-999-10	Sequence 10, Appl
421	342.5	16.6	546	6	5200340-6	Sequence 6, Appli	494	338	16.4	250	3	US-08-944-483-51	Sequence 51, Appl
422	342.5	16.6	546	6	5200340-6	Sequence 6, Appli	495	337.5	16.3	267	3	US-09-949-016-10711	Sequence 10711, A
423	342.5	16.6	713	4	US-09-949-016-9983	Sequence 9983, Ap	496	337	16.3	235	3	US-08-944-483-48	Sequence 48, Appl
424	342.5	16.6	790	2	US-08-469-486-54	Sequence 54, Appl	497	337	16.3	812	1	US-08-451-932-1	Sequence 1, Appli
425	342.5	16.6	790	2	US-08-469-658-54	Sequence 54, Appl	498	337	16.3	812	1	US-08-452-260-1	Sequence 1, Appli
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433	342.5	16.6	810	3	US-09-086-514-1	Sequence 1, Appli	506	337	16.3	812	4	US-09-335-325-1	Sequence 12, Appl
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435	342.5	16.6	810	4	US-09-701-265-1	Sequence 1, Appli	508	337	16.3	812	5	PCT-US95-05107-1	Sequence 1, Appli
436	342.5	16.6	810	6	5200340-8	Sequence 1, Appli	509	337	16.3	415	1	US-08-073-531B-1	Sequence 1, Appli
437	342.5	16.6	810	6	5200340-8	Sequence 1, Appli	510	336	16.3	415	2	US-08-766-288-1	Sequence 1, Appli
438	342.5	16.6	810	6	5200340-8	Sequence 1, Appli	511	336	16.3	790	4	US-08-991-761A-13	Sequence 13, Appl
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440	342	16.6	273	2	US-09-016-366A-19	Sequence 19, Appl	513	334.5	16.2	316	4	US-09-387-375-9	Sequence 9, Appli
441	342	16.6	273	2	US-08-978-404B-14	Sequence 14, Appl	514	334.5	16.2	316	4	US-10-041-400A-9	Sequence 9, Appli
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443	341.5	16.5	261	6	5270178-19	Sequence 6, Appli	516	334.5	16.2	446	4	US-10-177-661-4	Sequence 4, Appli
444	341.5	16.5	261	6	5270178-20	Sequence 6, Appli	517	334.5	16.2	477	4	US-10-177-661-2	Sequence 2, Appli
445	341.5	16.5	261	6	5270178-19	Sequence 6, Appli	518	334.5	16.2	562	4	US-09-879-792-12	Sequence 12, Appl
446	341.5	16.5	261	6	5270178-20	Sequence 6, Appli	519	333.5	16.1	290	4	US-09-386-653A-7	Sequence 7, Appli
447	341	16.5	261	6	5270178-21	Sequence 6, Appli	520	333.5	16.1	302	3	US-09-220-731-26	Sequence 26, Appl
448	341	16.5	261	6	5270178-21	Sequence 6, Appli	521	333.5	16.1	302	4	US-09-242-999-22	Sequence 22, Appl
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450	340.5	16.5	230	1	US-08-456-840-47	Sequence 47, Appl	523	333	16.1	415	2	US-08-955-471-2	Sequence 2, Appli

524	333	16.1	415	5	PCT-US92-10242-2	Sequence 2, Appli	597	324.5	15.7	461	4	US-09-949-016-8839	Sequence 8839, Ap
525	332.5	16.1	638	2	US-08-681-151-3	Sequence 3, Appli	598	324.5	15.7	466	1	US-07-882-202A-4	Sequence 4, Appli
526	332.5	16.1	810	1	US-08-991-761A-11	Sequence 11, Appl	599	324.5	15.7	466	1	US-08-021-615A-4	Sequence 4, Appli
527	331	16.0	295	3	US-08-338-368-2	Sequence 2, Appli	600	324.5	15.7	466	1	US-08-321-777-4	Sequence 4, Appli
528	331	16.0	579	1	US-08-295-411-4	Sequence 4, Appli	601	324.5	15.7	466	1	US-09-009-217-14	Sequence 14, Appl
529	331	16.0	579	2	US-08-955-471-4	Sequence 4, Appli	602	324.5	15.7	466	3	US-09-009-656-14	Sequence 14, Appl
530	331	16.0	579	3	US-09-117-708-14	Sequence 14, Appl	603	324.5	15.7	466	5	PCT-US93-04493-4	Sequence 4, Appli
531	331	16.0	579	5	PCT-US92-10242-4	Sequence 4, Appli	604	324.5	15.7	483	4	US-09-949-016-9523	Sequence 17, Appl
532	331	16.0	615	1	US-07-998-972A-3	Sequence 3, Appli	605	323.5	15.7	275	2	US-09-016-366A-17	Sequence 17, Appl
533	331	16.0	615	1	US-08-463-953-3	Sequence 3, Appli	606	323.5	15.7	275	2	US-08-978-404B-12	Sequence 12, Appl
534	331	16.0	615	1	US-08-462-261-3	Sequence 3, Appli	607	322.5	15.6	255	2	US-09-027-337-7	Sequence 7, Appli
535	331	16.0	615	5	PCT-US92-11357-3	Sequence 3, Appli	608	322.5	15.6	255	4	US-09-644-600-7	Sequence 7, Appli
536	331	16.0	622	3	US-08-952-967-8	Sequence 8, Appli	609	322.5	15.6	255	4	US-09-654-600A-7	Sequence 7, Appli
537	331	16.0	622	4	US-09-054-272-42	Sequence 42, Appl	610	322.5	15.6	560	4	US-09-912-559-4	Sequence 4, Appli
538	330.5	16.0	560	4	US-09-949-016-6458	Sequence 6458, Ap	611	322	15.6	207	4	US-10-000-483-54	Sequence 54, Appl
539	330.5	16.0	560	4	US-09-912-559-3	Sequence 3, Appli	612	321.5	15.6	418	4	US-10-177-661-6	Sequence 6, Appli
540	330	16.0	221	3	US-08-944-483-54	Sequence 54, Appl	613	321.5	15.6	809	4	US-08-991-761A-9	Sequence 9, Appli
541	330	16.0	222	1	US-08-456-840-46	Sequence 46, Appl	614	321	15.5	248	2	US-08-851-974-3	Sequence 3, Appli
542	330	16.0	222	1	US-08-266-407A-46	Sequence 46, Appl	615	321	15.5	248	2	US-09-213-390-3	Sequence 3, Appli
543	330	16.0	222	1	US-08-892-544-46	Sequence 46, Appl	616	321	15.5	269	2	US-08-978-404B-10	Sequence 10, Appl
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545	330	16.0	222	6	5223425-6	Patent No. 5223425	618	321	15.5	300	1	US-08-448-937A-1	Sequence 1, Appli
546	329.5	15.9	230	4	US-09-601-318-3	Sequence 3, Appli	619	321	15.5	315	4	US-09-386-653A-9	Sequence 9, Appli
547	329.5	15.9	283	4	US-09-244-111-2	Sequence 2, Appli	620	321	15.5	655	1	US-08-148-910-12	Sequence 12, Appl
548	329.5	15.9	285	4	US-09-023-942A-26	Sequence 26, Appl	621	321	15.5	655	1	US-08-448-937A-12	Sequence 12, Appl
549	329.5	15.9	376	2	US-08-558-269-10	Sequence 10, Appl	622	320.5	15.5	254	3	US-08-944-483-50	Sequence 50, Appl
550	329.5	15.9	376	3	US-09-410-882-10	Sequence 10, Appl	623	319.5	15.5	240	1	US-08-278-091-11	Sequence 11, Appl
551	329	15.9	259	3	US-08-944-483-52	Sequence 52, Appl	624	319.5	15.5	240	1	US-08-483-859-11	Sequence 11, Appl
552	328.5	15.9	238	3	US-08-944-483-64	Sequence 64, Appl	625	319.5	15.5	240	1	US-08-472-173-11	Sequence 11, Appl
553	328.5	15.9	338	4	US-08-991-761A-10	Sequence 10, Appl	626	319.5	15.5	240	2	US-08-487-167-11	Sequence 11, Appl
554	328	15.9	255	1	US-08-650-129-5	Sequence 5, Appli	627	319.5	15.5	240	2	US-08-482-816-11	Sequence 11, Appl
555	328	15.9	255	3	US-08-984-417-5	Sequence 5, Appli	628	319.5	15.5	240	2	US-08-296-149-11	Sequence 11, Appl
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557	328	15.9	717	4	US-09-949-016-11182	Sequence 11182, A	630	319.5	15.5	240	2	US-08-615-271-11	Sequence 11, Appl
558	327.5	15.9	151	3	US-09-518-046-21	Sequence 21, Appl	631	319.5	15.5	240	3	US-09-074-660-11	Sequence 11, Appl
559	327.5	15.9	154	3	US-09-261-416-7	Sequence 7, Appli	632	319.5	15.5	240	3	US-09-074-669-11	Sequence 11, Appl
560	327	15.8	241	3	US-08-944-483-60	Sequence 60, Appl	633	319.5	15.5	240	3	US-09-106-468-11	Sequence 11, Appl
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562	325.5	15.8	261	3	US-08-163-919A-2	Sequence 2, Appli	635	319.5	15.5	240	3	US-09-106-467-11	Sequence 11, Appl
563	325.5	15.8	261	4	US-08-462-515-2	Sequence 2, Appli	636	318.5	15.4	234	4	US-09-513-999C-7815	Sequence 7815, Ap
564	325.5	15.8	261	5	PCT-US94-14073-2	Sequence 2, Appli	637	318	15.4	295	4	US-10-163-442-3	Sequence 3, Appli
565	325.5	15.8	492	1	US-08-469-486-2	Sequence 2, Appli	638	317.5	15.4	245	3	US-08-944-483-69	Sequence 69, Appl
566	325.5	15.8	492	2	US-08-469-658-2	Sequence 2, Appli	639	317	15.3	232	3	US-08-944-483-45	Sequence 45, Appl
567	325	15.7	226	1	US-08-650-129-4	Sequence 4, Appli	640	317	15.3	295	4	US-10-165-442-1	Sequence 1, Appli
568	325	15.7	226	3	US-08-984-417-4	Sequence 4, Appli	641	316.5	15.3	226	1	US-07-929-198-2	Sequence 2, Appli
569	324.5	15.7	228	1	US-08-278-091-10	Sequence 10, Appl	642	316.5	15.3	226	1	US-07-929-198-6	Sequence 6, Appli
570	324.5	15.7	228	1	US-08-483-859-10	Sequence 10, Appl	643	316.5	15.3	226	2	US-08-557-146-15	Sequence 15, Appl
571	324.5	15.7	228	1	US-08-472-173-10	Sequence 10, Appl	644	316.5	15.3	226	2	US-09-154-344-15	Sequence 15, Appl
572	324.5	15.7	228	2	US-08-487-167-10	Sequence 10, Appl	645	316.5	15.3	226	3	US-08-944-483-43	Sequence 43, Appl
573	324.5	15.7	228	2	US-08-483-816-10	Sequence 10, Appl	646	316	15.3	246	3	US-08-906-769-127	Sequence 127, App
574	324.5	15.7	228	2	US-08-296-149-10	Sequence 10, Appl	647	316	15.3	246	3	US-08-906-616-127	Sequence 127, App
575	324.5	15.7	228	2	US-08-801-499-10	Sequence 10, Appl	648	316	15.3	246	3	US-08-639-075A-127	Sequence 127, App
576	324.5	15.7	228	2	US-08-615-271-10	Sequence 10, Appl	649	316	15.3	246	3	US-09-012-431-127	Sequence 127, App
577	324.5	15.7	228	3	US-09-074-660-10	Sequence 10, Appl	650	316	15.3	246	3	US-09-012-692-127	Sequence 127, App
578	324.5	15.7	228	3	US-09-074-659-10	Sequence 10, Appl	651	316	15.3	246	3	US-08-906-613-127	Sequence 127, App
579	324.5	15.7	228	3	US-09-106-468-10	Sequence 10, Appl	652	316	15.3	259	4	US-10-165-442-4	Sequence 4, Appli
580	324.5	15.7	228	3	US-09-106-466A-10	Sequence 10, Appl	653	315.5	15.3	254	3	US-09-578-303-5	Sequence 5, Appli
581	324.5	15.7	228	3	US-09-106-467-10	Sequence 10, Appl	654	315.5	15.3	292	4	US-09-578-303-5	Sequence 5, Appli
582	324.5	15.7	406	1	US-08-293-778-24	Sequence 24, Appl	655	315.5	15.3	300	3	US-08-705-875A-4	Sequence 4, Appli
583	324.5	15.7	406	1	US-08-295-411-5	Sequence 5, Appli	656	315.5	15.3	300	3	US-09-220-731-21	Sequence 21, Appl
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585	324.5	15.7	406	4	US-09-782-587B-1	Sequence 1, Appli	658	315.5	15.3	487	1	US-08-469-486-53	Sequence 53, Appl
586	324.5	15.7	406	4	US-09-782-587B-3	Sequence 3, Appli	659	315.5	15.3	487	2	US-08-469-658-53	Sequence 53, Appl
587	324.5	15.7	406	5	PCT-US92-10242-5	Sequence 5, Appli	660	315	15.2	259	4	US-10-165-442-2	Sequence 2, Appli
588	324.5	15.7	444	1	US-08-475-845-2	Sequence 2, Appli	661	315	15.2	691	4	US-09-949-016-7775	Sequence 7775, Ap
589	324.5	15.7	444	2	US-08-327-690-2	Sequence 2, Appli	662	314	15.2	855	2	US-09-027-337-2	Sequence 2, Appli
590	324.5	15.7	444	2	US-08-660-289-2	Sequence 2, Appli	663	314	15.2	855	4	US-09-644-600-2	Sequence 2, Appli
591	324.5	15.7	444	2	US-08-537-807-2	Sequence 2, Appli	664	314	15.2	855	4	US-09-654-600A-2	Sequence 2, Appli
592	324.5	15.7	444	2	US-08-871-003-2	Sequence 2, Appli	665	313.5	15.2	226	1	US-07-929-198-4	Sequence 4, Appli
593	324.5	15.7	444	3	US-08-464-233-2	Sequence 2, Appli	666	312.5	15.1	242	4	US-09-954-392-34	Sequence 34, Appl
594	324.5	15.7	444	3	US-08-189-607-2	Sequence 2, Appli	667	312	15.1	248	3	US-08-944-483-71	Sequence 71, Appl
595	324.5	15.7	444	3	US-09-378-907-2	Sequence 2, Appli	668	311.5	15.1	251	3	US-08-944-483-47	Sequence 47, Appl
596	324.5	15.7	444	5	PCT-US94-05779-2	Sequence 2, Appli	669	311	15.1	383	2	US-08-558-269-6	Sequence 6, Appli

670	311	15.1	383	3	US-09-410-882-6	Sequence 6, Appli	743	304	14.7	355	6	5223256-1	Patent No. 5223256
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672	311	15.1	798	4	US-08-794-042-2	Sequence 2, Appli	745	304	14.7	356	1	US-08-427-640-4	Sequence 4, Appli
673	311	15.1	798	5	PCT-US94-00616-2	Sequence 2, Appli	746	304	14.7	356	1	US-08-427-640-8	Sequence 8, Appli
674	311	15.1	812	4	US-09-192-012-9	Sequence 9, Appli	747	304	14.7	378	3	US-09-553-498-10	Sequence 10, Appli
675	311	15.1	1042	4	US-09-959-392-2	Sequence 2, Appli	748	304	14.7	378	4	US-09-618-869-10	Sequence 10, Appli
676	310.5	15.0	247	2	US-08-978-404B-47	Sequence 47, Appli	749	304	14.7	433	4	US-09-949-016-8220	Sequence 8220, Ap
677	310.5	15.0	314	4	US-09-636-382A-2	Sequence 2, Appli	750	304	14.7	472	2	US-08-811-949-63	Sequence 63, Appli
678	309.5	15.0	241	4	US-09-657-986B-2	Sequence 2, Appli	751	304	14.7	527	1	US-07-609-510B-16	Sequence 16, Appli
679	309.5	15.0	492	4	US-09-685-166A-895	Sequence 895, App	752	304	14.7	527	4	US-09-612-314A-51	Sequence 51, Appli
680	309.5	15.0	492	4	US-09-789-752-14	Sequence 14, Appli	753	304	14.7	527	5	PCT-US91-01025A-2	Sequence 2, Appli
681	309.5	15.0	492	4	US-09-679-426-895	Sequence 895, App	754	304	14.7	527	6	5185259-8	Patent No. 5185259
682	309.5	15.0	492	4	US-09-759-143-895	Sequence 895, App	755	304	14.7	527	6	5185259-8	Patent No. 5185259
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685	308.5	14.9	317	4	US-09-386-629-7	Sequence 7, Appli	758	304	14.7	562	4	US-08-883-795A-38	Sequence 38, Appli
686	308.5	14.9	317	4	US-09-907-794A-263	Sequence 263, App	759	304	14.7	562	4	US-09-703-695A-4	Sequence 4, Appli
687	308.5	14.9	317	4	US-09-905-125A-263	Sequence 263, App	760	304	14.7	562	4	US-10-443-701-4	Sequence 4, Appli
688	308.5	14.9	317	4	US-09-902-775A-263	Sequence 263, App	761	304	14.7	562	6	5185259-3	Patent No. 5185259
689	308.5	14.9	317	4	US-09-906-700-263	Sequence 263, App	762	304	14.7	562	6	5200340-2	Patent No. 5200340
690	308.5	14.9	317	4	US-09-903-603A-263	Sequence 263, App	763	304	14.7	562	6	5244676-5	Patent No. 5244676
691	308.5	14.9	317	4	US-09-904-920A-263	Sequence 263, App	764	304	14.7	562	6	5344773-2	Patent No. 5344773
692	308.5	14.9	317	4	US-09-908-084-263	Sequence 263, App	765	304	14.7	562	6	5185259-3	Patent No. 5185259
693	308.5	14.9	317	4	US-09-906-381A-263	Sequence 263, App	766	304	14.7	562	6	5200340-2	Patent No. 5200340
694	308.5	14.9	317	4	US-09-906-618-263	Sequence 263, App	767	304	14.7	562	6	5244676-5	Patent No. 5244676
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713	305	14.8	247	2	US-08-851-974-4	Sequence 4, Appli	786	302	14.6	389	2	US-08-811-949-65	Sequence 65, Appli
714	305	14.8	247	2	US-09-213-390-1	Sequence 1, Appli	787	302	14.6	477	2	US-08-560-098A-51	Sequence 51, Appli
715	305	14.8	247	2	US-09-213-390-4	Sequence 4, Appli	788	302	14.6	527	4	US-09-600-985-2	Sequence 2, Appli
716	305	14.8	247	4	US-09-949-016-6457	Sequence 6457, Ap	789	302	14.6	527	4	US-09-600-985-3	Sequence 3, Appli
717	305	14.8	255	3	US-08-944-483-67	Sequence 67, Appli	790	301.5	14.6	226	3	US-08-944-483-41	Sequence 41, Appli
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719	304.5	14.7	258	3	US-09-004-731-16	Sequence 16, Appli	792	301	14.6	527	6	5520913-1	Patent No. 5520913
720	304.5	14.7	258	3	US-09-004-731-19	Sequence 19, Appli	793	301	14.6	527	6	5520913-1	Patent No. 5520913
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727	304.5	14.7	492	3	US-09-342-749-2	Sequence 2, Appli	800	297	14.4	253	2	US-09-027-337-8	Sequence 8, Appli
728	304.5	14.7	492	4	US-09-691-840-2	Sequence 2, Appli	801	297	14.4	253	4	US-09-644-600-8	Sequence 8, Appli
729	304.5	14.7	492	4	US-09-759-143-932	Sequence 932, App	802	297	14.4	253	4	US-09-654-600A-8	Sequence 8, Appli
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733	304	14.7	268	4	US-09-613-822B-2	Sequence 2, Appli	806	297	14.4	393	2	US-09-560-098A-44	Sequence 44, Appli
734	304	14.7	327	4	US-09-386-629-8	Sequence 8, Appli	807	297	14.4	521	4	US-09-949-016-11081	Sequence 11081, A
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738	304	14.7	355	1	US-08-427-640-6	Sequence 6, Appli	811	296.5	14.4	224	1	US-08-483-859-12	Sequence 12, Appli
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740	304	14.7	355	1	US-08-217-616-1	Sequence 1, Appli	813	296.5	14.4	224	2	US-08-487-167-12	Sequence 12, Appli
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742	304	14.7	355	3	US-08-794-528-1	Sequence 1, Appli	815	296.5	14.4	224	2	US-08-296-149-12	Sequence 12, Appli

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817	296.5	14.4	224	2	US-08-615-271-12	Sequence 12, Appl	890	286.5	13.9	228	4	US-09-004-729-10	Sequence 10, Appl
818	296.5	14.4	224	2	US-09-074-660-12	Sequence 12, Appl	891	284.5	13.8	225	3	US-09-004-731-13	Sequence 13, Appl
819	296.5	14.4	224	3	US-09-074-659-12	Sequence 12, Appl	892	284.5	13.8	225	4	US-08-749-699-13	Sequence 13, Appl
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822	296.5	14.4	224	3	US-09-106-467-12	Sequence 12, Appl	895	284.5	13.8	225	3	US-08-906-616-83	Sequence 83, Appl
823	296.5	14.4	224	2	US-08-560-098A-49	Sequence 49, Appl	896	284.5	13.8	225	3	US-08-817-795-83	Sequence 83, Appl
824	296.5	14.4	276	4	US-09-880-503-5	Sequence 5, Appl	897	284.5	13.8	225	3	US-08-639-075A-83	Sequence 83, Appl
825	296.5	14.4	306	2	US-08-560-098A-45	Sequence 45, Appl	898	284.5	13.8	225	3	US-09-012-431-83	Sequence 83, Appl
826	296.5	14.4	331	2	US-08-560-098A-46	Sequence 46, Appl	899	284.5	13.8	225	3	US-09-012-692-83	Sequence 83, Appl
827	296.5	14.4	365	1	US-08-093-741-83	Sequence 83, Appl	900	284.5	13.8	225	3	US-08-906-613-83	Sequence 83, Appl
828	296.5	14.4	365	1	US-08-720-012-83	Sequence 83, Appl	901	284.5	13.8	225	5	PCT-US95-14442A-83	Sequence 83, Appl
829	296.5	14.4	393	3	US-08-967-024C-24	Sequence 24, Appl	902	283.5	13.7	268	3	US-09-032-215-42	Sequence 42, Appl
830	296.5	14.4	393	3	US-08-967-024C-25	Sequence 25, Appl	903	282.5	13.7	144	4	US-09-618-259-4	Sequence 4, Appl
831	296.5	14.4	403	4	US-09-880-503-6	Sequence 6, Appl	904	282	13.6	244	3	US-08-944-483-74	Sequence 74, Appl
832	296.5	14.4	411	1	US-08-087-163-1	Sequence 1, Appl	905	279	13.5	488	4	US-09-367-777-44	Sequence 44, Appl
833	296.5	14.4	411	1	US-08-286-748B-18	Sequence 18, Appl	906	279	13.5	488	4	US-09-367-791A-27	Sequence 27, Appl
834	296.5	14.4	411	1	US-08-153-799-18	Sequence 18, Appl	907	279	13.5	902	4	US-09-644-600-10	Sequence 10, Appl
835	296.5	14.4	411	2	US-08-560-098A-48	Sequence 48, Appl	908	279	13.5	902	4	US-09-654-600A-10	Sequence 10, Appl
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837	296.5	14.4	430	6	5219569-2	Patent No. 5219569	910	278	13.5	306	1	US-08-474-042-1	Sequence 1, Appl
838	296.5	14.4	430	6	5219569-2	Patent No. 5219569	911	278	13.5	306	1	US-08-484-558-1	Sequence 1, Appl
839	296.5	14.4	431	4	US-09-101-272G-1	Sequence 1, Appl	912	278	13.5	306	1	US-08-774-592-1	Sequence 1, Appl
840	296.5	14.4	431	6	5188829-1	Patent No. 5188829	913	278	13.5	437	1	US-08-487-037-2	Sequence 2, Appl
841	296.5	14.4	431	6	5188829-1	Patent No. 5188829	914	278	13.5	448	1	US-08-295-411-3	Sequence 3, Appl
842	296.5	14.4	432	2	US-08-560-098A-47	Sequence 47, Appl	915	278	13.5	448	1	US-08-955-471-3	Sequence 3, Appl
843	296	14.3	269	4	US-09-715-994-2	Sequence 2, Appl	916	278	13.5	448	5	PCT-US92-10068-1	Sequence 1, Appl
844	295.5	14.3	283	3	US-08-807-151-1	Sequence 1, Appl	917	278	13.5	448	5	PCT-US92-10242-3	Sequence 3, Appl
845	295.5	14.3	283	3	US-09-478-957-1	Sequence 1, Appl	918	278	13.5	488	1	US-08-487-037-1	Sequence 1, Appl
846	295.5	14.3	454	3	US-09-518-046-2	Sequence 2, Appl	919	278	13.5	488	1	US-08-487-037-1	Sequence 1, Appl
847	294	14.2	256	3	US-09-032-215-32	Sequence 32, Appl	920	277.5	13.4	242	3	US-09-949-016-9524	Sequence 524, Ap
848	293.5	14.2	239	3	US-08-944-483-61	Sequence 61, Appl	921	276	13.4	254	1	US-08-330-978-3	Sequence 3, Appl
849	293.5	14.2	411	4	US-09-403-736-2	Sequence 2, Appl	922	276	13.4	254	1	US-08-474-042-3	Sequence 3, Appl
850	293.5	14.2	430	1	US-07-942-157A-3	Sequence 3, Appl	923	276	13.4	254	1	US-08-484-558-3	Sequence 3, Appl
851	292	14.1	235	2	US-08-557-146-14	Sequence 14, Appl	924	276	13.4	254	1	US-08-484-558-4	Sequence 4, Appl
852	292	14.1	235	2	US-09-154-344-14	Sequence 14, Appl	925	274.5	13.3	211	3	US-09-220-731-25	Sequence 25, Appl
853	292	14.1	235	3	US-08-944-483-42	Sequence 42, Appl	926	274.5	13.3	211	4	US-09-242-999-20	Sequence 20, Appl
854	292	14.1	237	3	US-09-004-731-22	Sequence 22, Appl	927	274	13.3	241	1	US-08-330-978-4	Sequence 4, Appl
855	292	14.1	237	3	US-08-749-699-22	Sequence 22, Appl	928	274	13.3	241	1	US-08-474-042-4	Sequence 4, Appl
856	292	14.1	237	4	US-09-004-729-22	Sequence 22, Appl	929	274	13.3	241	1	US-08-484-558-4	Sequence 4, Appl
857	292	14.1	256	3	US-08-906-769-89	Sequence 89, Appl	930	274	13.3	241	1	US-08-774-592-4	Sequence 4, Appl
858	292	14.1	256	3	US-08-906-616-89	Sequence 89, Appl	931	273	13.2	251	3	US-08-944-483-28	Sequence 28, Appl
859	292	14.1	256	3	US-08-817-795-89	Sequence 89, Appl	932	272	13.2	253	3	US-08-906-769-91	Sequence 131, App
860	292	14.1	256	3	US-08-639-075A-89	Sequence 89, Appl	933	272	13.2	253	3	US-08-906-616-131	Sequence 131, App
861	292	14.1	256	3	US-09-012-431-89	Sequence 89, Appl	934	272	13.2	253	3	US-08-639-075A-131	Sequence 131, App
862	292	14.1	256	3	US-09-012-692-89	Sequence 89, Appl	935	272	13.2	253	3	US-09-012-431-131	Sequence 131, App
863	292	14.1	256	3	US-08-906-613-89	Sequence 89, Appl	936	272	13.2	253	3	US-09-012-692-131	Sequence 131, App
864	292	14.1	256	5	PCT-US95-14442A-89	Sequence 89, Appl	937	272	13.2	253	3	US-08-906-613-131	Sequence 131, App
865	292	14.1	414	4	US-09-270-767-46426	Sequence 46426, A	938	271.5	13.1	256	4	US-08-395-456C-23	Sequence 23, Appl
866	291.5	14.1	242	3	US-08-944-483-57	Sequence 57, Appl	939	271.5	13.1	256	4	US-08-487-453A-23	Sequence 23, Appl
867	291.5	14.1	253	3	US-08-944-483-73	Sequence 73, Appl	940	270.5	13.1	256	4	US-09-949-016-6271	Sequence 6271, Ap
868	291	14.1	416	2	US-09-000-846-2	Sequence 2, Appl	941	270	13.1	437	1	US-09-902-540-9796	Sequence 9796, Ap
869	290	14.0	235	3	US-08-807-151-3	Sequence 3, Appl	942	267.5	12.9	266	3	US-08-487-037-3	Sequence 3, Appl
870	290	14.0	235	3	US-09-478-957-3	Sequence 3, Appl	943	267.5	12.9	266	3	US-09-004-731-24	Sequence 24, Appl
871	289	14.0	223	1	US-07-956-848A-41	Sequence 41, Appl	944	267.5	12.9	266	3	US-08-749-699-24	Sequence 24, Appl
872	289	14.0	223	1	US-08-471-956-41	Sequence 41, Appl	945	266.5	12.9	256	4	US-09-949-016-6271	Sequence 6271, Ap
873	289	14.0	583	4	US-09-976-594-837	Sequence 837, App	946	266	12.9	352	4	US-08-230-428B-4	Sequence 48, Appl
874	288.5	14.0	255	3	US-08-906-769-91	Sequence 91, Appl	947	265.5	12.9	197	1	US-08-456-840-48	Sequence 48, Appl
875	288.5	14.0	255	3	US-08-906-616-91	Sequence 91, Appl	948	265.5	12.9	197	1	US-08-266-407A-48	Sequence 48, Appl
876	288.5	14.0	255	3	US-08-817-795-91	Sequence 91, Appl	949	265.5	12.9	197	2	US-08-892-544-48	Sequence 48, Appl
877	288.5	14.0	255	3	US-08-639-075A-91	Sequence 91, Appl	950	264.5	12.8	248	2	US-08-491-204A-18	Sequence 18, Appl
878	288.5	14.0	255	3	US-09-012-431-91	Sequence 91, Appl	951	264.5	12.8	248	2	US-08-238-130-2	Sequence 2, Appl
879	288.5	14.0	255	3	US-09-012-692-91	Sequence 91, Appl	952	264.5	12.8	248	2	US-08-921-426-4	Sequence 4, Appl
880	288.5	14.0	255	3	US-08-906-613-91	Sequence 91, Appl	953	264.5	12.8	248	2	US-08-815-915-4	Sequence 4, Appl
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882	288	13.9	268	1	US-08-270-584A-2	Sequence 2, Appl	955	264.5	12.8	249	3	US-09-578-303-2	Sequence 2, Appl
883	288	13.9	268	2	US-08-765-192-2	Sequence 2, Appl	956	264.5	12.8	251	4	US-09-949-016-6112	Sequence 6112, Ap
884	288	13.9	267	3	US-09-199-793-2	Sequence 2, Appl	957	264.5	12.8	250	4	US-09-949-016-9690	Sequence 9690, Ap
885	287	13.9	228	3	US-08-944-483-40	Sequence 40, Appl	958	264	12.8	255	3	US-08-944-483-68	Sequence 68, Appl
886	287	13.9	407	3	US-09-734-675-4	Sequence 4, Appl	959	263	12.7	252	3	US-08-906-769-103	Sequence 103, App
887	286.5	13.9	218	3	US-09-578-303-3	Sequence 3, Appl	960	263	12.7	252	3	US-08-906-616-103	Sequence 103, App
888	286.5	13.9	228	3	US-09-004-731-10	Sequence 10, Appl	961	263	12.7	252	3	US-08-817-795-103	Sequence 103, App

962	263	12.7	252	3	US-08-639-075A-103	Sequence 103, App	1035	227	11.0	258	4	US-09-023-942A-8	Sequence 8, Appli
963	263	12.7	252	3	US-09-012-431-103	Sequence 103, App	1036	227	11.0	259	3	US-08-906-769-190	Sequence 190, App
964	263	12.7	252	3	US-09-012-692-103	Sequence 103, App	1037	227	11.0	259	3	US-08-906-616-190	Sequence 190, App
965	263	12.7	252	3	US-08-906-613-103	Sequence 103, App	1038	227	11.0	259	3	US-08-639-075A-190	Sequence 190, App
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967	262.5	12.7	222	1	US-07-969-931-9	Sequence 9, Appli	1040	227	11.0	259	3	US-09-012-431-190	Sequence 190, App
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972	262.5	12.7	233	3	US-09-004-729-27	Sequence 27, Appli	1045	227	11.0	259	3	US-08-700-5190-18	Sequence 18, Appli
973	258.5	12.5	255	4	US-09-270-767-44361	Sequence 44361, A	1046	226.5	11.0	215	6	US-08-700-5190-18	Sequence 18, Appli
974	257.5	12.5	224	1	US-08-553-516-2	Sequence 2, Appli	1047	226.5	11.0	215	6	5180819-2	Patent No. 5180819
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976	256	12.4	267	3	US-08-906-616-145	Sequence 145, App	1049	226	10.9	697	2	US-08-167-641C-50	Sequence 50, Appli
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1018	245	11.9	228	2	US-08-766-982-11	Sequence 11, Appli	1091	219	10.6	223	3	US-08-906-769-141	Sequence 141, App
1019	245	11.9	228	3	US-08-944-483-55	Sequence 55, Appli	1092	216	10.5	185	3	US-08-906-616-141	Sequence 141, App
1020	245	11.9	228	3	US-09-296-219-11	Sequence 11, Appli	1093	216	10.5	185	3	US-08-639-075A-141	Sequence 141, App
1021	244.5	11.8	304	3	US-09-088-651-2	Sequence 2, Appli	1094	216	10.5	185	3	US-09-012-431-141	Sequence 141, App
1022	242	11.7	214	6	5180819-3	Patent No. 5180819	1095	216	10.5	185	3	US-09-012-692-141	Sequence 141, App
1023	242	11.7	214	6	5180819-3	Patent No. 5180819	1096	216	10.5	185	3	US-08-906-613-141	Sequence 141, App
1024	242	11.7	455	3	US-09-261-416-2	Sequence 2, Appli	1097	216	10.5	185	3	US-08-906-613-141	Sequence 141, App
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1029	232.5	11.3	185	4	US-09-242-999-5	Sequence 5, Appli	1102	211	10.2	223	2	US-08-482-130C-17	Sequence 17, Appli
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1109	211	10.2	224	3	US-08-639-075A-17	Sequence 17, Appl	1182	168	8.1	141	3	US-08-906-613-135	Sequence 135, App
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1116	206	10.0	250	4	US-09-270-767-33709	Sequence 33709, A	1189	165	8.0	198	3	US-08-906-616-133	Sequence 133, App
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1121	204.5	9.9	178	3	US-08-639-075A-107	Sequence 107, App	1194	163	7.9	190	2	US-08-845-998-4	Sequence 4, Appl
1122	204.5	9.9	178	3	US-09-012-431-107	Sequence 107, App	1195	163	7.9	190	3	US-09-206-537-4	Sequence 4, Appl
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1124	204.5	9.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	7.8	178	3	US-09-220-731-24	Sequence 24, Appl
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1129	199.5	9.7	254	3	US-08-906-616-129	Sequence 129, App	1202	159	7.7	190	3	US-09-206-537-6	Sequence 6, Appl
1130	199.5	9.7	254	3	US-08-639-075A-129	Sequence 129, App	1203	159	7.7	190	3	US-09-430-854-6	Sequence 6, Appl
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1145	191	9.2	138	6	5200340-4	Patent No. 5200340	1218	154.5	7.5	204	3	US-08-906-616-147	Sequence 147, App
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1148	187	9.1	312	4	US-09-636-382A-15	Sequence 15, Appl	1221	154.5	7.5	204	3	US-09-012-692-147	Sequence 147, App
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1152	182	8.8	145	3	US-08-906-769-123	Sequence 123, App	1225	153.5	7.4	151	4	US-09-270-767-48395	Sequence 48395, A
1153	182	8.8	145	3	US-08-906-616-123	Sequence 123, App	1226	153.5	7.5	3122	4	US-10-237-551-201	Sequence 201, App
1154	182	8.8	145	3	US-08-639-075A-123	Sequence 123, App	1227	153.5	7.5	3122	4	US-10-237-551-250	Sequence 250, App
1155	182	8.8	145	3	US-09-012-692-123	Sequence 123, App	1228	152.5	7.4	139	4	US-09-270-767-33648	Sequence 33648, A
1156	182	8.8	145	3	US-08-906-613-123	Sequence 123, App	1229	152.5	7.4	200	3	US-09-008-271A-5	Sequence 5, Appl
1157	182	8.8	346	4	US-09-949-016-9000	Sequence 9000, Ap	1230	151.5	7.4	425	4	US-09-252-991A-31834	Sequence 31834, A
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1159	181	8.8	133	4	US-09-949-016-7471	Sequence 7471, Ap	1232	151	7.4	328	4	US-09-253-991A-24003	Sequence 24003, A
1160	180	8.7	144	3	US-09-012-431-123	Sequence 123, App	1233	150.5	7.3	79	4	US-09-270-767-33666	Sequence 33666, A
1161	180	8.7	348	4	US-09-949-016-6979	Sequence 6979, Ap	1234	150.5	7.3	79	4	US-09-270-767-48883	Sequence 48883, A
1162	178.5	8.6	164	3	US-09-020-956-178	Sequence 178, App	1235	150	7.4	595	4	US-09-370-838-187	Sequence 187, App
1163	178.5	8.6	164	3	US-09-030-607-178	Sequence 178, App	1236	150	7.4	595	4	US-09-854-133-187	Sequence 187, App
1164	178.5	8.6	164	3	US-09-439-313-178	Sequence 178, App	1237	150	7.3	2508	4	US-09-627-650B-7	Sequence 7, Appl
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1168	178.5	8.6	164	4	US-09-636-215-178	Sequence 178, App	1241	150	7.3	2601	4	US-09-627-650B-9	Sequence 9, Appl
1169	178.5	8.6	164	4	US-09-685-166A-178	Sequence 178, App	1242	150	7.2	2601	4	US-09-436-063C-9	Sequence 9, Appl
1170	178.5	8.6	164	4	US-09-115-453-178	Sequence 178, App	1243	149	7.3	77	3	US-09-439-313-329	Sequence 329, App
1171	178.5	8.6	164	4	US-09-688-489-178	Sequence 178, App	1244	149	7.2	77	3	US-09-352-616A-329	Sequence 329, App
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1173	178.5	8.6	164	4	US-09-759-143-178	Sequence 178, App	1246	149	7.2	77	4	US-09-636-215-329	Sequence 329, App
1174	178.5	8.6	164	4	US-09-651-236-178	Sequence 178, App	1247	149	7.2	77	4	US-09-685-166A-329	Sequence 329, App
1175	175.5	8.5	481	4	US-09-949-016-9748	Sequence 9748, Ap	1248	149	7.2	77	4	US-09-688-489-329	Sequence 329, App
1176	173.5	8.4	218	4	US-09-270-767-44299	Sequence 44299, A	1249	149	7.2	77	4	US-09-679-426-329	Sequence 329, App
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1178	168	8.1	141	3	US-08-906-616-135	Sequence 135, App	1251	149	7.2	77	4	US-09-651-236-329	Sequence 329, App
1179	168	8.1	141	3	US-08-639-075A-135	Sequence 135, App	1252	149	7.3	419	4	US-09-252-991A-32949	Sequence 32949, A
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c1255	145	7.1	416	4	US-09-252-991A-30923	Sequence 30923, A	1328	135.5	6.6	794	4	US-09-252-991A-28569	Sequence 28569, A
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c1259	143.5	6.9	72	3	US-08-908-769-87	Sequence 87, Appl	c1332	135	6.6	480	4	US-09-252-991A-26799	Sequence 26799, A
c1260	143.5	6.9	72	3	US-08-906-616-87	Sequence 87, Appl	c1333	135	6.6	511	4	US-09-252-991A-26078	Sequence 26078, A
c1261	143.5	6.9	72	3	US-08-817-795-87	Sequence 87, Appl	c1334	135	6.6	1000	4	US-09-252-991A-31361	Sequence 31361, A
c1262	143.5	6.9	72	3	US-08-639-075A-87	Sequence 87, Appl	1335	135	6.5	1128	4	US-09-627-063B-11	Sequence 11, Appl
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c1267	143.5	6.9	635	4	US-09-252-991A-31646	Sequence 31646, A	1340	134.5	6.5	595	4	US-09-252-991A-18995	Sequence 18995, A
c1268	143.5	6.9	772	4	US-09-252-991A-30446	Sequence 30446, A	c1341	134.5	6.5	622	4	US-09-270-767-42577	Sequence 42577, A
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c1272	142.5	6.9	208	3	US-08-639-075A-151	Sequence 151, App	c1345	134	6.6	218	4	US-09-252-991A-23272	Sequence 23272, A
c1273	142.5	6.9	208	3	US-09-012-431-151	Sequence 151, App	1346	134	6.5	251	4	US-09-252-991A-20606	Sequence 20606, A
c1274	142.5	6.9	208	3	US-09-012-692-151	Sequence 151, App	c1347	134	6.6	290	4	US-09-252-991A-27441	Sequence 27441, A
c1275	142.5	6.9	208	3	US-08-906-613-151	Sequence 151, App	1348	134	6.5	328	4	US-09-252-991A-21969	Sequence 21969, A
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c1277	142.5	6.9	798	4	US-09-252-991A-23774	Sequence 23774, A	c1350	134	6.6	352	4	US-09-252-991A-17906	Sequence 17906, A
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c1279	142	6.9	666	4	US-09-248-796A-15507	Sequence 15507, A	c1352	134	6.5	615	4	US-09-252-991A-26695	Sequence 26695, A
c1280	141.5	6.8	85	4	US-09-270-767-33231	Sequence 33231, A	c1353	134	6.6	707	4	US-09-252-991A-24045	Sequence 24045, A
c1281	141.5	6.8	85	4	US-09-270-767-48448	Sequence 48448, A	1354	134	6.5	726	4	US-09-252-991A-20675	Sequence 20675, A
c1282	141.5	6.8	802	4	US-09-823-240A-2	Sequence 2, Appl	c1355	134	6.6	748	4	US-09-252-991A-18427	Sequence 18427, A
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c1284	141	6.9	450	4	US-09-252-991A-16659	Sequence 16659, A	c1357	133.5	6.6	2294	4	US-09-252-991A-17231	Sequence 17231, A
c1285	140.5	6.8	278	4	US-09-602-777A-76	Sequence 76, Appl	c1358	133.5	6.6	351	4	US-09-252-991A-18476	Sequence 18476, A
c1286	140.5	6.8	1400	3	US-08-630-915A-37	Sequence 37, Appl	c1359	133.5	6.6	457	4	US-09-252-991A-25131	Sequence 25131, A
c1287	140.5	6.8	1400	3	US-09-879-957-37	Sequence 37, Appl	c1360	133.5	6.6	552	3	US-09-219-849-7	Sequence 7, Appl
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c1294	139	6.7	87	3	US-09-012-692-161	Sequence 161, App	1367	132.5	6.4	226	4	US-09-252-991A-20432	Sequence 20432, A
c1295	139	6.7	87	3	US-08-906-613-161	Sequence 161, App	1368	132.5	6.4	263	4	US-09-252-991A-16906	Sequence 16906, A
c1296	139	6.7	89	3	US-08-906-769-165	Sequence 165, App	1369	132.5	6.4	326	4	US-09-538-082-1019	Sequence 1019, Ap
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c1298	139	6.7	89	3	US-08-639-075A-165	Sequence 165, App	1371	132.5	6.4	343	4	US-09-949-016-11007	Sequence 11007, A
c1299	139	6.7	89	3	US-09-012-431-165	Sequence 165, App	1372	132.5	6.4	371	4	US-09-252-991A-32348	Sequence 32348, A
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c1302	139	6.7	213	4	US-09-252-991A-23426	Sequence 23426, A	1375	132.5	6.4	1461	4	US-10-142-231-86	Sequence 86, Appl
c1303	139	6.8	553	4	US-09-252-991A-17984	Sequence 17984, A	1376	132.5	6.4	1652	4	US-09-627-650B-1	Sequence 1, Appl
c1304	139	6.7	1497	4	US-09-060-854B-2	Sequence 2, Appl	1377	132.5	6.4	1652	4	US-09-436-063C-1	Sequence 1, Appl
c1305	139	6.7	1497	4	US-09-529-904-3	Sequence 3, Appl	1378	132.5	6.4	2732	4	US-09-086-436-30	Sequence 30, Appl
c1306	138.5	6.8	957	4	US-09-252-991A-20408	Sequence 20408, A	c1379	132	6.5	335	4	US-09-252-991A-24899	Sequence 24899, A
c1307	138	6.7	361	4	US-09-252-991A-24085	Sequence 24085, A	c1380	132	6.5	479	4	US-09-252-991A-32994	Sequence 32994, A
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c1311	137.5	6.7	1027	4	US-09-252-991A-17886	Sequence 17886, A	1384	132	6.4	694	4	US-09-252-991A-30396	Sequence 30396, A
c1312	137.5	6.8	1078	3	US-08-963-825-21	Sequence 21, Appl	c1385	132	6.5	720	4	US-09-252-991A-23212	Sequence 23212, A
c1313	137.5	6.8	1078	3	US-09-500-811-21	Sequence 21, Appl	1386	131.5	6.4	219	4	US-09-252-991A-19313	Sequence 19313, A
c1314	137.5	6.8	1078	3	US-09-548-608-21	Sequence 21, Appl	1387	131.5	6.4	246	4	US-09-252-991A-25102	Sequence 25102, A
c1315	137.5	6.8	1078	3	US-09-548-608-21	Sequence 21, Appl	1388	131.5	6.4	267	4	US-09-252-991A-31452	Sequence 31452, A
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c1317	137	6.7	693	4	US-09-252-991A-26071	Sequence 26071, A	c1390	131.5	6.5	442	4	US-09-252-991A-19788	Sequence 19788, A
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c1319	137	6.6	1388	4	US-09-463-048A-6	Sequence 6, Appl	1392	131.5	6.4	518	4	US-09-252-991A-25203	Sequence 25203, A
c1320	136.5	6.7	482	4	US-09-252-991A-31492	Sequence 31492, A	c1393	131.5	6.5	540	4	US-09-252-991A-22219	Sequence 22219, A
c1321	136.5	6.6	522	4	US-09-252-991A-28065	Sequence 28065, A	1394	131.5	6.4	588	4	US-09-252-991A-30690	Sequence 30690, A
c1322	136.5	6.7	763	4	US-09-252-991A-30146	Sequence 30146, A	c1395	131.5	6.5	611	4	US-09-252-991A-32402	Sequence 32402, A
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c1324	136	6.6	203	4	US-09-270-767-47748	Sequence 47748, A	c1397	131.5	6.5	1065	1	US-08-642-255-72	Sequence 72, Appl
c1325	136	6.7	312	4	US-09-252-991A-21508	Sequence 21508, A	c1398	131	6.4	391	4	US-09-252-991A-20111	Sequence 20111, A
c1326	135.5	6.6	200	4	US-09-252-991A-27257	Sequence 27257, A	c1399	131	6.4	397	4	US-09-252-991A-25695	Sequence 25695, A



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1402	131	6.3	437	4	US-09-252-991A-23739	Sequence 23739, A	Sequence 23739, A	1475	127	6.1	137	4	US-09-252-991A-23652	Sequence 23652, A
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1421	129.5	6.4	412	4	US-09-252-991A-19536	Sequence 19536, A	Sequence 19536, A	1494	126.5	6.2	513	4	US-09-252-991A-18177	Sequence 18177, A
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1423	129.5	6.4	420	4	US-09-252-991A-20033	Sequence 20033, A	Sequence 20033, A	1496	126.5	6.2	630	4	US-09-252-991A-25626	Sequence 25626, A
1424	129.5	6.3	462	4	US-09-252-991A-20410	Sequence 20410, A	Sequence 20410, A	1497	126.5	6.2	683	4	US-09-252-991A-29859	Sequence 29859, A
1425	129.5	6.3	466	4	US-09-252-991A-26545	Sequence 26545, A	Sequence 26545, A	1498	126.5	6.2	1806	4	US-09-919-497-56	Sequence 56, Appli
1426	129.5	6.4	539	4	US-09-252-991A-27717	Sequence 27717, A	Sequence 27717, A	1499	126	6.1	142	3	US-08-906-769-155	Sequence 155, App
1427	129.5	6.4	973	4	US-09-252-991A-21386	Sequence 21386, A	Sequence 21386, A	1500	126	6.1	142	3	US-08-906-616-155	Sequence 155, App
1428	129	6.3	229	4	US-09-252-991A-26254	Sequence 26254, A	Sequence 26254, A							
1429	129	6.3	366	4	US-09-252-991A-32385	Sequence 32385, A	Sequence 32385, A							
1430	129	6.3	425	4	US-09-252-991A-26326	Sequence 26326, A	Sequence 26326, A							
1431	129	6.3	437	4	US-09-252-991A-23739	Sequence 23739, A	Sequence 23739, A							
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1433	129	6.3	481	4	US-09-949-016-9748	Sequence 9748, Ap	Sequence 9748, Ap							
1434	129	6.3	516	4	US-09-252-991A-21880	Sequence 21880, A	Sequence 21880, A							
1435	129	6.2	560	4	US-09-252-991A-26107	Sequence 26107, A	Sequence 26107, A							
1436	129	6.2	623	4	US-09-949-016-6530	Sequence 6530, Ap	Sequence 6530, Ap							
1437	129	6.2	693	4	US-09-949-016-7806	Sequence 7806, Ap	Sequence 7806, Ap							
1438	129	6.3	743	4	US-09-252-991A-28327	Sequence 28327, A	Sequence 28327, A							
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1443	129	6.2	2088	4	US-09-548-373D-13	Sequence 13, Appl	Sequence 13, Appl							
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1446	129	6.2	2972	3	US-09-579-181-2	Sequence 2, Appli	Sequence 2, Appli							
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1448	128.5	6.2	231	4	US-09-252-991A-27608	Sequence 27608, A	Sequence 27608, A							
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1450	128.5	6.3	338	4	US-09-252-991A-16820	Sequence 16820, A	Sequence 16820, A							
1451	128.5	6.3	459	4	US-09-252-991A-23042	Sequence 23042, A	Sequence 23042, A							
1452	128.5	6.3	546	4	US-09-252-991A-24620	Sequence 24620, A	Sequence 24620, A							
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1454	128.5	6.3	735	4	US-09-949-016-10120	Sequence 10120, A	Sequence 10120, A							
1455	128.5	6.2	863	4	US-09-252-991A-19574	Sequence 19574, A	Sequence 19574, A							
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1457	128.5	6.3	1411	4	US-09-252-991A-28408	Sequence 28408, A	Sequence 28408, A							
1458	128	6.2	246	4	US-09-370-838-60	Sequence 60, Appl	Sequence 60, Appl							
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1463	128	6.3	421	4	US-09-252-991A-17785	Sequence 17785, A	Sequence 17785, A							
1464	128	6.3	428	4	US-09-252-991A-25955	Sequence 25955, A	Sequence 25955, A							
1465	128	6.2	462	4	US-09-252-991A-20814	Sequence 20814, A	Sequence 20814, A							
1466	128	6.3	474	4	US-09-252-991A-17459	Sequence 17459, A	Sequence 17459, A							
1467	128	6.3	478	4	US-09-252-991A-25191	Sequence 25191, A	Sequence 25191, A							
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1469	128	6.2	2142	4	US-09-538-092-1142	Sequence 1142, Ap	Sequence 1142, Ap							
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1471	127.5	6.3	426	1	US-07-918-023-2	Sequence 2, Appli	Sequence 2, Appli							
1472	127.5	6.3	539	4	US-09-252-991A-17070	Sequence 17070, A	Sequence 17070, A							

## ALIGNMENTS

## RESULT 1

US-09-949-016-6948  
; Sequence 6948, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6948  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6948

Alignment Scores:  
Pred. No.: 5,28e-101 Length: 254  
Score: 1372.50 Matches: 253  
Percent Similarity: 85.52% Conservative: 1  
Best Local Similarity: 85.19% Mismatches: 0  
Query Match: 66.43% Indels: 43  
DB: 4 Gaps: 1

US-10-015-385A-193 (1-1091) x US-09-949-016-6948 (1-254)

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QY 181 AAGATTTTCAATGGCAGCTGAGTGGGGCTGAAGTCAAGCCGTGGCAGGTGGGCTGTTT 240  
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Qy	301	GCT	CAT	CTC	AGC	GGC	GAG	CAG	GTA	CTG	GGT	TGG	CGC	CTG	GGG	GGG	AA	CA	CAG	CTC	CA	CGC	360
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Qy	361	GAC	TGG	ACC	CGA	GAG	CAT	CCG	CA	GCG	GCT	CTC	TGT	GAC	CCC	ATC	CCC	GGT	TAC	CTG	GGG	420	
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Qy	421	GCT	CTC	AGC	AGC	CA	CAG	CA	CAC	CTC	CGG	TGT	CTG	CGG	CTG	CGC	CTG	CGC	CTG	CGC	CGT	480	
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Db	161	Cys	Leu	Asn	Leu	Ser	Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	180	
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Qy	721	GGG	GGC	CCC	CTG	TGT	GTG	GGG	GAG	TCT	CTC	CA	GCT	CTG	GTG	TCT	CTG	GGG	GCT	CTG	GGG	780	
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Qy	781	CC	TGT	GG	CA	AG	AT	G	G	CAT	CC	CT	GG	AG	TCT	TAC	AC	TAT	AT	T	T	840	
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178 ilePheProGlnLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal 197  
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RESULT 5

US-09-070-526-2  
; Sequence 2, Application US/09070526  
; Patent No. 6100059  
; GENERAL INFORMATION:  
; APPLICANT: SOUTHAN, CHRISTOPHER  
; APPLICANT: CLINKENBEARD, HELEN  
; APPLICANT: BURGESS, NICOLA  
; TITLE OF INVENTION: No. 6100059el Compounds  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-Seq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,526  
; FILING DATE: 30-APR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9711952.3  
; FILING DATE: 9-JUN-1997  
; APPLICATION NUMBER: EP 97309646.4  
; FILING DATE: 1-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-30353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 260 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-070-526-2

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Pred. No.: 6,53e-42 Length: 260  
Score: 628.50 Matches: 124  
Percent Similarity: 57.98% Conservative: 25  
Best Local Similarity: 48.25% Mismatches: 95  
Query Match: 30.42% Indels: 13  
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-070-526-2 (1-260)

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148 -----TGTGTTCTTTGGGCTCAGCCAGGAGCCACACCGAGATTTTCAATGGCACT 198  
18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyGlyHis 37  
199 GAGTGTGGGCTTACTCACAGCCGTGAGCTGGGGCTGTTTGGAGGACCCAGGCTGGCG 258  
38 GluCysGlnProHisSerGlnProTrpGlnAlaLeuPheGlnGlyGlnLeuLeu 57  
259 TGGCGGGGTGTCTTATTGACACAGAGTGGGTCTCTACAGCGGTCTACTGTCAGCGGAGC 318  
58 CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysLysPro 77  
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RESULT 6

US-09-008-271A-7  
; Sequence 7, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:

APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/008, 271A
  FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: <Unknown>
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Mohan-Peterson, Sheila
  REGISTRATION NUMBER: 41,201
  REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-845-0555
  TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  LENGTH: 260 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
IMMEDIATE SOURCE:
  LIBRARY: COLNOT27
  CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Alignment Scores:
Pred. No.: 1,368-41 Length: 260
Score: 624.50 Matches: 124
Percent Similarity: 57.69% Conservative: 26
Best Local Similarity: 47.69% Mismatches: 97
Query Match: 30.23% Indels: 13
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-008-271A-7 (1-260)
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DB 118 AsnHisAspLeuMetLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLys 137
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DB 138 ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTrp 157
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RESULT 7
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1020091
US-09-025-059-3

Alignment Scores:
Pred. No.: 1,968-41 Length: 260
Score: 622.50 Matches: 121
Percent Similarity: 60.32% Conservative: 28
Best Local Similarity: 48.99% Mismatches: 93
Query Match: 30.13% Indels: 5
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DB: 3 Gaps: 3

US-10-015-385A-193 (1-1091) x US-09-025-059-3 (1-260)

QY 133 ATCTTTTTCCTCTGTGTGTT- - - - -CTTGGGCTCAGCCAGCCACACCGAAG 183  
Db 13 IleLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32  
QY 184 ATTTTCAATGGCAGTGTGGGGCTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGGAG 243  
Db 33 IleLeuGluGlyArgGluCysIleProHisSerGlnProTrpGlnAlaLeuPheGln 52  
QY 244 GGCACAGCCTCGCTGGGGGGTGTCTTATTGACACAGTGGGTCTCACAGCGCT 303  
Db 53 GlyGluArgLeuIleCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72  
QY 304 CACTCAGCGGCGAGGAGTGTGGTGGCCCTGGCCGAGGAGGAGGAGGAGGAGGAGGAGG 363  
Db 73 HisCysLysLysGlnLysTyrSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp 92  
QY 364 TGGACCGAGCAGATCCGGCAGCGGCTTCTGTGACCCATCCCGGCTACCTGGGAGCC 423  
Db 93 GlnProGluGlnGluIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer 112  
QY 424 TCG- - -ACGAGCCAGCAGCAGCTCCGGCTGTGTGGGCTGGCTGGCTGGCTGGCTGG 480  
Db 113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132  
QY 481 ACCAGCAGGTTCAACCCCTGCCCTGCCATGACTGTGCAACCGCTGGCAGCAGTGC 540  
Db 133 GlyAspLysValLeuProValGlnLeuAlaAsnLeuCysProLysValGlyGlnLysCys 152  
QY 541 CACGTCCTCAGGTCGGGGGATCACCAACCAACCAACCAACCAACCAACCAACCAACCA 600  
Db 153 IleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172  
QY 601 TGCCTCAACCTTCCTCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCAT 660  
Db 173 CysAlaGluValLysIleTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle 192  
QY 661 ACAGCAACATGGTGTGGGGAGTCCCTTCAAGGTCTGTGCTGTGGGGTCTGTGGGG 720  
Db 193 ThrGluGlyMetValCysAlaGlySerSerAsnGlyAlaAspThrCysGlnGlyAspSer 212  
QY 781 CCCTGTGACAAAGATGGCATCCCTGGAGTCTACACTATATTGCAAGTATGTGACTGG 840  
Db 232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp 251  
QY 841 ATCCGGATGATCATGAGGAAC 861  
Db 252 IleLysLysThrMetAspAsn 258

## RESULT 8

US-09-618-259-8  
; Sequence 8, Application US/09618259  
; Patent No. 6642013  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
; FILE REFERENCE: D6020IP2  
; CURRENT APPLICATION NUMBER: US/09/618,259  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 09/127,444  
; PRIOR FILING DATE: 1998-08-21  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 8  
; LENGTH: 260  
; TYPE: PRT

; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous  
; to TADG-14; accession no. D30785  
US-09-618-259-8

Alignment Scores:  
Pred. No.: 1,96e-41 Length: 260  
Score: 622.50 Matches: 121  
Percent Similarity: 60.32% Conservative: 28  
Best Local Similarity: 48.99% Mismatches: 93  
Query Match: 30.13% Indels: 5  
DB: 4 Gaps: 3

US-10-015-385A-193 (1-1091) x US-09-618-259-8 (1-260)

QY 133 ATCTTTTTCCTCTGTGTGTT- - - - -CTTGGGCTCAGCCAGCCACACCGAAG 183  
Db 13 IleLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32  
QY 184 ATTTTCAATGGCAGTGTGGGGCTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGGAG 243  
Db 33 IleLeuGluGlyArgGluCysIleProHisSerGlnProTrpGlnAlaLeuPheGln 52  
QY 244 GGCACAGCCTCGCTGGGGGGTGTCTTATTGACACAGTGGGTCTCACAGCGCT 303  
Db 53 GlyGluArgLeuIleCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72  
QY 304 CACTCAGCGGCGAGGAGTGTGGTGGCCCTGGCCGAGGAGGAGGAGGAGGAGGAGG 363  
Db 73 HisCysLysLysGlnLysTyrSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp 92  
QY 364 TGGACCGAGCAGATCCGGCAGCGGCTTCTGTGACCCATCCCGGCTACCTGGGAGCC 423  
Db 93 GlnProGluGlnGluIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer 112  
QY 424 TCG- - -ACGAGCCAGCAGCAGCTCCGGCTGTGTGGGCTGGCTGGCTGGCTGGCTGG 480  
Db 113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132  
QY 481 ACCAGCAGGTTCAACCCCTGCCCTGCCATGACTGTGCAACCGCTGGCAGCAGTGC 540  
Db 133 GlyAspLysValLeuProValGlnLeuAlaAsnLeuCysProLysValGlyGlnLysCys 152  
QY 541 CACGTCCTCAGGTCGGGGGATCACCAACCAACCAACCAACCAACCAACCAACCAACCA 600  
Db 153 IleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172  
QY 601 TGCCTCAACCTTCCTCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCAT 660  
Db 173 CysAlaGluValLysIleTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle 192  
QY 661 ACAGCAACATGGTGTGGGGAGTCCCTTCAAGGTCTGTGCTGTGGGGTCTGTGGGG 720  
Db 193 ThrGluGlyMetValCysAlaGlySerSerAsnGlyAlaAspThrCysGlnGlyAspSer 212  
QY 721 GGGGGCCCCCTGTGTGGGGGAGTCCCTTCAAGGTCTGTGCTGTGGGGTCTGTGGGG 780  
Db 213 GlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGlySer- - -Asp 231  
QY 781 CCCTGTGACAAAGATGGCATCCCTGGAGTCTACACTATATTGCAAGTATGTGACTGG 840  
Db 232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp 251  
QY 841 ATCCGGATGATCATGAGGAAC 861  
Db 252 IleLysLysThrMetAspAsn 258

## RESULT 9

US-09-205-258-427  
; Sequence 427, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:



QY 778 GGGCCCTGTGACAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTGGAC 837  
|||||  
Db 222 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 241  
|||||

QY 838 TGGATCCGGATGATCATGAGGAACAAC 864  
|||||  
Db 242 TrpIleGlnGluThrMetLysAsnAsn 250  
|||||

## RESULT 10

US-09-025-059-1  
; Sequence 1, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guglier, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 282 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGTU10  
; CLONE: 2723646  
US-09-025-059-1

Alignment Scores:  
Pred. No.: 4,15e-41 Length: 282  
Score: 618.50 Matches: 120  
Percent Similarity: 62.25% Conservative: 35  
Best Local Similarity: 48.19% Mismatches: 89  
Query Match: 29.94% Indels: 5  
DB: 3 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-025-059-1 (1-282)

QY 127 CTCGACATCTTTTGTCTCTGTGTCTTGTGGCTCAGCCAGGCACACCGAAGATT 186  
|||||  
Db 36 LeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGluThr---ArgIle 54  
|||||  
QY 187 TTCATGGCAGTACGTGGGGGTAACTCACAGCGTGGCAGGTGGGGTGTTCAGGGC 246  
|||||

Db 55 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGluLys 74  
QY 247 ACCAGCCTCGGCTCGGGGGTGTCTTATTGACACACAGGTGGTCTCTCACAGCGGCTCAC 306  
|||||  
Db 75 ThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHis 94  
|||||  
QY 307 TGCAGCGGACAGAGTACTGGGTGGCTGGCGGGGAACACAGCCTCAGCCAGCTCGATGG 366  
|||||  
Db 95 CysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGly 114  
|||||  
QY 367 ACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCC-- 423  
|||||  
Db 115 CysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu 134  
|||||  
QY 424 --TCGACGACGACGACGACGACCTCGGCTGTGGGGCTGCGCTGCGCTGCGCGTA 480  
|||||  
Db 135 ProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIle 154  
|||||  
QY 481 ACCAGCAGCGTTCAACCCCTGCGCTGCGCAATGACTGTGCAACCGTGGCACCGAGTGC 540  
|||||  
Db 155 ThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCys 174  
|||||  
QY 541 CACGTCTCAGCTGGGCGCATCACCAACCCACGACCAACCATTCCTCCGATCTGCTCCAG 600  
|||||  
Db 175 LeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArg 194  
|||||  
QY 601 TGCCTCAACCTCTCATCGTCTCCCATGCCACCTCGTGTGTGTATCCCGGGAGATC 660  
|||||  
Db 195 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 214  
|||||  
QY 661 ACAGCACAACATGGTGTGTGAGGC--GGCTCCCGGGGAGGATGCTGCCAGGTGAT 717  
|||||  
Db 215 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 234  
|||||  
QY 718 TCTGGGGCCCCCTGTGTGTGGGGAGTCTCTCAAGTCTGTGTCTCTGGGGTCTGTG 777  
|||||  
Db 235 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln--- 253  
|||||  
QY 778 GGGCCCTGTGACCAAGATGGCATCCCTGGAGTCTACACCTATATTGCAAGTATGTGGAC 837  
|||||  
Db 254 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 273  
|||||  
QY 838 TGGATCCGGATGATCATGAGGAACAAC 864  
|||||  
Db 274 TrpIleGlnGluThrMetLysAsnAsn 282  
|||||

## RESULT 11

US-09-386-642-13  
; Sequence 13, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

Alignment Scores:  
Pred. No.: 7,79e-40 Length: 288  
Score: 602.50 Matches: 116  
Percent Similarity: 60.35% Conservative: 21



Best Local Similarity: 51.10% Mismatches: 87  
Query Match: 29.16% Indels: 3  
DB: 4 Gaps: 3

US-10-015-385A-193 (1-1091) x US-09-386-642-13 (1-288)

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QY 181 AAGATTTCATGGCACTGAGTGT---GGGCGTAACACACAGCCGTGGCAGGTGGGGCTG 237
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Db 51 LysIleValGlyGlyTyrAsnCysLeuGluProHisSerGlnProTrpGlnAlaLeu 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 TTTGAGGCGACAGCGCTGCGTGGCGGTGCTTATTGACACAGGTGGGTCTCTACA 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 PheGlnGlyGlnLeuLeuCysGlyValLeuValGlyGlyAsnTrpValLeuThr 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 GCGGCTCACTGACGCGGACAGGACTGCTGGGTGCGCTGGGGAAACACAGCCTCAGCCAG 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 AlaAlaHisCysLysLysProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsn 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTCGACTGACGACAGATCCGGCACAGCGCTTCTGTGACCCATCCCGGCTACCTG 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 LysAspGlyProGluGlnGluIleProValValGlnSerIleProHisProCysTyrAsn 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 GGAGCTCGACG---AGCCAGGACGACGACCTCCGCTGCTGCGGTGCGCTGCCCTG 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 SerSerAspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAla 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 GCGGTAAACAGCAGCGGTTCACCCCTGCGCCCTGCGCAATGCTGTCACACCGCTGCCACC 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 SerLeuGlySerLysValLysProLysLeuAlaAspHisCysThrGlnProGlyGln 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 GAGTCCGCTCACTGAGGTGGGGATCACCACACCGAACCCATTCGCGGATCTG 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 LysCysThrValSerGlyTrpGlyThrValThrSerProArgGluAsnPheProAspThr 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 CTCGAGTCCCTCAACTCTCCATCTCTCCCATGCCACCTGCGATGCTGTATCCCGG 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 LeuAsnCysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGly 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 AGAATCAGCAGCAACATGCTGTGTGTCAGCGCGCTCCCGGCGAGATGCCCTGCCAGGCT 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 GlnIleThrAspGlyMetValCysAlaGlySerSerLysGlyAlaAspThrCysGlnGly 230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 715 GATTCTGGGGGCCCTGCTGTGTGGGGAGTCTTCAAGTCTGTGTGCTGGGGTCT 774
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 AspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 775 GTGGGGCCCTGTGGACAGATGGCATCCCTGTGAGTCTACACCTATATTGCAAGTATGTG 834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 ---AspProCysGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeu 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 835 GACTGGATCCGGATCATGATCATG 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 270 AspTrpIleLysIleIle 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 12

US-09-386-642-14

; Sequence 14, Application US/09386642

; Patent No. 6420157

; GENERAL INFORMATION:

; APPLICANT: Darrow, Andrew

; APPLICANT: Qi, Jensen

; APPLICANT: Andrade-Gordon, Patricia

; TITLE OF INVENTION: Zymogen Activation System

; FILE REFERENCE: ORT-1028

; CURRENT APPLICATION NUMBER: US/09/386,642

; CURRENT FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14

## Alignment Scores:

Pred. No.: 1,62e-39 Length: 289  
Score: 598.50 Matches: 114  
Percent Similarity: 63.79% Conservative: 34  
Best Local Similarity: 49.14% Mismatches: 79  
Query Match: 28.97% Indels: 5  
DB: 4 Gaps: 4

US-10-015-385A-193 (1-1091) x US-09-386-642-14 (1-289)

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QY 181 AAGATTTCATGGCACTGAGTGT---GGGCGTAACACACAGCCGTGGCAGGTGGGGCTG 237
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Db 51 LysIleValGlyGlyTyrAsnCysLeuGluLysHisSerGlnProTrpGlnAlaLeu 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 TTTGAGGCGACAGCGCTGCGTGGCGGTGCTTATTGACACAGGTGGGTCTCTACA 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 PheGluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThr 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 GCGGCTCACTGACGCGGACAGGACTGCTGGGTGCGCTGGGGAAACACAGCCTCAGCCAG 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 AlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTCGACTGGACGACGACAGATCCGGCACAGCGCTTCTGTGACCCATCCCGGCTACCTG 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 GGAGCC-----TCGACGAGCCACGAGCAGACCTCCCGGCTGCTGGGTGCGCTGCCCTGCC 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 GTCCCGCTAAACAGCAGCGGTTCACCCCTGCGCCCTGCCATGATGCTGTCACACCGCTGCG 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 ACCGAGTCCACGCTCTCAGGTGGGGCATCACCAACACCCACCGAACCCATTCCCGGAT 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHis 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 CTGCTCCAGTGCCTCAACTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTGTATCCC 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 ThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrPro 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 652 GGGAGAATCAGAGCAACATGCTGTGTGTCAGGC---GGGCTCCCGGGCAGGATGCCTGC 708
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 709 CAGGTGTATCTGGGGGCCCTGCTGTGTGGGGAGTCTTCAAGGTCTGTGTCTCTGG 768
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 769 GGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTGCAAG 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 GlyGln---AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLys 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 829 TATGTGGACTGATCCGGATGATCATGAGGAACAAC 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 270 TyrValAspTrpIleGlnGluThrMetLysAsnAsn 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 13

US-08-944-483-24

; Sequence 24, Application US/08944483

; Patent No. 6232456

; GENERAL INFORMATION:

; APPLICANT: COHEN, MAURICE

; APPLICANT: COLPITTS, TRACEY L.

; APPLICANT: FRIEDMAN, PAULA N.

; APPLICANT: GRANADOS, EDWARD N.

; APPLICANT: KLASS, MICHAEL R.

; APPLICANT: RUSSELL, JOHN C.





Db 311 ValCysArgTyrThrAsnTrpIleGln 319

Search completed: March 5, 2005, 23:08:24  
Job time : 54 secs

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OM nucleic - protein search, using frame plus n2p model

Run on: March 5, 2005, 23:00:19 ; Search time 49 Seconds  
(without alignments)  
4284.591 Million cells

**Title:** US-10-015-385A-193

Perfect score: 2066  
Sequence: 1 caaqcaqqtcatccccttgg.....agggcaaaaaaaaaaaaaaa 1091

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

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Fgapop	6.0	, Fgapext	7.0
Delop	6.0	, Delext	7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

**Command line parameters:**

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Command-line parameters:
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Database :

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2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	622.5	30.1	260	2	I56559	neuropsin - mouse
2	569.5	27.6	248	2	S55066	trypsin (EC 3.4.21
3	567	27.4	248	2	S55067	trypsin (EC 3.4.21
4	561	27.2	231	1	TRGOTR	trypsin (EC 3.4.21
5	555	26.9	243	2	A35871	trypsin (EC 3.4.21
6	555	26.9	253	2	A53968	serine proteinase
7	553	26.8	246	2	B25528	trypsin (EC 3.4.21
8	552	26.7	229	1	TRBOTR	trypsin (EC 3.4.21
9	550	26.6	247	2	S13813	trypsin (EC 3.4.21
10	546	26.4	247	1	TRDG	trypsin (EC 3.4.21
11	545	26.4	246	1	ADG547	trypsin (EC 3.4.21
12	544.5	26.4	247	2	TR27547	trypsin (EC 3.4.21
13	543	26.3	246	1	TRRT1	trypsin (EC 3.4.21
14	540	26.1	238	2	S31779	trypsin (EC 3.4.21

trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
7S nerve growth factor	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
7S nerve growth factor	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
trypsin	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
semenogelase	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
gamma-aminocaproic acid amidohydrolase	(EC 3.4.21.2)
venom plasminogen activator	(EC 3.4.21.2)
kallikrein, glandular	(EC 3.4.21.2)
snake venom factor	(EC 3.4.21.2)
gamma-renin	(EC 3.4.21.2)
venombin A	(EC 3.4.21.2)
venombin B	(EC 3.4.21.2)
snake venom factor	(EC 3.4.21.2)
venombin A	(EC 3.4.21.2)
venombin AB	(EC 3.4.21.2)
venombin A	(EC 3.4.21.2)
venombin A	(EC 3.4.21.2)
pancreatic elastase	(EC 3.4.21.2)
polyprotein - Afri-	(EC 3.4.21.2)
tissue kallikrein	(EC 3.4.21.2)
chymotrypsin-like complement factor	(EC 3.4.21.2)
complement factor	(EC 3.4.21.2)
probable serine protease	(EC 3.4.21.2)
prostatin	(EC 3.4.21.2)
complement factor	(EC 3.4.21.2)
venombin A	(EC 3.4.21.2)
chymotrypsin	(EC 3.4.21.2)
pancreatic elastase	(EC 3.4.21.2)

88	370.5	17.9	638	1	KQHUP	plasma kallikrein	161	327	15.8	244	2	S72219	chymotrypsin B - A
89	366	17.7	258	1	S36783	venombin A (EC 3.4	162	327	15.8	259	2	S68424	allergen Der f III
90	364	17.6	156	2	B23863	tissue kallikrein	163	326.5	15.8	248	1	PMSC2	granzyme C (EC 3.4
91	362.5	17.5	246	2	S64707	chymase (EC 3.4.21	164	326.5	15.8	266	1	ELPG	pancreatic elastas
92	359.5	17.4	277	2	S35340	trypsin (EC 3.4.21	165	326	15.8	248	2	S33755	granzyme-like prot
93	359.5	17.4	1019	2	A38738	coagulation factor	166	325.5	15.8	492	1	KFHU7	coagulation factor
94	359	17.4	443	2	I46932	coagulation factor	167	324.5	15.7	466	1	EXBO	coagulation factor
95	358.5	17.4	263	2	A31299	chymotrypsin (EC 3	168	324	15.7	274	2	A45754	trypsin (EC 3.4.2
96	358	17.3	812	1	PLBO	plasma (EC 3.4.21	169	324	15.7	459	2	J00419	coagulation factor
97	357	17.3	262	1	A31372	granzyme A (EC 3.4	170	324	15.7	1019	1	A56318	enteropeptidase (E
98	357	17.3	271	2	S29239	chymotrypsin (EC 3	171	322	15.6	265	2	T10495	chymotrypsin (EC 3
99	355.5	17.2	276	2	A38654	mast cell proteina	172	322	15.6	460	2	B61545	plasmin (EC 3.4.21
100	354.5	17.2	263	2	S47537	chymotrypsin (EC 3	173	321.5	15.6	251	2	JC2125	chymase (EC 3.4.21
101	354	17.1	260	2	A45061	granzyme A (EC 3.4	174	321.5	15.6	436	2	JX0172	acrosin (EC 3.4.21
102	354	17.1	271	2	A25528	pancreatic elastas	175	321	15.5	226	1	KCUF	bradykinin (EC 3.4
103	353.5	17.1	270	2	S56160	mast cell trypsin	176	321	15.5	226	2	S69370	chymase - bovine
104	353	17.0	274	2	JC4171	trypsin (EC 3.4.2	177	321	15.5	247	2	S64708	chymase (EC 3.4.21
105	352	17.0	461	1	JX0210	protein C (activat	178	321	15.5	248	2	A43520	natural killer cel
106	351	17.0	456	1	KXBO	protein C (activat	179	321	15.5	269	2	B32410	mastocytoma protei
107	349.5	16.9	269	2	B26823	pancreatic elastas	180	321	15.5	655	1	A46688	hepatocyte growth
108	348	16.8	267	2	S40006	trypsin (EC 3.4.21	181	320.5	15.5	247	1	PMSC1	granzyme B (EC 3.4
109	347	16.8	461	1	KXHU	protein C (activat	182	320	15.5	431	2	S47538	acrosin (EC 3.4.21
110	346.5	16.8	244	2	S26042	chymase (EC 3.4.21	183	319.5	15.5	559	1	A29941	t-plasminogen acti
111	346.5	16.8	461	1	S18994	protein C (activat	184	319	15.4	1034	1	A53663	enteropeptidase (E
112	344	16.7	275	2	B35863	trypsin (EC 3.4.2	185	318	15.4	271	2	I46580	factor IX - pig (f
113	343.5	16.6	273	2	A47246	trypsin (EC 3.4.2	186	318	15.4	274	2	I47078	coagulation factor
114	343.5	16.6	274	2	S35339	trypsin (EC 3.4.21	187	318	15.4	618	2	A35827	thrombin (EC 3.4.2
115	343.5	16.6	558	2	JC5878	plasma hyaluronan-	188	317.5	15.4	245	1	KVBOB	chymotrypsin (EC 3
116	343	16.6	275	2	A32410	trypsin (EC 3.4.2	189	317.5	15.4	246	2	A32692	cytotoxic T-lympho
117	342.5	16.6	437	2	S18407	acrosin (EC 3.4.21	190	317	15.3	249	2	A55634	granzyme M (EC 3.4
118	342.5	16.6	810	1	PLHU	plasmin (EC 3.4.21	191	316.5	15.3	246	1	A46504	chymase (EC 3.4.21
119	342	16.6	275	2	C35863	trypsin (EC 3.4.2	192	316.5	15.3	433	1	JN0560	u-plasminogen acti
120	342	16.6	275	2	A35863	trypsin (EC 3.4.2	193	316	15.3	482	1	EXRT	coagulation factor
121	341.5	16.5	258	2	I58220	trypsin (EC 3.4.2	194	315.5	15.3	254	1	TRWV3Y	trypsin-like prote
122	340.5	16.5	246	2	B38678	mast cell proteina	195	315.5	15.3	266	1	ELRT1	pancreatic elastas
123	339.5	16.4	258	2	A45161	serine proteinase	196	315.5	15.3	392	1	A30100	serine proteinase
124	339.5	16.4	267	4	A56615	probable pancreati	197	315	15.2	248	2	S43259	granzyme-like prot
125	339	16.4	257	2	B45061	granzyme A (EC 3.4	198	315	15.2	275	2	S40005	trypsin (EC 3.4.21
126	339	16.4	461	1	KFHU1	coagulation factor	199	315	15.2	617	2	S10511	thrombin (EC 3.4.2
127	339	16.4	625	1	KFHU1	coagulation factor	200	315	15.2	686	1	A59271	Ra-reactive factor
128	338	16.4	625	1	TBBO	thrombin (EC 3.4.2	201	314	15.2	418	2	A37344	acrosin (EC 3.4.21
129	337.5	16.3	238	1	TRWV5Y	trypsin-like prote	202	313	15.2	613	2	S15468	complement C3b/C4b
130	337.5	16.3	264	2	S65566	granzyme 3 (EC 3.4	203	313	15.2	855	2	JC7731	membrane-bound arg
131	337	16.3	434	1	A35005	u-plasminogen acti	204	312.5	15.1	274	2	S40004	trypsin-related pr
132	337	16.3	812	1	PLMS	plasmin (EC 3.4.21	205	312.5	15.1	615	1	KFHU12	coagulation factor
133	336.5	16.3	251	2	T10262	mast cell serine p	206	311.5	15.1	761	2	JC5759	brain-specific ser
134	336.5	16.3	251	2	PC1235	29K serine protein	207	311	15.1	261	2	S40162	cathepsin G (EC 3.
135	336.5	16.3	638	1	KQMSPL	plasma kallikrein	208	311	15.1	421	2	S29599	acrosin (EC 3.4.21
136	336	16.3	416	1	KFBO	coagulation factor	209	311	15.1	559	1	A5029	t-plasminogen acti
137	336	16.3	790	1	PLFG	plasmin (EC 3.4.21	210	311	15.1	1035	1	A43090	enteropeptidase (E
138	335.5	16.2	258	4	S70439	pancreatic elastas	211	310.5	15.0	247	1	PRRTG	factor IX - rabbit
139	334	16.2	245	1	KYBOA	chymotrypsin (EC 3	212	310	15.0	275	2	I46712	oviductin (EC 3.4.
140	333.5	16.1	263	1	KYRTB	chymotrypsin (EC 3	213	308.5	14.9	1004	2	T30338	hepsin (EC 3.4.21
141	333	16.1	285	2	I48144	coagulation factor	214	308	14.9	417	1	S00845	serine proteinase
142	333	16.1	810	2	I46260	plasmin (EC 3.4.21	215	307	14.9	250	2	S55493	chymotrypsin (EC 3
143	332.5	16.1	638	1	KQRTPL	plasma kallikrein	216	307	14.9	259	1	S49129	limulus clotting e
144	332.5	16.1	810	2	B30848	trypsin (EC 3.4.21	217	306.5	14.8	375	1	A23689	thrombin (EC 3.4.2
145	331.5	16.0	256	1	TRFF	trypsin-like prote	218	305.5	14.8	236	2	I42696	hypothetical prote
146	331.5	16.0	275	2	S40007	trypsin (EC 3.4.21	219	305	14.8	196	2	T08808	granzyme B (EC 3.4
147	331	16.0	622	1	TBHU	thrombin (EC 3.4.2	220	305	14.8	281	1	A61021	tissue kallikrein
148	330.5	16.0	237	2	S68702	chymase (EC 3.4.2	221	304	14.7	149	1	KQMSM	thrombin (EC 3.4.2
149	330.5	16.0	247	1	KYHUCM	plasma hyaluronan-	222	304	14.7	268	2	C42696	pancreatic elastas
150	330.5	16.0	560	1	JC4795	coagulation factor	223	304	14.7	236	2	S68825	t-plasminogen acti
151	330	16.0	282	2	I84621	apoptein(a) (EC	224	304	14.7	562	1	UKHTU	chymase (EC 3.4.21
152	330	16.0	4548	1	S00657	myonase (EC 3.4.-	225	303.5	14.7	244	2	A46721	coagulation factor
153	329.5	15.9	226	2	JE0151	pancreatic elastas	226	303.5	14.7	309	2	B49878	cathepsin G (EC 3.
154	329.5	15.9	269	2	C26823	apolipoprotein(a)	227	303	14.7	255	2	A27122	mast cell proteina
155	329.5	15.9	1420	2	A32869	serine proteinase	228	302.5	14.6	244	2	A43910	trypsin-related pr
156	328.5	15.9	455	2	A61545	plasmin (EC 3.4.21	229	302.5	14.6	273	2	S40003	low-density lipopr
157	328.5	15.9	786	1	A47547	serine proteinase	230	302.5	14.6	1113	2	JE0315	pancreatic elastas
158	328	15.9	452	1	A30351	coagulation factor	231	302	14.6	268	2	S68826	trypsin homolog -
159	328	15.9	699	1	I54763	Ra-reactive factor	232	302	14.6	281	2	T13596	t-plasminogen acti
160	327.5	15.9	266	2	S54146	trypsin (EC 3.4.21	233	302	14.6	394	2	J50600	

234	302	14.6	477	1	A34369	t-plasminogen acti	307	247	12.0	243	2	A56338	venom proteinase (
235	302	14.6	477	2	JS0598	t-plasminogen acti	308	245.5	11.9	711	1	A47136	macrophage-stimula
236	301	14.6	431	2	JS0599	t-plasminogen acti	309	243.5	11.8	705	1	CIHURB	complement subcomp
237	301	14.6	442	1	UKPG	u-plasminogen acti	310	239.5	11.6	265	2	I48679	neutrophil elastas
238	300	14.5	245	2	A48598	kallikrein-like se	311	237.5	11.5	232	2	S32398	serine proteinase
239	300	14.5	433	1	UKWS	u-plasminogen acti	312	237	11.5	716	1	JCS061	macrophage-stimula
240	299.5	14.5	235	2	A42696	thrombin (EC 3.4.2	313	235.5	11.4	198	2	S06176	cytotoxic T-lympho
241	299.5	14.5	246	2	A38678	mast cell proteina	314	235	11.4	96	2	A05308	tissue kallikrein
242	299.5	14.5	258	1	A44184	chymotrypsin (EC 3	315	235	11.4	230	2	A27802	hypodermis C (EC 3
243	299	14.5	260	2	S26043	chymase (EC 3.4.21	316	234.5	11.4	219	1	TRPGA2	azurocidin - pig
244	299	14.5	421	1	S11674	acrosin (EC 3.4.21	317	234	11.3	230	2	I48685	mast cell proteina
245	298.5	14.4	191	2	S54115	complement factor	318	227.5	11.0	267	1	ELHUL	leukocyte elastase
246	298.5	14.4	249	1	A35842	chymase (EC 3.4.21	319	227.5	11.0	272	2	JC4170	trypsin-like prote
247	298.5	14.4	270	2	B29934	pancreatic elastas	320	227	11.0	259	1	TRSMG	trypsin (EC 3.4.21
248	298.5	14.4	407	1	KFB07	coagulation factor	321	226	10.9	728	1	JH0579	hepatocyte growth
249	297	14.4	237	1	TRCY1	trypsin (EC 3.4.21	322	225	10.9	548	2	D82175	probable trypsin V
250	297	14.4	477	2	JS0597	t-plasminogen acti	323	217.5	10.5	710	1	I51283	hepatocyte growth
251	296.5	14.4	248	1	S01007	granzyme F (EC 3.4	324	216	10.5	728	1	A35644	hepatocyte growth
252	295.5	14.3	239	2	A42696	thrombin (EC 3.4.2	325	216	10.5	728	1	A60185	hepatocyte growth
253	294	14.2	247	2	S23504	chymase (EC 3.4.21	326	204.5	9.9	177	2	S23505	chymase (EC 3.4.21
254	294	14.2	303	2	T13598	u-plasminogen acti	327	201.5	9.8	248	2	S49323	chymotrypsin (EC 3
255	293.5	14.2	431	1	UKHU	u-plasminogen acti	328	201	9.7	214	2	S17680	fibrinolytic prote
256	293	14.2	234	2	F42696	thrombin (EC 3.4.2	329	197.5	9.6	213	2	S17537	fibrinolytic prote
257	293	14.2	247	2	S59135	mast cell proteina	330	192.5	9.3	763	2	I50807	complement factor
258	293	14.2	265	2	A38894	serine proteinase	331	189.5	9.2	94	2	PC2013	tissue kallikrein
259	293	14.2	265	2	JS0260	serine proteinase	332	182	8.8	104	2	S15395	tissue kallikrein-
260	293	14.2	433	1	UKBAY	u-plasminogen acti	333	182	8.8	348	1	HPHUR	haptoglobin-relate
261	292.5	14.2	236	2	A28566	T-cell suppressor	334	180.5	8.7	377	2	C88710	protein C43G2.5 (i
262	291.5	14.1	216	1	KYVH20	chymotrypsin (EC 3	335	180	8.7	258	2	G02959	haptoglobin - rhes
263	291	14.1	271	2	S41308	serine proteinase	336	179.5	8.7	149	2	S35208	serine proteinase
264	291	14.1	415	1	A43170	acrosin (EC 3.4.21	337	177	8.6	347	1	HPHU1	haptoglobin precur
265	290.5	14.1	420	2	A55283	acrosin (EC 3.4.21	338	177	8.6	406	1	HPHU2	haptoglobin precur
266	289.5	14.0	248	2	A33412	cytotoxic T-lympho	339	176.5	8.5	760	1	C2MS	classical compleme
267	289	14.0	583	2	A29154	complement factor	340	176	8.5	735	2	T35778	probable fusidic a
268	288.5	14.0	270	2	A29934	pancreatic elastas	341	175.5	8.5	330	2	B82415	probable serine pr
269	288.5	14.0	1047	2	A55617	masquerade precurs	342	174	8.4	161	2	I48158	coagulation factor
270	288	13.9	268	2	QJ1473	pancreatic elastas	343	172	8.3	346	2	I36942	haptoglobin - chlm
271	287.5	13.9	235	2	H42696	thrombin (EC 3.4.2	344	171	8.3	159	2	S35202	proteinase 2 - buf
272	287.5	13.9	603	2	S28941	coagulation factor	345	171	8.3	258	2	I36945	haptoglobin Hp - c
273	286.5	13.9	218	1	KYVH2C	chymotrypsin (EC 3	346	171	8.3	345	2	I36941	haptoglobin - chlm
274	286	13.8	254	2	S35585	chymotrypsin-like	347	170	8.2	347	2	G00006	haptoglobin - blac
275	285.5	13.8	235	2	D42696	thrombin (EC 3.4.2	348	169	8.2	329	1	HPDG	haptoglobin precur
276	282.5	13.7	331	2	T27906	hypothetical prote	349	168	8.1	66	2	I52972	kallikrein - mouse
277	282	13.6	416	1	S33777	hepsin (EC 3.4.21	350	168	8.1	154	2	S35207	proteinase 7 - buf
278	280.5	13.6	366	2	JE0105	testicular serine	351	166	8.0	258	2	I36947	haptoglobin Hpp -
279	280	13.6	254	2	S65465	trypsin-like prote	352	166	8.0	349	2	I36944	haptoglobin - chlm
280	280	13.6	430	1	A24702	serine proteinase	353	166	8.0	752	1	C2HU	complement C2 prec
281	278.5	13.5	432	1	S18932	u-plasminogen acti	354	165	8.0	161	2	I62744	coagulation factor
282	278.5	13.5	593	2	S45281	coagulation factor	355	165	8.0	347	1	HPMS	haptoglobin precur
283	278	13.5	488	1	EXHU	coagulation factor	356	161.5	7.9	660	1	QBBE3	BHLFI protein - hu
284	277.5	13.4	266	2	JC4850	trypsin-like prote	357	159.5	7.7	152	2	S35209	serine proteinase
285	275.5	13.3	240	1	CPBOA3	procarboxypeptidas	358	159.5	7.7	805	2	T25795	hypothetical prote
286	275.5	13.3	265	2	T15451	hypothetical prote	359	159	7.7	126	2	A23473	chymotrypsin-like
287	275	13.3	237	2	S55378	serine proteinase	360	158.5	7.7	264	2	A28942	pancreatic elastas
288	275	13.3	688	1	CIHUS	complement subcomp	361	157.5	7.6	764	1	BBHU	complement factor
289	274.5	13.3	695	1	S05008	granzyme-like prot	362	157	7.6	407	2	C70816	hypothetical prote
290	273	13.2	247	2	S45113	coagulation factor	363	154.5	7.5	747	2	I51579	complement factor
291	272	13.2	475	1	EXCH	proteinase 3 (EC 3	364	153.5	7.4	761	1	BIMS	complement factor
292	271.5	13.1	256	1	PRHU3	nuclei protein prec	365	152.5	7.4	159	2	I84615	coagulation factor
293	271	13.1	2616	2	AS7096	complement subcomp	366	152	7.4	181	2	T08805	hypothetical prote
294	270	13.1	694	2	JC6554	granzyme-like prot	367	151.5	7.3	152	2	S35203	serine proteinase
295	269.5	13.0	248	2	S33756	azurocidin precurs	368	148	7.2	81	2	A18966	tissue kallikrein
296	264.5	12.8	251	1	TRHUAZ	trypsin (EC 3.4.21	369	147.5	7.2	825	2	JC4163	DNA-binding protei
297	264.5	12.8	256	2	T10109	trypsin-like prote	370	145.5	7.0	82	2	T46510	hypothetical prote
298	264.5	12.8	264	2	S32794	cytotoxic T-lympho	371	143.5	6.9	1357	2	T29265	collagen alpha 1(I
299	259	12.5	248	2	S01006	procytotoxic T-lym	372	142	7.0	673	1	CEBO6C	hypothetical prote
300	258.5	12.5	252	2	A34172	probable serine pr	373	140.5	6.8	1560	2	T00080	transcription fact
301	258.5	12.5	285	2	T35195	trypsin-like prote	374	139.5	6.8	639	2	G02919	hypothetical prote
302	257.5	12.5	254	2	S49328	probable trypsin V	375	139.5	6.8	1952	2	T48814	hypothetical prote
303	256	12.4	403	2	C82228	testicular serine	376	139	6.7	1087	2	T31100	probable potassium
304	255	12.3	367	2	JE0104	coagulation factor	377	138.5	6.7	158	2	S35201	serine proteinase
305	252	12.2	400	1	A48050	macrophage-stimula	378	138	6.7	153	2	S35204	proteinase 4 - buf
306	251	12.1	716	1	A40332		379	138	6.7	383	2	S32975	gene BCRF2 protein

380	137.5	6.7	660	1	QBEB3	BHLF1 protein - hu	453	124.5	6.0	464	2	S22697	extensin - Volvox
381	137	6.6	743	2	S34853	probable fusidic a	c 454	124.5	6.1	671	1	CGRTIS	collagen alpha 1(I)
382	136.5	6.6	152	2	S35206	serine proteinase	c 455	124.5	6.0	1691	1	S22917	collagen alpha 5(I)
383	135.5	6.6	46	2	I49416	glandular kallikre	c 456	124	6.1	677	2	S23296	collagen alpha 2(I)
384	135.5	6.6	1794	2	T38459	hypothetical diver	457	124	6.0	708	1	QBEB8	UL80 protein - hum
c 385	135	6.6	460	2	T33110	hypothetical prote	458	124	6.0	759	2	T44142	DRI protein (impor
c 386	135	6.6	1027	2	S28774	collagen alpha cha	c 459	124	6.1	1024	2	S18251	collagen alpha 1(X
c 387	135	6.6	1049	1	CGB078	collagen alpha 1(I)	460	124	6.0	3020	2	A43932	mucin 2 precursor,
c 388	134	6.6	435	2	T15143	hypothetical prote	461	123.5	6.0	137	2	S55364	serine proteinase,
c 389	133.5	6.5	699	2	C43674	US4 protein - huma	462	123.5	6.0	151	2	S35205	protease 5 - buf
390	132.5	6.4	292	2	S24169	mucin - rat	463	123.5	6.0	574	2	T43556	Wiskott-Aldrich sy
391	132.5	6.4	326	2	S34427	tristetrapoline p	464	123.5	6.0	715	2	G86239	protein F20B24.6 l
c 392	132.5	6.5	640	2	T08179	LRG5 protein - Chl	c 465	123.5	6.1	1486	1	B40333	collagen alpha 1(I)
c 393	132.5	6.5	1042	1	CGCH18	collagen alpha 1(I)	c 466	123.5	6.0	1492	2	A40333	collagen alpha 1(I)
c 394	132.5	6.5	3436	2	S55659	tegument protein 6	467	123.5	6.1	2715	2	T13049	eyelid - fruit fly
395	132.5	6.4	3570	2	T45025	mucin MUC5B, trach	468	123.5	6.0	2944	2	A54849	collagen alpha 1(V
396	132	6.4	347	1	HPRT	haptoglobin precur	c 469	123	6.0	375	1	A45225	pulmonary surfacta
397	132	6.4	2232	2	T34434	hypothetical prote	c 470	123	6.0	635	2	A57131	collagen alpha 2(V
398	131	6.3	839	2	T04859	extensin homolog F	c 471	123	6.0	688	2	A53330	collagen alpha 2(I)
399	131	6.3	1151	2	T18535	high molecular mas	c 472	123	6.0	1100	2	JC8033	leukocyte formin p
c 400	130	6.3	396	1	KX802	plasma protein 2 -	c 473	123	6.0	1418	2	T45467	collagen alpha 1(I)
c 401	130	6.4	438	2	S53787	collagen alpha cha	c 474	123	6.0	1464	1	CGHUIS	collagen alpha 1(I)
402	130	6.3	573	2	A33533	cell surface glyco	475	122.5	5.9	75	2	A37002	catroxin 1 (EC 3
c 403	130	6.3	775	1	EDBE11	immediate-early pr	c 476	122.5	6.0	684	2	I58166	protein-tyrosine k
c 404	130	6.4	1466	1	CGHU7L	collagen alpha 1(I)	477	122.5	5.9	1091	2	S33596	rabphilin-3A - rat
405	129.5	6.3	817	2	S51342	verprolin - yeast	478	122.5	5.9	3164	1	WNBEH6	U136 protein - hum
406	129.5	6.3	1585	2	T31611	hypothetical prote	c 479	122	6.0	931	2	S13580	collagen alpha 1(I)
c 407	129	6.3	308	2	T37286	collagen 40 - Caen	480	122	5.9	1049	1	CGBOY8	collagen alpha 1(I)
408	129	6.2	721	2	E70766	hypothetical prote	481	122	5.9	1188	2	S49915	extensin-like prot
409	129	6.2	3530	2	A59266	unconventional myo	482	122	5.9	1520	2	T00273	hypothetical prote
c 410	128.5	6.2	320	2	JC1255	TIS11 protein - ra	c 483	122	5.9	1575	2	S68448	synaptotagmin, 170K
411	128.5	6.2	1006	2	G86292	hypothetical prote	c 484	122	6.0	1744	2	S40991	collagen alpha 1(I)
412	128	6.2	256	2	A60533	tumor-associated a	485	121.5	5.9	435	2	T15143	hypothetical prote
413	128	6.2	296	2	A31219	collagen 1 Caeno	486	121.5	5.9	610	2	S35049	mucin JERS7 - huma
414	128	6.2	301	2	T21314	hypothetical prote	487	121.5	5.9	825	1	EDBEXD	immediate-early pr
c 415	128	6.2	649	1	A46500	hypothetical prote	c 488	121.5	6.0	1487	1	CGHU6C	collagen alpha 1(I)
c 416	128	6.3	1546	2	CGHU2E	collagen alpha 2(X	489	121	5.9	363	2	T16755	hypothetical prote
417	128	6.2	2142	2	B35098	MHC class III hiet	490	121	5.9	620	2	S06733	hydroxyproline-ric
418	127.5	6.2	69	2	S28195	tissue kallikrein	c 491	121	5.9	680	2	S31216	collagen alpha 1(X
c 419	127.5	6.2	72	2	S28196	tissue kallikrein	492	121	5.9	780	2	T00366	hypothetical prote
c 420	127.5	6.3	431	2	S09824	hypothetical prote	493	121	5.9	862	2	T46289	hypothetical prote
421	127.5	6.2	507	2	T47468	antifreeze glycope	c 494	121	5.9	1142	2	JX0369	collagen alpha 1(X
422	127.5	6.2	1433	2	A46053	bullous pemphigoid	c 495	121	5.9	1373	1	A43291	collagen alpha 2(I)
423	127	6.1	548	2	S52735	CW17R protein - mo	496	121	5.9	1487	1	EDBEF6	155K transcription
424	127	6.1	754	2	A55267	collagen alpha 5(I)	c 497	120.5	5.9	329	2	T32783	hypothetical prote
c 425	127	6.1	805	2	T43385	hypothetical prote	498	120.5	5.8	635	2	T75477	hypothetical prote
c 426	127	6.2	1414	1	S23809	collagen alpha 2(I)	499	120.5	5.8	666	2	B70803	hypothetical prote
c 427	127	6.2	1453	2	S21626	collagen alpha 1(I)	500	120.5	5.8	963	2	T19140	hypothetical prote
c 428	126.5	6.2	290	2	T23416	hypothetical prote	c 501	120.5	5.9	1106	2	JQ0405	hypothetical 119.5
c 429	126.5	6.2	488	2	A27353	collagen alpha 1(I)	c 502	120.5	5.9	1733	1	B45344	probable nuclear a
430	126.5	6.1	522	2	A41819	nucleoporin p62 -	503	120.5	5.8	1896	1	RNPF2L	DNA-directed RNA p
431	126.5	6.1	839	2	F75518	hypothetical prote	c 504	120	5.9	490	2	T09084	phosphatidylinosit
c 432	126.5	6.1	1201	2	G86441	unknown protein [i	505	120	5.8	779	1	CGBOIS	collagen alpha 1(I)
c 433	126.5	6.2	1806	1	CGHU1E	collagen alpha 1(X	506	120	5.8	1006	2	T42731	atrophin-1 related
434	126	6.1	80	2	A05324	gamma-renin (EC 3.	c 507	120	5.9	1460	2	EDBEIF	immediate-early pr
c 435	126	6.1	323	2	T27450	hypothetical prote	508	120	5.8	1464	2	S59856	collagen alpha 1(I)
c 436	126	6.2	779	1	CGBO1S	collagen alpha 1(I)	c 509	120	5.9	1759	2	T29351	collagen alpha 2(I)
c 437	126	6.1	1334	2	T50568	probable multi-dom	c 510	120	5.9	1958	2	B40505	hypothetical prote
c 438	126	6.2	1464	2	S59856	collagen alpha 1(I)	511	119.5	5.8	309	1	S09257	homeotic protein H
c 439	126	6.1	3149	1	QBEB8	BPLF1 protein - hu	c 512	119.5	5.9	636	2	S41067	collagen alpha 1(I)
c 440	125.5	6.2	371	2	E88633	protein F56B3.1 [i	513	119.5	5.8	705	2	A35363	synapsin I splice
c 441	125	6.1	348	2	T29288	hypothetical prote	514	119	5.8	227	2	C29149	proline-rich prote
c 442	125	6.1	426	2	JQ1696	hypothetical prote	515	119	5.8	310	2	I50696	collagen alpha 1(I)
443	125	6.1	558	2	JC2004	pistil extensin-li	c 516	119	5.8	480	2	A40815	transcription fact
c 444	125	6.1	707	2	T38819	nuclear factor-kap	517	119	5.8	528	2	I47141	gastric mucin (clo
c 445	125	6.1	574	2	A46302	wiskott-aldrich sy	518	119	5.8	680	1	CGHUID	collagen alpha 1(X
c 446	125	6.1	886	2	I50694	PTB-associated epl	c 519	119	5.8	1763	2	S16366	collagen alpha 2(I)
c 447	125	6.1	1603	2	S23810	collagen alpha 1(I	c 520	119	5.8	1775	2	A31893	collagen alpha 1(I)
448	125	6.1	1970	1	S21054	collagen alpha 1(X	521	118.5	5.7	526	2	A56573	collagen alpha 1(I)
449	125	6.1	1370	2	T25048	DNA-directed RNA p	522	118.5	5.7	586	2	T29695	nuclear pore compl
c 450	124.5	6.1	312	2	T25048	RNA polymerase II	523	118.5	5.7	742	2	F84643	hypothetical prote
451	124.5	6.0	402	2	E86185	hypothetical prote	c 524	118.5	5.8	920	2	B34493	hypothetical prote
c 452	124.5	6.1	418	2	T15142	hypothetical prote	c 525	118.5	5.8	939	2	G75481	sensory box/GGDEF



C 526	118.5	5.8	1147	1	MWAXIB	myosin heavy chain
C 527	118.5	5.8	1366	1	CGH02S	collagen alpha 2(I
C 528	118.5	5.8	1736	2	T00391	hypothetical prote
C 529	118.5	5.8	1758	2	T29350	hypothetical prote
C 530	118.5	5.8	2944	2	A54849	collagen alpha 1(V
C 531	118	5.7	303	2	T19289	hypothetical prote
C 532	118	5.7	330	2	T26004	hypothetical prote
C 533	118	5.8	373	2	A47234	homeobox protein H
C 534	118	5.7	1285	2	T14171	ataxin-2 - mouse
C 535	118	5.7	1453	2	S21626	collagen alpha 1(I
C 536	118	5.7	1487	1	EDBEE1	immediate-early pr
C 537	117.5	5.8	312	2	A61183	hypothetical prote
C 538	117.5	5.7	878	2	T21621	hypothetical prote
C 539	117.5	5.7	1388	2	A53317	collagen alpha 1(X
C 540	117.5	5.7	1494	2	T14355	protein-tyrosine-p
C 541	117.5	5.7	1914	2	T42635	tenascin Y precurs
C 542	117.5	5.7	1959	1	AGRT	agrin - rat
C 543	117	5.7	279	2	S53363	mucin 5AC (clone J
C 544	117	5.7	290	2	A32249	collagen - sea urc
C 545	117	5.7	383	2	S32975	gene BCRF2 protein
C 546	117	5.7	393	2	PQ0479	pistil extensin-I
C 547	117	5.7	471	2	T33997	hypothetical prote
C 548	117	5.7	487	2	A24442	nuclear protein B3
C 549	117	5.7	488	2	S42753	collagen alpha 1(I
C 550	117	5.7	525	2	A35596	nuclear pore glyco
C 551	117	5.7	605	2	T33913	hypothetical prote
C 552	117	5.7	1299	2	T47182	hypothetical prote
C 553	117	5.7	1532	2	A61262	collagen alpha 1(X
C 554	117	5.7	1870	2	S37671	MHC class III hist
C 555	117	5.7	1872	2	S36152	MHC class III hist
C 556	117	5.7	3124	2	A40020	collagen alpha 1(X
C 557	117	5.7	3511	2	A59295	unconventional myo
C 558	116.5	5.6	614	2	T33149	hypothetical prote
C 559	116.5	5.6	1146	2	A38587	collagen, cornea-s
C 560	116.5	5.6	1255	2	T31065	diaphanous protein
C 561	116.5	5.7	1497	2	T149607	procollagen type V
C 562	116	5.7	474	2	A41782	transcription fact
C 563	116	5.7	684	2	T36771	probable integral
C 564	116	5.7	825	1	EDBEXD	immediate-early pr
C 565	116	5.7	862	2	T46289	hypothetical prote
C 566	116	5.6	865	2	A47282	calcium-binding pr
C 567	116	5.7	964	1	CGCH2S	collagen alpha 2(I
C 568	116	5.6	1367	1	S48478	glucan 1,4-alpha-g
C 569	116	5.7	1549	2	I48103	type VII collagen
C 570	115.5	5.7	300	2	T19929	hypothetical prote
C 571	115.5	5.6	303	2	T28999	hypothetical prote
C 572	115.5	5.6	304	2	T22602	hypothetical prote
C 573	115.5	5.6	422	1	KXH0Z	plasma protein 2 p
C 574	115.5	5.7	676	1	EDBE22	immediate-early pr
C 575	115.5	5.6	749	2	I38488	trophinin - human
C 576	115.5	5.6	1132	2	T03844	telomerase catalyt
C 577	115.5	5.6	1199	2	A0670	nuclear envelope p
C 578	115.5	5.6	1400	2	T31555	hypothetical prote
C 579	115.5	5.6	1414	1	S23809	collagen alpha 2(I
C 580	115.5	5.7	1419	2	A41182	collagen alpha 1(I
C 581	115.5	5.7	1487	2	B41182	collagen alpha 1(I
C 582	115	5.6	285	1	A43556	homeotic protein H
C 583	115	5.6	461	2	T51044	related to spore c
C 584	115	5.7	632	2	S42731	collagen alpha 1 c
C 585	115	5.7	698	2	T17261	hypothetical prote
C 586	115	5.7	775	1	EDBE11	immediate-early pr
C 587	115	5.6	1142	2	JX0369	collagen alpha 1(X
C 588	115	5.6	1207	2	T00378	hypothetical glyci
C 589	115	5.7	1381	2	E70806	adenomatous polyo
C 590	115	5.7	2874	2	T30258	Bassoon protein -
C 591	115	5.6	3942	2	T42730	elastase (EC 3.4.2
C 592	114.5	5.5	85	2	S44461	hypothetical prote
C 593	114.5	5.5	290	2	T24586	collagen col-34 -
C 594	114.5	5.5	298	2	JC1448	hypothetical prote
C 595	114.5	5.6	304	2	T23801	hypothetical prote
C 596	114.5	5.6	310	2	T29731	hypothetical prote
C 597	114.5	5.5	319	2	A36600	growth factor-indu
C 598	114.5	5.5	377	2	A48018	mucin 7 precursor,

C 599	114.5	5.6	405	4	A61181	homeotic protein H
C 600	114.5	5.6	452	2	C41602	transcription fact
C 601	114.5	5.6	469	2	A24450	collagen alpha 2(V
C 602	114.5	5.5	797	1	VBEX1	GTP-binding regula
C 603	114.5	5.5	846	2	S52418	hypothetical prote
C 604	114.5	5.5	914	2	T25220	collagen alpha 1(I
C 605	114.5	5.6	921	2	S40495	collagen alpha 1(I
C 606	114.5	5.5	961	2	A55380	faciogenital dyspl
C 607	114.5	5.6	1496	1	CGHU2V	collagen alpha 2(V
C 608	114.5	5.5	1670	1	CGHU3B	collagen alpha 3(I
C 609	114	5.6	204	2	JQ0321	hypothetical 19.8K
C 610	114	5.6	738	2	E87627	hypothetical prote
C 611	114	5.5	929	2	C96623	hypothetical prote
C 612	114	5.5	1323	2	S27224	N-methyl-D-asparta
C 613	114	5.5	1549	2	I48103	type VII collagen
C 614	113.5	5.5	307	2	T16842	hypothetical prote
C 615	113.5	5.5	319	2	T32250	hypothetical prote
C 616	113.5	5.5	383	2	T46707	proteophosphoglyca
C 617	113.5	5.6	452	2	T30082	hypothetical prote
C 618	113.5	5.5	456	2	T35474	50kD proline rich
C 619	113.5	5.5	593	2	S49525	glycoprotein G - s
C 620	113.5	5.5	647	2	T43952	hypothetical prote
C 621	113.5	5.6	676	1	EDB823	immediate-early pr
C 622	113.5	5.5	729	2	E70803	hypothetical prote
C 623	113.5	5.5	818	2	A59433	KIAA0672 protein l
C 624	113.5	5.5	987	2	I48652	mouse developmenta
C 625	113.5	5.5	987	2	I48953	eph-related recept
C 626	113.5	5.5	1001	2	T16419	hypothetical prote
C 627	113.5	5.5	1032	2	T34433	hypothetical prote
C 628	113.5	5.5	1165	2	T16420	hypothetical prote
C 629	113.5	5.6	1838	1	CGHU1V	collagen alpha 1(V
C 630	113.5	5.5	2187	2	T30826	nascent polypeptid
C 631	113.5	5.5	3938	2	T42761	Bassoon protein -
C 632	113	5.6	381	2	S16506	hypothetical prote
C 633	113	5.5	543	2	S35047	mucin JUL7 - human
C 634	113	5.6	618	2	S34436	collagen alpha 2(I
C 635	113	5.5	727	2	C84534	hypothetical prote
C 636	113	5.5	730	2	A36226	collagen alpha 1 c
C 637	113	5.5	753	2	JQ0532	Op protein - Kenne
C 638	113	5.5	786	2	T16509	hypothetical prote
C 639	113	5.5	812	2	S31521	collagen COLF1 - f
C 640	113	5.5	1356	1	C45219	N-methyl-D-asparta
C 641	113	5.5	1611	2	T38236	hypothetical prote
C 642	113	5.6	1712	1	CGHU2B	collagen alpha 2(I
C 643	113	5.5	1759	2	T29351	collagen alpha 2(I
C 644	113	5.5	3124	2	A40020	collagen alpha 1(X
C 645	112.5	5.4	317	2	T19143	hypothetical prote
C 646	112.5	5.5	330	2	S46657	collagen alpha 1(X
C 647	112.5	5.4	394	2	T33641	hypothetical prote
C 648	112.5	5.5	401	2	A48423	engrailed homeodom
C 649	112.5	5.5	1039	2	T35878	hypothetical prote
C 650	112.5	5.5	1051	2	A35763	collagen alpha 2 c
C 651	112.5	5.4	1400	2	T52359	hypothetical prote
C 652	112	5.5	305	2	T20906	hypothetical prote
C 653	112	5.5	319	2	F75420	hypothetical prote
C 654	112	5.4	492	2	S49147	ERF-2 protein - hu
C 655	112	5.4	591	2	T44868	probable membrane
C 656	112	5.4	600	2	D87232	conserved membrane
C 657	112	5.5	730	2	A36226	collagen alpha 1 c
C 658	112	5.4	980	2	S54986	regulatory protein
C 659	112	5.5	1007	2	T01437	hypothetical prote
C 660	112	5.4	1096	2	H86237	protein F14N23.29
C 661	112	5.4	1203	2	I55466	N-methyl-D-asparta
C 662	112	5.5	1215	2	T32734	myosin-IA - Acanth
C 663	112	5.4	1224	2	T40765	webi protein homol
C 664	112	5.4	1251	2	A57293	latent transformin
C 665	111.5	5.4	302	2	A31921	collagen dpy-13 pr
C 666	111.5	5.5	306	2	T21939	hypothetical prote
C 667	111.5	5.5	314	2	T34269	hypothetical prote
C 668	111.5	5.4	325	2	T32248	hypothetical prote
C 669	111.5	5.5	397	2	T35289	probable multifunc
C 670	111.5	5.5	405	2	T29167	hypothetical prote
C 671	111.5	5.4	413	2	T12533	hypothetical prote

c 672	111.5	5.5	510	2	A42750	insulinoma-associat	745	109.5	5.3	4957	2	T03455	ALR protein - huma
c 673	111.5	5.5	627	1	JC5534	protein kinase 1 (	746	109	5.3	317	2	S55316	mucin (clone PGM-2
c 674	111.5	5.4	907	2	E96636	hypothetical prote	c 747	109	5.4	587	2	T41653	probable transcrip
675	111.5	5.4	1132	2	A35098	MHC class III hist	748	109	5.3	615	2	A05289	collagen alpha 1(I
676	111.5	5.4	1323	2	I78557	N-methyl-D-asparta	749	109	5.3	760	2	F86387	probable Pto kinase
c 677	111.5	5.5	1670	1	CGH3B	collagen alpha 3(I	c 750	109	5.4	780	2	T00366	hypothetical prote
c 678	111.5	5.5	3573	2	S23070	erythronolide synt	c 751	109	5.4	783	2	T35389	probable serine-th
679	111	5.4	317	2	A28996	proline-rich prote	752	109	5.3	815	2	B56708	extracellular sign
680	111	5.4	437	2	S05478	properdin - mouse	753	109	5.3	873	2	A47283	calphostin - fruit
681	111	5.4	439	2	A36385	surface antigen se	c 754	109	5.4	914	2	H70987	hypothetical glyci
682	111	5.4	533	2	T33912	hypothetical prote	c 755	109	5.4	920	2	A45748	collagen alpha 1(V
c 683	111	5.5	794	2	T10519	pre-pro-legumini -	756	109	5.3	931	2	S13580	collagen alpha 1(I
c 684	111	5.5	888	2	A55318	serine/threonine p	757	109	5.3	1069	2	S27922	nuclear antigen EB
685	111	5.4	921	2	G02326	transcription fact	c 758	109	5.4	1170	2	A53612	laminin B1k chain
686	111	5.4	990	2	T14756	hypothetical prote	c 759	109	5.4	1752	2	A45407	collagen alpha 3(I
c 687	111	5.5	1184	2	S50832	atrophin-1 - huma	c 760	109	5.3	3002	2	A47221	fibrillin 1 precu
c 688	111	5.5	1428	2	T13926	probable protein p	761	108.5	5.3	282	2	T16036	cuticle collagen c
689	111	5.4	1777	2	T34369	hypothetical prote	c 762	108.5	5.3	313	2	T22828	hypothetical prote
690	110.5	5.3	221	2	T02086	zinc inducible pro	c 763	108.5	5.3	316	2	S08169	collagen col-12 pr
691	110.5	5.3	240	2	A24264	proline-rich prote	c 764	108.5	5.3	316	2	S08170	collagen col-13 pr
692	110.5	5.3	256	2	A56593	trypsin-related pr	c 765	108.5	5.3	325	2	T32248	hypothetical prote
693	110.5	5.3	347	2	A43815	transforming prote	766	108.5	5.3	424	2	T33663	hypothetical prote
694	110.5	5.3	632	2	S42731	collagen alpha 1 c	767	108.5	5.3	522	2	S52216	viral proteinase -
695	110.5	5.3	642	1	S34416	transcription fact	768	108.5	5.3	571	2	T43456	hypothetical prote
696	110.5	5.3	920	2	B34493	collagen alpha 1(I	769	108.5	5.3	667	2	S74254	homeotic protein s
c 697	110.5	5.4	921	2	S42617	collagen alpha 1(I	770	108.5	5.3	796	2	JC7555	C14orf4 protein -
698	110.5	5.3	1137	2	A86335	T20H2.9 protein -	771	108.5	5.3	886	2	I50694	collagen alpha 1(I
699	110.5	5.3	1497	2	I49607	procollagen type V	772	108.5	5.3	915	2	T09575	smoothelin - huma
c 700	110.5	5.4	1690	1	CGHUIB	collagen alpha 4(I	c 773	108.5	5.3	949	2	E75352	glycine cleavage s
701	110.5	5.3	1820	2	A55494	latent transformin	774	108.5	5.3	1496	1	CGHU2V	collagen alpha 2(V
702	110.5	5.3	2090	2	S26058	probable transform	c 775	108.5	5.3	1538	2	H70846	hypothetical prote
703	110.5	5.3	3436	2	S55659	tegument protein 6	c 776	108.5	5.3	1572	2	T00027	brain-specific ang
704	110	5.3	302	2	T32711	hypothetical prote	777	108.5	5.3	1613	2	S39059	protein BRG1 - hum
c 705	110	5.4	311	2	T15268	hypothetical prote	778	108.5	5.3	1618	2	S21424	neatin - human
706	110	5.3	333	2	S11484	CABP1 protein - si	779	108.5	5.3	1647	2	S45252	SNF2beta protein -
c 707	110	5.4	401	2	E70563	hypothetical prote	c 780	108.5	5.3	1691	1	T22917	collagen alpha 5(I
708	110	5.3	455	2	A87913	protein B0205.10 l	781	108	5.2	316	2	T20497	hypothetical prote
709	110	5.3	534	2	S21961	proline-rich prote	782	108	5.2	333	2	T15257	hypothetical prote
c 710	110	5.3	589	2	C70767	probable pknJ - My	783	108	5.2	384	2	T29422	hypothetical prote
c 711	110	5.4	594	2	G70545	hypothetical glyci	784	108	5.2	677	2	S23296	collagen alpha 2(I
c 712	110	5.4	603	2	T45093	hypothetical prote	785	108	5.2	684	2	T36771	probable integral
713	110	5.3	624	2	JC5471	regulatory protein	c 786	108	5.3	744	2	S15435	collagen alpha 1(V
714	110	5.3	628	2	S01955	hypothetical prote	787	108	5.2	969	2	T15446	hypothetical prote
715	110	5.3	671	1	CGRT1S	collagen alpha 1(I	788	108	5.2	987	2	A75496	conserved hypotet
716	110	5.3	784	2	JQ0317	hypothetical 82K p	789	108	5.2	1054	2	T43226	translatin initia
717	110	5.3	1135	2	T30561	Scythe protein - A	790	108	5.2	1184	2	S50832	atrophin-1 - huma
718	110	5.3	1184	2	G01763	insulin receptor s	791	108	5.2	1241	2	T18311	hypothetical prote
719	110	5.3	1242	2	JS0670	submaxillary mucin	792	108	5.2	1360	2	T33922	hypothetical prote
720	110	5.3	1589	2	T42233	hypothetical prote	793	108	5.2	1546	1	CGHU2E	collagen alpha 2(X
721	110	5.3	1758	2	T29350	hypothetical prote	c 794	108	5.3	1712	2	A38261	masking protein pr
c 722	110	5.4	1843	2	S18803	collagen alpha 1(V	c 795	108	5.3	3149	1	Q0BE8	BPLF1 protein - hu
723	110	5.3	2124	2	T28658	polyketide synthas	c 796	108	5.3	3198	2	A43426	collagen alpha 2 f
724	109.5	5.3	61	2	PS0049	serine proteinase	c 797	108	5.3	3530	2	A59266	unconventional myo
725	109.5	5.3	142	2	B41132	collagen-related p	c 798	108	5.3	3942	2	T42730	Bassoon protein -
726	109.5	5.3	290	2	T24590	hypothetical prote	799	107.5	5.2	211	2	C87462	hypothetical prote
c 727	109.5	5.4	294	2	S13141	hypothetical prote	800	107.5	5.2	227	2	G70555	hypothetical prote
c 728	109.5	5.4	295	2	B48013	proline-rich prote	c 801	107.5	5.3	282	2	J50168	collagen col-8 - C
c 729	109.5	5.4	297	2	T18638	hypothetical prote	c 802	107.5	5.3	282	2	T16036	cuticle collagen c
730	109.5	5.3	299	1	FRSMBG	streptogrisin B (E	c 803	107.5	5.3	300	2	T24482	hypothetical prote
731	109.5	5.3	348	2	JQ0431	hypothetical 35.5K	804	107.5	5.2	301	2	B31219	collagen 2 - Caeno
c 732	109.5	5.4	374	1	A42046	surfactant protein	c 805	107.5	5.3	304	2	T22482	hypothetical prote
733	109.5	5.3	379	2	T05441	proline-rich prote	c 806	107.5	5.3	339	2	S20880	homeotic protein H
734	109.5	5.3	379	2	D85257	extensin-like prote	c 807	107.5	5.3	356	2	T22827	hypothetical prote
c 735	109.5	5.4	428	2	T24769	hypothetical prote	808	107.5	5.2	379	2	S31719	proline-rich prote
c 736	109.5	5.4	614	2	T33149	hypothetical prote	809	107.5	5.2	458	2	T31631	hypothetical prote
c 737	109.5	5.4	632	2	T00084	hypothetical prote	810	107.5	5.2	510	2	H84824	En/Spm-like transp
738	109.5	5.3	649	2	JQ0103	hypothetical 70K p	c 811	107.5	5.3	511	1	A48560	probable mucin Dkf
c 739	109.5	5.4	656	2	AC0573	outer membrane est	c 812	107.5	5.2	580	2	T43481	hypothetical prote
740	109.5	5.3	1042	1	CGCH1S	collagen alpha 1(I	c 813	107.5	5.3	725	2	T00492	proline-rich prote
741	109.5	5.3	1126	2	T20801	hypothetical prote	c 814	107.5	5.2	728	2	I38487	hypothetical prote
c 742	109.5	5.4	1168	1	MWAXIC	myosin heavy chain	c 815	107.5	5.3	1747	2	A41121	tastin - human
c 743	109.5	5.4	1660	2	A70869	hypothetical glyci	816	107	5.2	186	2	C54132	collagen-related p
744	109.5	5.3	1707	2	A33526	collagen alpha 2(I	817	107	5.2	240	2	B24264	proline-rich prote

818	107	5.2	264	2	D34768	ORF4 protein - Orf	c 891	105.5	5.2	812	2	S31521	collagen COLP1 - f
c 819	107	5.3	304	2	T26185	hypothetical prote	892	105.5	5.1	873	2	F96615	probable Myb-famil
c 820	107	5.3	304	2	T26184	hypothetical prote	893	105.5	5.1	898	2	T14764	hypothetical prote
821	107	5.2	388	2	JC5437	spliceosome-associ	894	105.5	5.1	968	2	T00353	hypothetical prote
822	107	5.2	395	2	H75457	hypothetical prote	895	105.5	5.1	1063	2	T03743	bifocal protein -
823	107	5.2	432	2	A25483	env polyprotein, r	896	105.5	5.1	1106	1	TVHUGL	transforming prote
824	107	5.2	432	2	A25483	hypothetical prote	c 897	105.5	5.2	1122	2	T14180	exif protein - Myc
c 825	107	5.3	573	2	JQ0135	hypothetical prote	c 898	105.5	5.2	1198	2	T28678	polyketide synthas
c 826	107	5.3	576	2	T36729	probable serine/th	c 899	105.5	5.1	1603	2	S23810	collagen alpha 1(X
c 827	107	5.2	592	2	D70863	hypothetical prote	c 900	105.5	5.2	1691	1	CGHU6B	collagen alpha 6(I
c 828	107	5.3	615	2	A05269	collagen alpha 1(I	901	105.5	5.1	2774	2	A43359	microtubule-associ
c 829	107	5.2	616	2	JQ1441	hypothetical 67K p	902	105.5	5.1	2776	2	T17428	FK506 polyketide s
c 830	107	5.2	635	2	F96660	protein FK11.10 [	903	105	5.1	297	2	T27525	hypothetical prote
c 831	107	5.3	675	2	S20819	collagen alpha 3(I	904	105	5.1	304	2	T22482	hypothetical prote
c 832	107	5.2	738	2	S40992	hypothetical prote	905	105	5.1	380	2	T28888	hypothetical prote
c 833	107	5.3	744	1	A32426	collagen alpha 1(V	906	105	5.1	439	1	A48099	cuticle collagen d
c 834	107	5.3	744	1	S23298	collagen alpha 1(V	c 907	105	5.2	440	2	S71795	transcription fact
835	107	5.2	801	2	T29018	hypothetical prote	c 908	105	5.1	505	2	S72273	actin-depolymerizi
836	107	5.2	847	1	A53800	mixed-lineage prot	c 909	105	5.2	517	2	T10927	3C3.18c protein -
837	107	5.2	967	2	S66852	hypothetical prote	c 910	105	5.2	518	2	T23745	hypothetical prote
838	107	5.2	1040	2	T29092	TSC-22 protein hom	c 911	105	5.2	532	2	T07903	tubulin delta chai
c 839	107	5.3	1306	2	A70934	hypothetical glyci	c 912	105	5.2	542	2	T29707	hypothetical prote
c 840	107	5.3	1323	2	T78557	N-methyl-D-asparta	c 913	105	5.2	589	2	T29299	hypothetical prote
841	107	5.2	1464	1	CGHUI8	collagen alpha 1(I	914	105	5.1	628	2	S19150	hypothetical prote
842	107	5.2	1466	1	CGHUI7	collagen alpha 1(I	915	105	5.1	636	2	D84823	hypothetical prote
843	107	5.2	1574	2	T13954	MEGF6 protein - ra	916	105	5.1	660	2	JW0067	chitinase (EC 3.2.
844	107	5.2	1669	1	CGHU4B	collagen alpha 1(I	917	105	5.1	674	2	S13301	collagen alpha 1(X
845	107	5.2	1752	2	A45407	collagen alpha 3(I	c 918	105	5.2	680	2	S21323	probable endogluca
846	107	5.2	2649	2	T51023	hypothetical prote	c 919	105	5.2	969	2	AB3388	soluble lytic mure
847	107	5.2	3534	2	T42567	tegument protein 2	c 920	105	5.2	1151	2	T18535	high molecular mas
c 848	106.5	5.2	302	2	T15936	hypothetical prote	921	105	5.1	1231	2	S30185	insulin receptor s
c 849	106.5	5.2	316	2	T20497	hypothetical prote	c 922	105	5.2	2182	2	T14320	calcineurin inhibi
850	106.5	5.2	355	2	T29932	hypothetical prote	c 923	105	5.2	3176	2	CGHU3A	collagen alpha 3(V
851	106.5	5.2	514	2	H70699	probable ppp prote	c 924	105	5.2	3707	2	S18252	heparan sulfate pr
c 852	106.5	5.2	529	2	T45134	hypothetical prote	925	104.5	5.1	164	2	I53641	mucin SAC - human
853	106.5	5.2	635	2	A57131	collagen alpha 2(V	926	104.5	5.1	266	2	T22706	hypothetical prote
854	106.5	5.2	684	2	T25603	hypothetical prote	c 927	104.5	5.1	267	1	UUCH	major prion protei
855	106.5	5.2	823	2	T02812	probable membrane	928	104.5	5.1	287	2	T15779	hypothetical prote
856	106.5	5.2	876	2	T49801	hypothetical prote	929	104.5	5.1	300	2	T19929	hypothetical prote
857	106.5	5.2	915	2	S36327	ciathrin assembly	930	104.5	5.1	306	2	T09067	extensin-like prot
858	106.5	5.2	1298	1	EDBE75	immediate-early pr	931	104.5	5.1	313	2	T22828	hypothetical prote
859	106.5	5.2	1373	1	A43291	collagen alpha 2(I	932	104.5	5.1	341	2	S09913	hypothetical prote
860	106.5	5.2	1892	2	T18314	hypothetical prote	933	104.5	5.1	356	2	T22827	hypothetical prote
861	106.5	5.2	13288	2	T03099	mucin, submaxillar	c 934	104.5	5.1	379	2	S49999	40K protein - frog
862	106	5.1	149	2	A41132	collagen-related p	c 935	104.5	5.1	380	2	A48295	collagen 1 - marin
c 863	106	5.2	297	2	T27525	hypothetical prote	936	104.5	5.1	510	2	A42750	inulinoma-associa
864	106	5.1	304	2	T26185	hypothetical prote	937	104.5	5.1	589	2	T29299	hypothetical prote
c 865	106	5.1	304	2	T26184	hypothetical prote	c 938	104.5	5.1	636	2	S41067	collagen alpha 1(I
c 866	106	5.2	314	2	T32985	hypothetical prote	c 939	104.5	5.1	641	1	Q0BE31	nuclear antigen EB
867	106	5.1	509	2	D86911	conserved hypotet	c 940	104.5	5.1	674	2	S13301	collagen alpha 1(X
868	106	5.1	509	2	T10013	probable phosphopr	941	104.5	5.1	684	2	A56154	Abl substrate ena
c 869	106	5.2	704	2	A48097	rabphilin-3A - bov	942	104.5	5.1	708	2	D96711	hypothetical prote
c 870	106	5.1	814	2	T49207	receptor kinase-li	943	104.5	5.1	924	2	S27923	gene Lf3 protein -
c 871	106	5.2	832	2	B87673	ABC transporter, H	944	104.5	5.1	1048	1	XPBEA9	large structural p
872	106	5.1	873	2	B75514	penicillin-binding	945	104.5	5.1	1402	2	I46707	translation initia
c 873	106	5.2	1079	2	B70807	hypothetical glyci	c 946	104.5	5.1	1638	2	A42091	transcription acti
874	106	5.1	1176	2	T49482	hypothetical prote	c 947	104.5	5.1	2240	2	T37057	probable multi-dom
c 875	106	5.2	1237	2	T45070	protein kinase hom	c 948	104.5	5.1	3002	2	A47221	fibrillin 1 precur
876	106	5.1	1843	2	S18803	collagen alpha 1(V	949	104	5.0	49	2	B24696	tissue kallikrein
c 877	106	5.2	2715	2	T13049	collagen alpha 1(V	950	104	5.0	270	2	H83619	hypothetical prote
c 878	105.5	5.2	177	2	S37749	eyelid - fruit fly	951	104	5.0	272	2	H87075	probable conserved
c 879	105.5	5.2	273	2	A6280	collagen alpha 2(X	952	104	5.0	283	2	E88597	protein Y47D38.6 l
880	105.5	5.1	291	2	T26576	prion protein - ch	953	104	5.0	287	2	S65765	chitinase (EC 3.2.
881	105.5	5.1	294	2	T22639	hypothetical prote	954	104	5.0	290	2	A32249	collagen - sea urc
c 882	105.5	5.1	307	2	B72677	hypothetical prote	955	104	5.0	310	1	PIHUSD	salivary proline-r
c 883	105.5	5.2	309	2	T28708	hypothetical prote	956	104	5.0	314	2	T32985	hypothetical prote
884	105.5	5.1	310	2	T22641	hypothetical prote	c 957	104	5.1	314	2	T32247	hypothetical prote
885	105.5	5.1	366	2	T70907	hypothetical prote	c 958	104	5.1	316	2	G84187	hypothetical prote
886	105.5	5.1	504	2	T34995	probable integral	c 959	104	5.1	358	1	WMBE38	infected cell prot
c 887	105.5	5.2	584	2	G70804	hypothetical glyci	960	104	5.0	365	2	T24955	hypothetical prote
888	105.5	5.1	626	2	B70754	probable serine/th	961	104	5.0	421	2	T30709	core protein homol
889	105.5	5.1	715	1	TNBE77	77K alpha trans-in	962	104	5.0	441	2	T23461	hypothetical prote
c 890	105.5	5.2	754	2	A55267	collagen alpha 5(I	c 963	104	5.1	469	1	S29126	properdin precurs

964	104	5.0	563	2	C70987	hypothetical prote	1037	102.5	5.0	390	4	S03158	hypothetical BCR/A
c 965	104	5.1	577	2	A40220	cleavage stimulat	c1038	102.5	5.0	438	2	S138946	melanoma ubiquitou
966	104	5.0	586	2	H86914	conserved hypothet	1039	102.5	5.0	439	2	S51939	chitinase (EC 3.2.
c 967	104	5.1	597	2	QJ0107	hypothetical 66K p	c1040	102.5	5.0	525	2	JN0059	hypothetical 57.4K
968	104	5.0	574	2	S23297	collagen alpha 1(X	c1041	102.5	5.0	528	2	B75310	conserved hypothet
c 969	104	5.1	784	2	QJ0317	hypothetical 82K p	1042	102.5	5.0	530	2	A45690	transactivator EBN
970	104	5.0	1029	2	T30351	mucin-like protein	1043	102.5	5.0	540	2	S21825	vicilin-like stora
971	104	5.0	1039	2	T35878	hypothetical prote	1044	102.5	5.0	542	2	A44358	zyxin - chicken
972	104	5.0	1257	2	S28764	neurocan precursor	1045	102.5	5.0	548	2	E70546	hypothetical prote
973	104	5.0	1428	2	T08852	lustrin A - Califo	1046	102.5	5.0	559	2	T02825	probable membrane
974	104	5.0	2205	1	MWVRN	nonstructural poly	1047	102.5	5.0	576	2	T36729	probable serine/th
975	103.5	5.0	64	2	A30981	prostatic arginine	1048	102.5	5.0	627	2	A70888	hypothetical prote
976	103.5	5.0	386	2	T36169	hypothetical prote	1049	102.5	5.0	631	2	S52257	episialin - mouse
977	103.5	5.0	410	2	T15142	hypothetical prote	1050	102.5	5.0	693	1	TVHUA2	bcr (breakpoint cl
978	103.5	5.0	440	2	JC7807	Wiskott-Aldrich sy	1051	102.5	5.0	698	2	T32594	hypothetical prote
979	103.5	5.0	461	2	T10741	extensin-like prot	c1052	102.5	5.0	767	2	S55618	hypothetical prote
980	103.5	5.0	469	1	S23126	properdin precursor	1053	102.5	5.0	867	2	S57795	probable deoxyribo
c 981	103.5	5.1	496	2	S28402	homeotic protein H	1054	102.5	5.0	900	2	B70694	probable infB - My
982	103.5	5.0	538	2	S65764	chitinase (EC 3.2.	1055	102.5	5.0	940	2	A38149	RNA-directed RNA p
983	103.5	5.0	688	2	A53330	collagen alpha 2(I	1056	102.5	5.0	992	1	GNWVR3	structural polypro
c 984	103.5	5.1	729	2	E70803	hypothetical prote	1057	102.5	5.0	1089	2	T30843	serine-repeat anti
985	103.5	5.0	772	2	T13078	KIAA0992 protein -	1058	102.5	5.0	1122	2	T47424	hypothetical prote
986	103.5	5.0	825	2	T23634	hypothetical prote	1059	102.5	5.0	1142	2	T00022	B120 protein - hum
987	103.5	5.0	866	2	T45462	membrane glycoprot	1060	102.5	5.0	1271	1	TVHUR	bcr (breakpoint cl
988	103.5	5.0	867	2	T45463	hypothetical 119.5	c1061	102.5	5.0	1334	2	T50568	probable multi-dom
989	103.5	5.0	1106	2	JQ0405	hypothetical prote	c1062	102.5	5.0	1571	2	T00062	hypothetical prote
990	103.5	5.0	1110	2	T19673	mucin, tracheobron	1063	102.5	5.0	1747	2	A45974	collagen alpha 1(X
991	103.5	5.0	1118	2	A48292	probable iron-sulf	1064	102.5	5.0	1791	2	T02345	hypothetical prote
992	103.5	5.0	1132	2	C75259	collagen, cornea-s	c1065	102	5.0	237	2	A88640	protein C34H4.4 li
c 993	103.5	5.1	1146	2	A38587	hypothetical prote	1066	102	4.9	255	2	JQ0320	hypothetical 24.7K
c 994	103.5	5.1	1216	2	T34101	hypothetical prote	c1067	102	5.0	267	2	S27953	Mx protein - pig (
c 995	103.5	5.1	1298	1	EDBE75	immediate-early pr	1068	102	4.9	286	2	S34665	collagen, cuticula
996	103.5	5.0	1460	1	EDBEIF	immediate-early pr	1069	102	4.9	315	2	T06806	proline rich prote
997	103.5	5.0	1487	1	CGHU6C	collagen alpha 1(I	1070	102	4.9	316	2	T19288	hypothetical prote
998	103.5	5.0	1621	2	T15264	hypothetical prote	1071	102	4.9	323	2	T19142	hypothetical prote
c 999	103.5	5.1	1855	2	T32633	hypothetical prote	c1072	102	5.0	416	2	T32458	hypothetical prote
1000	103.5	5.0	1838	1	CGHU1V	collagen alpha 1(V	1073	102	4.9	495	1	S31223	transcription fact
1001	103.5	5.0	1857	2	S31212	collagen alpha 1(X	1074	102	4.9	551	2	S57447	HPBIII-7 protein - hu
1002	103.5	5.0	1888	2	S78476	collagen alpha 1(X	c1075	102	5.0	575	2	JG0181	XIII2 protein - hu
1003	103.5	5.0	1964	2	T09059	notch4 - mouse	1076	102	4.9	665	1	VCVWEM	env polypeptin -
1004	103.5	5.0	2555	2	A40043	notch protein homo	1077	102	4.9	667	2	A41311	transcription fact
1005	103	5.0	214	2	T10737	extensin-like cell	c1078	102	5.0	680	1	CGHUID	collagen alpha 1(X
1006	103	5.0	219	2	T09854	proline-rich cell	1079	102	4.9	760	2	T16726	hypothetical prote
1007	103	5.0	269	2	T26957	hypothetical prote	1080	102	4.9	1001	2	T13807	potassium channel
c1008	103	5.1	303	2	T19289	hypothetical prote	1081	102	4.9	1008	2	T04462	hypothetical prote
c1009	103	5.1	363	2	T16831	hypothetical prote	1082	102	4.9	1069	2	D85383	hypothetical prote
c1010	103	5.1	401	1	OZQOAC	circumsporozoite p	c1083	102	5.0	1098	2	T08599	probable transcrip
1011	103	5.0	422	2	T51199	hypothetical prote	1084	102	4.9	1235	1	S16948	insulin receptor s
1012	103	5.0	464	2	T32812	endoglucanase I -	1085	102	4.9	2274	2	T30258	adenomatous polypo
1013	103	5.0	530	2	T32812	hypothetical prote	c1086	102	5.0	2414	2	A54277	transcription adap
c1014	103	5.1	566	2	T34842	probable transfera	c1087	102	5.0	13288	2	T03099	mucin, submaxillar
1015	103	5.0	600	2	S07638	spore coat protein	1088	101.5	4.9	210	2	B44984	collagen - nematod
c1016	103	5.1	623	2	A45137	collagen alpha 4(I	c1089	101.5	5.0	283	2	T29837	hypothetical prote
1017	103	5.0	646	2	T35002	probable respirato	c1090	101.5	5.0	294	2	T29839	hypothetical prote
c1018	103	5.1	679	2	T36426	probable oxidoredu	1091	101.5	4.9	312	2	A31846	hypothetical prote
1019	103	5.0	680	2	S31216	collagen alpha 1(X	1092	101.5	4.9	324	2	S13497	130K paracrystalli
1020	103	5.0	711	2	S43464	ecdysteroid-induce	1093	101.5	4.9	324	2	T34203	cAMP-binding prote
c1021	103	5.1	718	2	A36068	major ampuillate fi	1094	101.5	4.9	327	2	T34203	hypothetical prote
c1022	103	5.1	801	2	T29018	hypothetical prote	1095	101.5	4.9	371	2	F70555	hypothetical prote
1023	103	5.0	920	2	A45748	collagen alpha 1(V	c1096	101.5	5.0	379	2	S31719	proline-rich prote
1024	103	5.0	938	1	Q0BE24	nuclear antigen BB	1097	101.5	4.9	439	2	I57561	transcription fact
c1025	103	5.0	1076	2	C96620	protein T30E16.23	1098	101.5	4.9	449	2	A44993	cellulase (EC 3.2.
1026	103	5.1	1446	1	A45344	immediate-early pr	1099	101.5	4.9	583	1	S22544	transcription fact
c1027	103	5.1	1454	2	T13709	diacylglycerol kin	1100	101.5	4.9	592	2	T42078	serine/threonine p
1028	103	5.0	1589	2	T13606	hypothetical prote	c1101	101.5	5.0	635	2	F75477	hypothetical prote
c1029	103	5.1	1655	2	T13998	gene mastermind pr	c1102	101.5	5.0	638	2	AF3463	flagellar protein
1030	103	5.0	2321	2	S78549	notch3 protein - h	1103	101.5	4.9	725	2	A41258	a-agglutinin core
1031	102.5	5.0	221	2	C34768	ORF2 protein - Orf	c1104	101.5	5.0	749	2	A70812	hypothetical glyci
1032	102.5	5.0	282	2	JS0168	collagen col-8 - C	1105	101.5	4.9	880	2	D89756	protein T32E7.2b l
1033	102.5	5.0	283	2	T29837	hypothetical prote	1106	101.5	4.9	896	2	S36326	clathrin assembly
1034	102.5	5.0	289	2	T26812	hypothetical prote	c1107	101.5	5.0	918	2	S23377	collagen alpha 2(V
1035	102.5	5.0	294	2	T29839	hypothetical prote	1108	101.5	4.9	932	2	T21338	hypothetical prote
1036	102.5	5.0	357	2	T21152	hypothetical prote	1109	101.5	4.9	997	2	T28872	hypothetical prote

c1110	101.5	5.0	1022	2	S04111	collagen alpha 2(V	c1183	100.5	4.9	1264	2	S41603	type V adenylyl cy
c1111	101.5	4.9	1139	1	S61918	protein kinase C (	c1184	100.5	4.9	1486	1	B40333	collagen alpha 1(I
c1112	101.5	5.0	1329	2	S70917	hypothetical glyci	c1185	100.5	4.9	1560	2	T42727	proliferation pote
c1113	101.5	5.0	1356	1	C45219	N-methyl-D-asparta	c1186	100.5	4.9	1690	1	CGHUIB	collagen alpha 4(I
c1114	101.5	4.9	1797	2	T21889	hypothetical prote	c1187	100.5	4.9	1737	2	T00209	MEGF8 protein - hu
c1115	101.5	4.9	1805	2	T21888	hypothetical prote	c1188	100.5	4.9	1747	2	A45974	collagen alpha 1(X
c1116	101.5	5.0	1870	2	S37671	MHC class III hist	c1189	100.5	4.9	2526	2	T20531	hypothetical prote
c1117	101.5	5.0	1872	2	S36152	MHC class III hist	c1190	100.5	4.9	2722	2	T20532	hypothetical prote
c1118	101.5	5.0	2468	2	A83412	hypothetical prote	c1191	100.5	4.9	2738	2	E88320	protein F07A11.6 (
c1119	101.5	4.9	5262	2	T03454	ALR protein - huma	c1192	100	4.8	188	2	D29149	proline-rich prote
c1120	101.5	5.0	7576	2	T17428	FK506 polyketide s	c1193	100	4.8	263	2	A87149	conserved hypothet
c1121	101	4.9	232	2	A60095	larval glue protei	c1194	100	4.8	307	2	T27609	hypothetical prote
c1122	101	4.9	257	2	T10586	small nuclear ribo	c1195	100	4.8	346	2	T46916	hypothetical prote
c1123	101	5.0	279	2	T26125	hypothetical prote	c1196	100	4.8	394	2	C84905	collagen extensin
c1124	101	4.9	284	2	G75447	hypothetical prote	c1197	100	4.8	469	2	A24450	collagen alpha 2(V
c1125	101	4.9	299	2	T24833	hypothetical prote	c1198	100	4.9	591	2	I48141	acroganin I - guine
c1126	101	4.9	300	2	T24482	hypothetical prote	c1199	100	4.8	691	2	A25704	synapsin I - rat
c1127	101	4.9	302	2	T15936	hypothetical prote	c1200	100	4.8	731	2	T04455	hypothetical prote
c1128	101	4.9	326	2	T29810	hypothetical prote	c1201	100	4.8	977	2	I32657	seizure-related pr
c1129	101	4.9	326	2	JS0169	collagen col-14 -	c1202	100	4.9	1263	2	T13805	spalt-related prot
c1130	101	4.9	330	2	S46657	collagen alpha 1(X	c1203	100	4.8	1418	2	T45467	collagen alpha 1(I
c1131	101	4.9	387	2	T21370	hypothetical prote	c1204	100	4.8	1419	2	A41182	collagen alpha 1(I
c1132	101	5.0	414	2	T49916	hypothetical prote	c1205	100	4.8	1487	2	B41182	collagen alpha 1(I
c1133	101	5.0	474	2	I38240	transcription fact	c1206	100	4.9	1669	1	CGMS4B	collagen alpha 1(I
c1134	101	5.0	476	2	A38478	surface glycoprote	c1207	100	4.8	1691	1	CGHU6B	collagen alpha 6(I
c1135	101	5.0	491	2	T0916	hypothetical glyci	c1208	100	4.9	2142	2	B35098	MHC class III hist
c1136	101	5.0	532	2	F70580	hypothetical glyci	c1209	100	4.9	2639	2	T31328	fibroin - Chinese
c1137	101	4.9	656	2	E75468	hypothetical prote	c1210	99.5	4.8	208	2	T36390	hypothetical prote
c1138	101	4.9	706	2	E30411	synapsin Ia - bovi	c1211	99.5	4.8	237	2	S46964	microfilarial shea
c1139	101	5.0	720	1	A55160	Trg protein - frui	c1212	99.5	4.9	255	1	S04899	myb-related protei
c1140	101	4.9	798	2	T21369	hypothetical prote	c1213	99.5	4.9	270	2	A60830	keratin, 70k type
c1141	101	4.9	850	2	S56015	gastric mucin MUC5	c1214	99.5	4.8	271	2	D84199	hypothetical prote
c1142	101	5.0	808	2	TC0399	dual leucine zippe	c1215	99.5	4.9	290	2	T24586	hypothetical prote
c1143	101	4.9	966	2	T00039	hypothetical prote	c1216	99.5	4.8	296	2	T21070	hypothetical prote
c1144	101	4.9	948	2	A57640	retinoblastoma bin	c1217	99.5	4.9	307	2	B72677	hypothetical prote
c1145	101	5.0	1006	2	T42731	atrophin-1 related	c1218	99.5	4.8	307	2	T37287	collagen 36 - Caen
c1146	101	4.9	1317	2	T03748	apoptosis associat	c1219	99.5	4.9	318	2	JC4963	metalloproteinase
c1147	101	4.9	1446	1	A45344	immediate-early pr	c1220	99.5	4.8	325	2	A55558	albumin D-box bind
c1148	101	4.9	1459	2	T32271	hypothetical prote	c1221	99.5	4.9	340	2	T20807	hypothetical prote
c1149	101	4.9	1541	2	T02831	AAA protein L4171	c1222	99.5	4.8	340	2	T34423	hypothetical prote
c1150	101	5.0	3137	2	A37797	collagen alpha 3(V	c1223	99.5	4.8	343	2	H70517	probable lppd prot
c1151	100.5	4.9	242	2	S60143	cellulase (EC 3.2.	c1224	98.5	4.8	360	2	T37285	collagen dpy-2 - C
c1152	100.5	4.9	245	1	W4WZ5	E4 protein - human	c1225	99.5	4.8	363	2	T16831	hypothetical prote
c1153	100.5	4.9	267	2	A37372	prion protein homo	c1226	99.5	4.8	365	2	A34894	hepatic transcript
c1154	100.5	4.9	283	2	T29980	hypothetical prote	c1227	99.5	4.8	389	2	S27200	proline-rich prote
c1155	100.5	4.9	290	2	T24590	hypothetical prote	c1228	99.5	4.8	457	2	A33669	streptogrisin C (E
c1156	100.5	4.9	299	2	T25407	hypothetical prote	c1229	99.5	4.8	474	2	S65763	chitinase (EC 3.2.
c1157	100.5	4.9	301	2	B31219	collagen 2 - Caeno	c1230	98.5	4.9	486	1	A57601	transcription fact
c1158	100.5	4.9	305	2	I57039	genomic screen hom	c1231	99.5	4.8	535	2	S6762	chitinase (EC 3.2.
c1159	100.5	4.9	316	2	S08169	collagen col-12 pr	c1232	99.5	4.9	562	2	B70953	hypothetical glyci
c1160	100.5	4.9	316	2	S08170	collagen col-13 pr	c1233	99.5	4.9	674	2	S23297	collagen alpha 1(X
c1161	100.5	4.9	317	2	T19143	hypothetical prote	c1234	99.5	4.9	705	2	A35363	synapsin I splice
c1162	100.5	4.9	333	2	T20436	hypothetical prote	c1235	99.5	4.8	770	1	S30293	transcription fact
c1163	100.5	4.9	339	2	T22607	hypothetical prote	c1236	99.5	4.9	888	2	S28791	collagen alpha 1(X
c1164	100.5	4.9	402	1	CG8028	collagen alpha 2(I	c1237	99.5	4.8	921	2	S40495	collagen alpha 1(I
c1165	100.5	4.9	416	2	T34279	hypothetical prote	c1238	99.5	4.8	1101	2	T16840	hypothetical prote
c1166	100.5	4.9	440	2	I61183	transcription fact	c1239	99.5	4.9	1167	2	T42704	hypothetical prote
c1167	100.5	4.9	476	1	SGMSV	vitronectin precur	c1240	99.5	4.8	1258	2	JC5765	inositol polyphosp
c1168	100.5	4.9	486	2	T35445	probable integral	c1241	99.5	4.8	1275	2	T33369	hypothetical prote
c1169	100.5	4.9	516	2	C44479	collagen alpha 1(X	c1242	98.5	4.9	1323	2	S27224	N-methyl-D-asparta
c1170	100.5	4.9	538	2	T49849	related to DRPLA p	c1243	99.5	4.8	1329	2	T29074	hypothetical prote
c1171	100.5	4.9	538	2	S57459	hook-containing pr	c1244	99.5	4.8	1332	2	T15670	hypothetical prote
c1172	100.5	4.9	542	2	I39540	chitinase (EC 3.2.	c1245	99.5	4.8	1344	1	A35175	mucin 1 precursor,
c1173	100.5	4.9	552	2	F75311	ABC transporter, A	c1246	99.5	4.9	1532	2	A61262	collagen alpha 1(X
c1174	100.5	4.9	613	2	T42671	hypothetical prote	c1247	99.5	4.8	1655	2	T32633	hypothetical prote
c1175	100.5	4.9	745	2	S13586	triacylglycerol li	c1248	98.5	4.8	1669	1	CGMS4B	collagen alpha 1(I
c1176	100.5	4.9	883	2	S57653	brevican precursor	c1249	99.5	4.9	2297	2	T34918	polyketide synthas
c1177	100.5	4.9	888	2	S28791	collagen alpha 1(X	c1250	99.5	4.8	2440	2	S39162	transcription coac
c1178	100.5	4.9	896	2	T51891	hypothetical prote	c1251	99.5	4.8	3198	2	A43426	collagen alpha 2 f
c1179	100.5	4.9	963	2	T19140	hypothetical prote	c1252	99.5	4.9	5069	2	T17464	rifamycin polyketi
c1180	100.5	4.9	1038	2	JT0663	ras GTPase-activat	c1253	99	4.8	217	2	S29309	hypothetical prote
c1181	100.5	4.9	1045	2	A35199	endoglucanase B (E	c1254	99	4.8	283	2	T29980	hypothetical prote
c1182	100.5	4.9	1182	2	I48378	hairless protein -	c1255	99	4.9	296	2	T21070	hypothetical prote

c1256	99	4.9	298	2	T27644	hypothetical prote	1329	98.5	4.8	987	2	A54092	protein-tyrosine k
1257	99	4.8	309	2	G83013	polyhydroxyalkanoa	c1330	98.5	4.8	1101	2	G70951	probable ATP-depen
c1258	99	4.9	310	1	PIHUSD	salivary proline-r	1331	98.5	4.8	1213	2	A41724	limb deformity (ld
1259	99	4.8	312	2	T25048	hypothetical prote	1332	98.5	4.8	1282	2	JB0120	glycoprotein A - m
1260	99	4.8	328	2	C42756	hypothetical prote	c1333	98.5	4.8	1489	2	D70807	hypothetical glyci
1261	99	4.8	344	2	T40167	hypothetical prote	c1334	98.5	4.8	1857	2	S31212	collagen alpha 1(X
1262	99	4.8	346	2	S76923	hypothetical prote	1335	98.5	4.8	1859	1	A34092	DNA-directed RNA p
1263	99	4.9	347	2	H75253	hypothetical prote	1336	98.5	4.8	1862	2	T29959	collagen alpha 1(X
c1264	99	4.9	347	2	J06087	helix-loop-helix t	c1337	98.5	4.8	1888	2	S78476	collagen polyketid
1265	99	4.8	371	2	E88633	protein P56B3.1 li	c1338	98.5	4.8	2103	2	G86925	CREB-binding prote
c1266	99	4.9	391	2	D83021	hypothetical prote	c1339	98.5	4.8	3190	2	T13828	tenascin-X, bovin
c1267	99	4.9	392	2	B48423	homeotic protein e	c1340	98.5	4.8	4135	2	T42629	collagen-related p
c1268	99	4.9	404	2	T44590	tylosin biosynthes	1341	98	4.7	172	2	D41132	hypothetical prote
c1269	99	4.9	413	2	E70661	probable PE protei	1342	98	4.7	202	2	AB2378	hypothetical 24.7K
c1270	99	4.9	443	1	S29334	transcription fact	c1343	98	4.8	255	2	JQ0320	hypothetical prote
1271	99	4.8	470	2	A30136	developmental cont	c1344	98	4.8	261	1	WMBEXE	infected cell prot
1272	99	4.8	487	2	T49424	hypothetical prote	1345	98	4.7	291	2	T20083	hypothetical prote
c1273	99	4.9	512	1	WMBEY4	UL54 protein - hum	c1346	98	4.8	299	2	T00837	glycine-rich prote
c1274	99	4.9	517	2	T37225	hypothetical prote	1347	98	4.7	310	2	T29731	hypothetical prote
1275	99	4.8	548	2	S59133	ETS2 repressor fac	1348	98	4.7	317	2	T29960	hypothetical prote
1276	99	4.8	617	2	S52797	mufi protein - hum	1349	98	4.7	329	2	T32783	hypothetical prote
1277	99	4.8	628	2	JQ0110	hypothetical 69K p	1350	98	4.7	356	2	A96826	T8K14.10 [importe
1278	99	4.8	653	2	T08984	auxin response fac	1351	98	4.7	362	2	A44083	meq protein - Mare
1279	99	4.8	683	2	A82704	1,4-beta-cellobios	1352	98	4.7	384	2	H70580	hypothetical prote
1280	99	4.8	707	2	A46302	PTB-associated spl	1353	98	4.7	403	2	S52796	prpL2 protein - hu
c1281	99	4.9	710	2	A31641	daughterless (da)	1354	98	4.7	416	2	G71965	glycine hydroxymet
c1282	99	4.9	718	1	VCPVIM	coat protein VP1 -	1355	98	4.7	429	2	JC4965	elk1 protein - mou
c1283	99	4.9	733	2	JC7679	dendritic cell-der	1356	98	4.7	449	2	S16748	proline-rich prote
c1284	99	4.9	784	2	A26601	elastin precursor	1357	98	4.7	463	2	A48375	cellulase (EC 3.2.
c1285	99	4.9	841	2	C87331	ISCC2, transposase	1358	98	4.7	473	2	S50755	hypothetical prote
c1286	99	4.9	1028	1	CGHUIA	collagen alpha 1(V	1359	98	4.7	502	2	A48679	probable transcrip
1287	99	4.8	1032	2	DB3637	serine/threonine p	1360	98	4.7	587	2	T41653	hypothetical prote
c1288	99	4.9	1056	2	A53767	mucin MUC5B, trach	1361	98	4.7	589	2	G87485	hypothetical prote
c1289	99	4.9	1062	2	T30255	inversin - mouse	c1362	98	4.8	589	2	G87485	hypothetical prote
1290	99	4.8	1290	2	T00018	period protein hom	1363	98	4.7	602	2	T45760	neuron-derived rec
1291	99	4.8	1366	1	CGHU2S	collagen alpha 2(I	c1364	98	4.7	625	2	S71930	proflilaggrin - rat
c1292	99	4.9	1574	2	T13954	MEGF6 protein - ra	c1365	98	4.8	625	2	A34615	hypothetical prote
c1293	99	4.9	1618	2	S21424	nestin - human	1366	98	4.7	710	2	T00359	hypothetical prote
c1294	99	4.9	1669	1	CGHU4B	collagen alpha 1(I	1367	98	4.7	712	2	D96728	gag protein - silk
1295	99	4.8	2027	2	S60123	hypothetical prote	1368	98	4.7	722	2	T18195	glucan 1,4-alpha-g
1296	99	4.8	2056	2	G88564	protein R10E11.1 l	1369	98	4.7	748	2	T49633	granulocyte colony
1297	99	4.8	2395	1	S50820	surface protein ty	1370	98	4.7	771	2	B38252	hypothetical prote
c1298	99	4.9	3229	2	S27852	probable cell-surf	c1371	98	4.8	811	2	S08579	hypothetical glyci
c1299	98.5	4.8	152	2	T34649	hypothetical prote	c1372	98	4.8	853	2	A70896	probable beta-gluc
1300	98.5	4.8	213	2	E72548	hypothetical prote	c1373	98	4.8	859	2	T35785	protein-tyrosine k
1301	98.5	4.8	217	2	T09556	hypothetical prote	c1374	98	4.8	864	2	A48266	protein-tyrosine k
1302	98.5	4.8	234	1	Q0BE43	membrane antigen 9	1375	98	4.7	901	2	A44825	phosphoprotein, sy
1303	98.5	4.8	298	2	T27644	hypothetical prote	1376	98	4.7	903	2	T00705	N-chimerin homolog
1304	98.5	4.8	302	2	T32872	hypothetical prote	1377	98	4.7	1127	2	A25018	circadian rhythm p
1305	98.5	4.8	313	2	T26465	hypothetical prote	1378	98	4.7	1130	1	TVHUA	protein-tyrosine k
c1306	98.5	4.8	357	2	D84395	1-allo-threonine a	1379	98	4.7	1218	2	A26588	period clock prote
1307	98.5	4.8	363	2	D75423	hypothetical prote	1380	98	4.7	1218	2	A26427	period clock prote
c1308	98.5	4.8	381	2	T27806	hypothetical prote	c1381	98	4.8	1323	2	T30253	spalt protein - mo
c1309	98.5	4.8	404	2	S54729	RNA-binding protei	c1382	98	4.8	1329	2	T29074	hypothetical prote
1310	98.5	4.8	420	2	D70599	hypothetical prote	c1383	98	4.7	1575	2	T13998	synaptotagmin, 170K
1311	98.5	4.8	423	2	A41207	collagen 13, nonfi	1384	98	4.7	1655	2	T33998	gene mastermand pr
1312	98.5	4.8	430	2	S66671	neuron-derived rec	1385	98	4.7	1736	2	T00391	hypothetical prote
1313	98.5	4.8	499	2	S03880	hypothetical prote	c1386	98	4.8	6420	2	T30283	polyketide synthas
c1314	98.5	4.8	516	2	C44479	collagen alpha 1(X	1387	97.5	4.7	228	2	S46965	microfilament shea
c1315	98.5	4.8	532	2	JC5412	epidermal growth f	1388	97.5	4.7	273	2	A84332	hypothetical prote
c1316	98.5	4.8	537	2	B33485	spore coat protein	c1389	97.5	4.8	305	2	T30165	hypothetical prote
1317	98.5	4.8	589	2	JG0196	protein kinase DYR	1390	97.5	4.7	306	2	T52340	cell wall-plasma m
c1318	98.5	4.8	591	2	B70523	hypothetical glyci	1391	97.5	4.7	316	2	T19291	hypothetical prote
1319	98.5	4.8	598	2	A37251	probable nuclear h	c1392	97.5	4.8	348	2	A34705	collagen - Caenorh
1320	98.5	4.8	628	2	JC2493	neuron derived orp	1393	97.5	4.7	349	2	T43457	hypothetical prote
1321	98.5	4.8	629	2	JG0195	protein kinase DYR	1394	97.5	4.7	354	2	S39406	homeotic protein o
c1322	98.5	4.8	691	2	A40024	regulatory protein	1395	97.5	4.7	364	2	I48186	gene NKX6.1 protei
1323	98.5	4.8	698	2	T17261	hypothetical prote	1396	97.5	4.7	366	2	T26449	probable transmemb
c1324	98.5	4.8	775	2	A61228	collagen alpha 2(I	1397	97.5	4.7	396	2	T35659	transforming prote
1325	98.5	4.8	886	2	S29605	glycoprotein 350/2	1398	97.5	4.7	428	1	TVHUEK	tapasin 1 homolog,
1326	98.5	4.8	907	1	Q0BE21	membrane antigen 9	c1399	97.5	4.8	430	2	S09824	hypothetical prote
1327	98.5	4.8	913	2	S20590	exo-alpha-sialidas	1400	97.5	4.7	431	2	S09824	ribonucleoprotein
c1328	98.5	4.8	947	2	T02979	pyruvate, phosphat	1401	97.5	4.7	471	2	S33679	



```
QY 364 TGGACCGAGCATCCGGCACACGCGCTTCTGTGACCCATCCCGGTACCTACCTGGGAGCC 423
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 GlnProGluGlnIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer 112
QY 424 TCG---ACAGACGACAGACGACCTCCCGGTGCTGGCGGTGCGGCTGCCCTCCGCGTA 480
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132
QY 481 ACCAGCAGGTTCACCCCTGCCCTGCCATGACTGTGCAACCCGCTGGCACCAGATGC 540
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
133 GlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlnLysCys 152
QY 541 CACGCTCAGGTGGGGCATCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
153 IleIleSerGlyTyrGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172
QY 601 TGCCTCAACCTCCATCCTCCCATGCGACCTGCGTGTGATATCCCGGAGATC 660
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
173 CysAlaGluValLysIleTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle 192
QY 661 ACAGCAACATGCTGTGTCAGCGCGCTCCCGGCGCAGATGCTGCCAGGTGATTC 720
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 ThrGluGlyMetValCysAlaGlySerSerAsnGlyAlaAspThrCysGlnGlyAspSer 212
QY 721 GGGGGCCCTGCTGTGTGGGGAGTCTTCAAGGTCTGTGCTGCTGCGGGGTCTGTGGGG 780
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
213 GlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTyrGlySer---Asp 231
QY 781 CGCTGTGGACAGATGGCATCCCTGGAGTCTACACTATATTGCAAGTATGTGACTGG 840
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp 251
QY 841 ATCCGGATGATCATGAGGAAC 861
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N:Alternate names: trypsinogen II
C:Species: Gallus gallus (chicken)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S55066; S72347
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A:Title: Isolation and characterization of the chicken trypsinogen gene family.
A:Reference number: S55066; MUID:95251611; PMID:7733885
A:Accession: S55066
A:Molecule type: mRNA
A:Residues: 1-248 <WAN2>
A:Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A:Experimental source: clone 2-P29
A:Accession: S72347
A:Molecule type: DNA
A:Residues: 1-248 <WAN2>
A:Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A:Experimental source: clone 2-P29
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-25/Domain: activation peptide #status predicted <APT>
F:26-248/Product: trypsin II #status predicted <MAT>
F:26-241/Domain: trypsin homology <TRY>
F:65,109,202/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 3,98e-30 Length: 248
Score: 569.50 Matches: 116
Percent Similarity: 63.52% Conservative: 39
Best Local Similarity: 47.54% Mismatches: 78
Query Match: 27.57% Indels: 11
DB: 2 Gaps: 6
```

```
US-10-015-385a-193 (1-1091) x S55066 (1-248)
QY 133 ATCTTTTGTCTCTGTGTCTTGGGCTCAGC-----CAGSCAGCCACA 177
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4 LeuPheLeuIleLeuSerCysLeuGlyAlaValAlaPheProGlyGlyAlaAsp 23
QY 178 CCGAAGATTTTCAATGGCAGTGTGGGGGTAACTCACAGCCGCTGGCAGGTGGGGCTG 237
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
24 AspLysIleValGlyGlyTyrThrCysProGluHisSerValProTyrGlnValSerLeu 43
QY 238 TTTGAGGACACAGCTCGCTGCGGGGTTCCTTATTGACCAACAGTGGTGGTCTCTACA 297
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
44 AsnSerGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValLeuSer 62
QY 298 GCGGCTCACTCAGCGGACAGGTACTGGGTGGCGCTGGGGGAAACACAGCTCAGCCAG 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
63 AlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyLysLeuAsnVal 82
QY 358 CTCGACTGGACCGAGATCGGACAGCGGTCTTCTGTGACCCATCCCGGTACCTG 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
83 GlnGluAspSerGluValValArgSerSerValIleIleArgHisProLysTyr--- 101
QY 418 GGAGCCTCGACAGCAGCAGACGACCTCCGGCTGCTGGCGTGGCGCTGCCCTCCGCG 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
102 ---SerSerIleThrLeuAsnAsnAspIleMetLeuIleLysLeuAlaSerAlaValGlu 120
QY 478 GTAACACAGCAGGTTCACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCCGAG 537
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 TyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAlaLysAlaGlyThrGlu 140
QY 538 TGCCACGCTCAGGTGGGGCATCACCAACCAACCAACCAACCAACCAACCAACCAACCA 597
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
141 CysLeuIleSerGlyTyrGlyAsnThrLeuSerAsnGlyTyrAsnTyrProGluLeuLeu 160
QY 598 CAGTGCCTCAACCTCTCCATGCTCCCATGCCATGCCATGGTGTGTATCCCGGGAGA 657
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
161 GlnCysLeuAsnAlaProIleLeuSerAspGlnGluCysGlnGluAlaTyrProGlyAsp 180
QY 658 ATCAGACGACATGTGTGTGACGGCGCTGCCG---GGCAGAGATGCCTGCCAGGT 714
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 IleThrSerAsnMetIleCysValGlyPheLeuGluGlyLysAspSerCysGlnGly 200
QY 715 GATTCTGGGGCCCCCTGCTGTGTGGGGAGTCTTCAAGTCTGTGTCTGGGGGTCT 774
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 AspSerGlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGly--- 219
QY 775 GTGGGGCCCTGTGGACAGATGGCATCCCTGGAGTCTACACTATATTGCAAGTATCTG 834
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 IleGly---CysAlaLeuLysGlyTyrProGlyValTyrThrLysValCysAsnTyrVal 238
QY 835 GACTGGATCCGG 846
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 AspThrIleGln 242

RESULT 3
S55067
trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
N:Alternate names: trypsinogen I
C:Species: Gallus gallus (chicken)
C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S55067; S72345; S55065; S72346; S71155
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A:Title: Isolation and characterization of the chicken trypsinogen gene family.
A:Reference number: S55065; MUID:95251611; PMID:7733885
A:Accession: S55067
A:Molecule type: mRNA
A:Residues: 1-248 <WAN1>
A:Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:g603904
A:Experimental source: clone 1-P38
A:Accession: S72345
A:Molecule type: DNA
```







```

Score: 555.00 Matches: 115
Percent Similarity: 58.91% Conservative: 37
Best Local Similarity: 44.57% Mismatches: 90
Query Match: 26.86% Indels: 16
DB: 2 Gaps: 6

US-10-015-385A-193 (1-1091) x A53968 (1-253)

QY 121 ATGGGGCTCAGCATCTTTTGTGCTCTGTGTGTTCTTGGGCTCAGC----- 165
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 166 -----CAGGAGCCACACCAGAGATTTTCANTGCAGCTAGTGTGGGGTAACTCA 216
   ::|||::: |||::: |||::: |||::: |||::: |||:::
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 217 CAGCGTCGGCAGTGGGGCTGTTTCAGGAGCCACAGCTGCGCTGCGGGGGTCTCTATT 276
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 600

QY 277 GACCACAGGTGGTCTCACAGCGGCTCACTGCAGCGGACGAGGTACTGGCTGGCGCTG 336
   ::|||::: |||::: |||::: |||::: |||::: |||:::
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyThrValHisLeu 80

QY 337 GGGGAACACAGCTCAGCGAGCTCGACTGGACCGAGCAGATCCGGACACAGCGGTTCT 396
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 81 GlySerAspThrLeuGly-----AspArgArgAlaGlnArgIleLysAlaSerLysSer 98

QY 397 GTGACCATCCGGTACTTGGGAGCCTCGAGAGCCACGACGACGACTCCGGCTGCTG 456
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 99 PheArgHisProGlyTyr-----SerThrGlnThrHisValAsnAspLeuMetLeuVal 116

QY 457 CGGCTCGCCCTGCCGTCGCTCCGCTAACACAGCAGCGTTCAACCCCTCGCCCTGCCAATGAC 516
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 117 LysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArg 136

QY 517 TGTCAACCGTGGCAGCGAGTGCACGCTCTCAGCTGGGGCATCACCAACACCCACGG 576
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 137 CysGluProProGlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAsp 156

QY 577 AACCCATTCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCATGCCACCTGC 636
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 157 ValThrPheProSerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCys 176

QY 637 CATGCTGTGTATCCCGGAGAAATACAGACCAATGCTGTGTGCAGGGCGGCTCCCGGG 696
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 177 ThrLysValTyLysAspLeuLeuGlnAsnSerMetLeuCysAla--GlyIleProAsp 195

QY 697 -----CAGATGCTGCCAGGTGATTCGCGGGCCCTCGTGTGTGGGGAGTCTCT 750
   ::|||::: |||::: |||::: |||::: |||::: |||:::
Db 196 SerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeu 215

QY 751 CAAGTCTGTGTCTCTGGGGTCTGTGGGGCCCTGTGGACAGATGGCATCCTCGGATGC 810
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 216 GlnGlyLeuValSerTrpGlyThrPhe---ProCysGlyGlnProAsnAspProGlyVal 234

QY 811 TACACCTATATTTCAGATGTGTGACTGGATCCGGATGATCATGATGAGGAACAAC 864
   |||::: |||::: |||::: |||::: |||::: |||:::
Db 235 TyrThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetCysLysHis 252

RESULT 7
B25528
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1998 #sequence_revision 30-Jun-1998 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse elan
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>

```

## RESULT 8

A;Cross-references: UNIPROT:P07146; GB:X04574; NID:G54918; PIDN:CA28243.1; PID:G54919191  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-246/Product: trypsin #status predicted <MAT>  
F:24-239/Domain: trypsin homology <TRY>  
F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted  
F:63, 107, 200/Active site: His, Asp, Ser #status predicted  
F:75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:		
Pred. No.:	4.98-29	246
Score:	553.00	113
Percent Similarity:	62.45%	Conservative: 45
Best Local Similarity:	44.66%	Mismatches: 81
Query Match:	26.77%	Indels: 14
DB:	2	Gaps: 7

US-10-015-385A-193 (1-1091) x B25528 (1-246)

Qy	127	CTCAGCATCTTTTGTGCTCTCTGTGTGTTCTTGTGGCTACGCCAGGCA-----GCC	174
Db	1	MetSerAlaLeuLeuLeuLeuLeuValGlyAlaAlaValAlaPheProValAspAsp	20
Qy	175	ACCCGAGATTTTCAATGGCACTGAGTGTGGCGTAACTACACCGTGGCAGGTGGGG	234
Db	21	AspAspLysIleValGlyGlyTyrThrCysArgGluSerSerValProTyrGlnValSer	40
Qy	235	CTGTGTTGAGGGCACACGCTCGCTCGCGGGGTGCTTATTGACACACAGTGGGTCTTC	294
Db	41	LeuAsnAlaGlyTyrHisPhe--CysGlyGlySerLeuIleAsnAspGlnTrpValVal	59
Qy	295	ACAGCGGTCTACTGACGCGGCGCAGCAGGTACTGGGTGCGCTGGGGGAAACACAGCTCAGC	354
Db	60	SerAlaAlaHisCysTyrLysTyrArgIleGlnValArgLeuGlyGluHisAsnIleAsn	79
Qy	355	CAGCTCCAGTGGACCGAGCAGATCCGGCACACGGCTTCTCTGTGACCCATCCCGCTAC	414
Db	80	ValLeuGluGlyAsnGluGlnPheValAspSerAlaLysIleIleArgHisProAsnTyr	99
Qy	415	CTGGGAGCTCGACGACCGACGACGACGACCTCCGGCTGCTCGCGTGGCGCTGCCCGTC	474
Db	100	-----AsnSerTrpThrLeuAspAsnAspIleMetLeuIleLysLeuAlaSerProVal	117
Qy	475	CGCGTAACACGACAGGTTCAACCTCTGCCCTGCGCCCAATGACTGTGCACCGCTGGCAC	534
Db	118	ThrLeuAsnAlaArgValAlaSerValProLeuProSerSerCysAlaProAlaGlyThr	137
Qy	535	GAGTGCACAGTCTCAGGCTGGGGC-----ATCACCAACACCCACGGAACCATTC	588
Db	138	GlnCysLeuIleSerGlyTrpGlyAsnThrLeuSerAsnGlyValAsnAsn-----Pro	155
Qy	589	GATCTGCTCCAGTGCGCTCAACCTCTCCATCGTCTCCCATGCCACCTGCATGGTGTGTAT	648
Db	156	AspLeuLeuGlnCysValAspAlaProValLeuProGlnAlaAspCysGluAlaSerTyr	175
Qy	649	CCCGGGAGATCAACAGCAACATGGTGTGTGTGAGCGCGGTCCCG---GGGACAGATGCC	705
Db	176	ProGlyAspIleThrAsnAsnMetIleCysValGlyPheLeuGluGlyGlyLysAspSer	195
Qy	706	TGCCAGGTTGATCTGGGGGCCCTCGTGTGTGGGGAGTCTCTTCAGGTCGTGGTGTC	765
Db	196	CysGlnGlyAspSerGlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSer	215
Qy	766	TGGGGGTCTGTGGGGCCCTGTGGACAGATGCCATCCCTGGAGTCTACACCTATATTTC	825
Db	216	TrpGlyTyr-----GlyCysAlaGlnProAspAlaProGlyValTyrThrLysValCys	233
Qy	826	AAGTATGTGGACTGGATCCGGATGATCATGAGGACAAC	864
Db	234	AsnTyrValAspTrpIleGlnAsnThrIleAlaAspAsn	246

## RESULT 8

TRB0TR

trypsin (EC 3.4.21.4) precursor - bovine  
N:Contains: trypsinogen  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence revision 28-Feb-1986 #text\_change 18-Jul-1997  
C:Accession: A90164; A00946; S08774  
R:Mike, O.; Holeysovsky, V.; Tomasek, V.; Sorn, F.  
Biochem. Biophys. Res. Commun. 24, 346-352, 1966  
A:Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.  
A:Reference number: A90164; MUID:67168848; PMID:5967094  
A:Accession: A90164  
A:Molecule type: protein  
A:Residues: 157, 'Q', 59-67, 'Q', 69-150, 'N', 152-176, 'N', 178-229 <MIK>  
R:Hartley, B.S.  
Philos. Trans. R. Soc. Lond. B257, 77-87, 1970  
A:Reference number: A93755  
A:Contents: annotation; revisions  
R:Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.  
Biochemistry 14, 1358-1366, 1975  
A:Title: Amino acid sequence of dogfish trypsin.  
A:Reference number: A00950; MUID:75146445; PMID:1092332  
A:Contents: annotation; revisions  
A:Note: the sequence agrees with that shown  
R:Bode, W.; Schwager, P.  
J. Mol. Biol. 98, 693-717, 1975  
A:Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution  
A:Reference number: A92954; MUID:76072097; PMID:512  
A:Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and  
C:Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.  
C:Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal  
pseudotrypsin. A cleavage may also occur after Arg-105.  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F:1-229/Product: trypsinogen #status experimental <ZYM>  
F:1-6/Domain: activation peptide #status experimental <APT>  
F:7-222/Domain: trypsin homology <TRY>  
F:7-131,132-229/Product: alpha-trypsin #status experimental <MPT>  
F:6-7/Cleavage site: Lys-11e (enteropeptidase) #status experimental  
F:13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental  
F:46,90,183/Active site: His, Asp, Ser #status experimental  
F:58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental  
F:131-132/Cleavage site: Lys-Ser (autolytic) #status experimental

Alignment Scores:  
Pred. No.: 5,73e-29 Length: 229  
Score: 552.00 Matches: 106  
Percent Similarity: 63.76% Conservative: 40  
Best Local Similarity: 46.29% Mismatches: 77  
Query Match: 26.72% Indels: 6  
DB: 1 Gaps: 4

US-10-015-385A-193 (1-1091) x TRB0TR (1-229)

QY 181 AAGATTTCATGGCACTGAGTGGCGGTAACCTACAGCGTGGCAGGTGGCGCTGTTT 240  
Db 6 LyslleValGlyGlyThrCysGlyAlaAsnThrValProTyrGlnValSerLeuAsn 25  
QY 241 GAGGGCACCAGCCTCGCGCTCGGGGGTGCCTTATTGACACAGGTGGGTCTCAGCG 300  
Db 26 SerGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValValSerAla 44  
QY 301 GCTCACTGACGGCAGCAGTACTGGTGGCTGGGGAAACACAGCCTCAGCCAGCTC 360  
Db 45 AlaHisCysTyrLysSerGlylleGlnValArgLeuGlyGluAspAsnIleAenValVal 64  
QY 361 GACTGGACCAGACAGATCCGCGACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420  
Db 65 GluGlyAsnGluGlnPheIleSerAlaSerLysSerIleValHisProSerTyr----- 82  
QY 421 GCCTCGACGACCCACGACGACGACCTCCGCGCTGCTGCGGCTGCGCCGTCGCCGGA 480  
Db 83 AsnSerAsnThrLeuAsnAsnAspIleMetLeuIleLysLeuLysSerAlaAaSerLeu 102

QY	481	ACGAGCAGCGTTTCAACCCCTGCGCCCTGCGCAACCGTGGCACCGTGGCACCGAGTGC	544
Db	103	AsnSerArgValAlaLaSerIleSerLeuProThrSerCysAlaSerAlaGlyThrGlnCys	122
QY	541	CAGCTCTCAGGCTGGGGCATCACCAACCCACCGAAACCCATTCGCCGATCTGCTCCAG	600
Db	123	LeuIleSerGlyTrpGlyAsnThrLysSerSerGlyThrSerTyrrProAspValLeuLys	142
QY	601	TGCTCTCAACCTCTCCATCGTCTCCCATGCCACTGCGCATGGTGTGTATCCCGGAGATC	660
Db	143	CysLeuLysAlaProIleLeuSerAspSerSerCysLysSerAlaTyrrProGlyGlnIle	162
QY	661	ACGAGCAACATGGTGTCTGCAGCGGGCTCCCG- --GGGCAGGATCGCTGCCAGGCTGAT	717
Db	163	ThrSerAsnMetPheCysAlaGlyTyrLeuLysGlyGlyLysAspSerCysGlnGlyAsp	182
QY	718	TCTGGGGCCCCCTGGTGTGTGGGGAGTCCCTTCAAGGTCTGGTGCCTGGGGGTCTGG	777
Db	183	SerGlyGlyProValValCysSerGlyLysLeuGlnGlyIleValSerTrpGlySer---	201
QY	778	GGGCCCTGTGACAAGATGGCATCCCTGGAGTCTACACCTATATTTCGAAGTATGTGGAC	837
Db	202	---GlyCysAlaGlnLysAsnLysProGlyValTyrThrLysValCysAsnTyrrValSer	220
QY	838	TGGATCCGGATGATCATCGAGCAACAC 864	
Db	221	TrpIleLysGlnThrIleAlaSerAsn 229	
RESULT 9			
SI3813			
trypsin (EC 3.4.21.4) - bovine			
C:Species: Bos primigenius taurus (cattle)			
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004			
C:Accession: SI3813			
R:le Huerol, I.; Wicks, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.			
Eur. J. Biochem. 193, 767-773, 1990			
A:Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic			
A:Reference number: SI3813; MUID:91065383; PMID:1701147			
A:Accession: SI3813			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-247 <HUS>			
A:Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PIR			
C:Superfamily: trypsin; trypsin homology			
C:Keywords: hydrolase; protein digestion; serine proteinase			
F:24-239/Domain: trypsin homology <TRY>			
F:63,107,200/Active site: His, Asp, Ser #status predicted			
Alignment Scores:			
Pred. No.:		7,74e-29	Length:
Score:		550.00	Matches:
Percent Similarity:		61.94%	Conservative:
Best Local Similarity:		45.75%	Mismatches:
Query Match:		26.62%	Indels:
DB:		2	Gaps:
			5
US-10-015-385A-193 (1-1091) x SI3813 (1-247)			
QY	139	TGTCCTCTGTGTGTCTTGGGCTCAGCAGGCA-----GCCACCCGAAAGATT	186
Db	5	LeuIleLeuAlaPheValGlyAlaAlaValAlaPheProSerAspAspAspIle	24
QY	187	TTCAATGGCACTAGTGTGGGGTAACTCAAGCCGTGGGAGCGAGTGGGGCTGTTGAGGCG	246
Db	25	ValGlyGlyTyrrThrCysAlaGluAsnSerValProTyrrGlnValSerLeuAsnAlaGly	44
QY	247	ACGACCTCGCTGGGGGGGTGCTCTTATTGACACAGGTGGGTCTCTCACAGCGGCTCAC	306
Db	45	TyrHisPhe---CysGlyGlySerLeuIleAsnAspGlnTrpValValSerAlaAlaHis	63
QY	307	TGCAGCGGCAGCAGGCTACTGGGTGCGCTGGGGAAACACAGCCTCAGCCAGCTCGACTGG	366
Db	64	CysTyrrGlnTyrrHisIleGlnValArgLeuGlyGlyTyrrAsnIleAspValLeuGlyGly	83

```
QY 367 ACCGAGCAGATCCGGCAGACAGCGGCTTCTGTGTGACCCATCCGGCTACTCTGGAGCGCTCG 426
Db      |||||
84 GlyGluGlnPheIleAspAlaSerIlylleArgHisProLysTyr-----SerSer 101
QY 427 ACGAGCCAGCAGCAGCAGCTCCGGCTGCTGGCGCTCGCGCTCCGCTCCGCTACCAACG 486
Db      |||||
102 TrpThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 121
QY 487 ACGGTTCAACCCCTGCTCCCAATGACTGTGCAACCGCTGGCAGCCAGATGCCACGTC 546
Db      |||||
122 ArgValSerThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 141
QY 547 TCAGCTGGGGCATCACCAACCCAGCAACCGAACCATTCCCGGATCTGCTCAGTGCCTC 606
Db      |||||
142 SerGlyTrpGlyAsnThrLeuSerSerGlyValAsnTyrProAspLeuLeuGlnCysLeu 161
QY 607 AACCTCTCCATCGTCTCCATCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 666
Db      |||||
162 ValAlaProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 181
QY 667 AACATGGTGTGTGCGAGCGGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 723
Db      |||||
182 AsnMetIleCysAlaGlyPheLeuGluGlyGlyLysAspSerCysGlnGlyAspSerGly 201
QY 724 GCGCCCTGCTGTGTGGGGAGTCTCTCAAGTCTGTGTCTGTGTGTGTGTGTGTGTGTGT 783
Db      |||||
202 GlyProValAlaCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyTyr-----Gly 219
QY 784 TGTGACACAGATGGATCCCTGAGTCTACACTATATTTGCAAGTATGTGAGTGTGATC 843
Db      |||||
220 CysAlaGlnLysGlyLysProGlyValTyrThrLysValCysAsnTyrValAspTrpIle 239
QY 844 CGGATGATCATCAGGAACAAC 864
Db      |||||
240 GlnGluThrIleAlaAlaAsn 246

RESULT 10
TRDGC
trypsin (EC 3.4.21.4) precursor, anionic - dog
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26273
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequen
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: A26273
A:Molecule type: mRNA
A:Residues: 1-247 <PIN>
A:Cross-references: UNIPROT:P06872; GB:M11589; NID:gl64094; PIDN:AAA30899.1; PID:gl64095
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-247/Product: trypsin, anionic #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 1,42e-28 Length: 247
Score: 546.00 Matches: 113
Percent Similarity: 60.8% Conservative: 38
Best Local Similarity: 45.5% Mismatches: 85
Query Match: 26.43% Indels: 12
DB: 1 Gaps: 6

US-10-015-385a-193 (1-1091) x TRDGC (1-247)
QY 139 TTGCTCTGTGTGTTCTTGGGCTCAGCCAGCAGCCACACCG-----AAG 183
```

```
Db      |||||
5 LeuIleLeuAlaPheLeuGly---AlaAlaValAlaThrProThrAspAspAspAspLys 23
QY 184 ATTTTCAATGGCAGTGTGGCGGTAACTCACAGCCGTGGCAGGTGGGTGGTGTGGAG 243
Db      |||||
24 IleValGlyGlyTyrThrCysGluGluAsnSerValProTyrGlnValSerLeuAla 43
QY 244 GGCACAGCTCGCTGGGGGTGTCTTTATGACACAGTGGGTCTCTCAGCGGCT 303
Db      |||||
44 GlyTyrHisPhe--CysGlySerLeuIleSerAspGlnTrpValValSerAlaAla 62
QY 304 CACTCAGCGGCGAGCTACTGGTGGCTGGGGGAAACACAGCTCAGCCAGCTCGAC 363
Db      |||||
63 HisCysTyrLysSerArgIleGlnValArgLeuGlyGlyTyrAsnIleAspValLeuGlu 82
QY 364 TGGACCGGAGCAGATCCGACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTCGGAGCC 423
Db      |||||
83 GlyAsnGluGlnPheIleAsnSerAlaLysValIleArgHisProAsnTyr-----Asn 100
QY 424 TGCAGAGCCAGCAGACGACCTCCGGTGTGTGGCGTGTGGCGTGTGGCGTGTGGCGTAA 483
Db      |||||
101 SerTrpIleLeuAspAsnAspIleMetLeuIleLysLeuSerSerProAlaValLeuAsn 120
QY 484 AGCAGCGTTCACCCCTGCCCTGCCATGACTGTGCAACCGCTGGCAGCCAGTCCAC 543
Db      |||||
121 AlaArgValAlaThrIleSerLeuProArgAlaCysAlaAlaProGlyThrGlnCysLeu 140
QY 544 GTCTCAGGCTGGGGCATCACCAACCCACCGAACCATTCCCGGATCTGTCTCAGTGC 603
Db      |||||
141 IleSerGlyTrpGlyAsnThrLeuSerSerGlyThrAsnTyrProGluLeuGlnCys 160
QY 604 CTCACCTCTCCATCGTCTCCATCCACCTCCCATGTGTGTGTGTGTGTGTGTGTGTGT 663
Db      |||||
161 LeuAspAlaProIleLeuThrGlnAlaGlnCysGluAlaSerTyrProGlyGlnIleThr 180
QY 664 AGCAACATGCTGTGTGGCGGCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCT 720
Db      |||||
181 GluAsnMetIleCysAlaGlyPheLeuGluGlyLysAspSerCysGlnGlyAspSer 200
QY 721 GGGGGCCCTCGTGTGTGGGGAGTCTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db      |||||
201 GlyGlyProValValCysAsnGlyGluLeuGlnGlyIleValSerTrpGlyTyr----- 218
QY 781 CCCTGTGGACAGATGGATCCCTGAGTCTACACTATATTTGCAAGTATGTGAGCTGG 840
Db      |||||
219 GlyCysAlaGlnLysAsnLysProGlyValTyrThrLysValCysAsnPheValAspTrp 238
QY 841 ATCCGGATGATCATGAGGAACAAC 864
Db      |||||
239 IleGlnSerThrIleAlaAlaAsn 246

RESULT 11
TRDGC
trypsin (EC 3.4.21.4) precursor, cationic - dog
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26273
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequen
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: B26273
A:Molecule type: mRNA
A:Residues: 1-246 <PIN>
A:Cross-references: UNIPROT:P06871; GB:M11590; NID:gl64096; PIDN:AAA30900.1; PID:gl64097
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-246/Product: trypsin, cationic #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
```

F:63,107,200/Active site: His, Asp, Ser #status predicted  
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

## Alignment Scores:

Pred. No.: 1.66e-28 Length: 246  
Score: 545.00 Matches: 111  
Percent Similarity: 61.35% Conservatives: 43  
Best Local Similarity: 44.22% Mismatches: 87  
Query Match: 26.36% Indels: 10  
DB: 1 Gaps: 6

US-10-015-385A-193 (1-1091) x TRDGC (1-246)

```
QY 127 CTCAGCATCTTTTCTCTCTGTGTCTTCTGGGCTCAGCCAGGCA-----GCC 174
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 1 MetLysThrPheLeuAlaLeuLeuGlyAlaThrValAlaPheProIleAspAsp 20
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||

QY 175 ACACCGAAGATTTTCAATGGCACTGAGTGGGGCTAACTACACCGTGGGAGTGGG 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 AspAspLysIleValGlyGlyThrCysSerArgAsnSerValProTyrGlnValSer 40
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 235 CTGTTTGGGGCACCAGCCTGGCTGGCTGGGGGTCTTATTGACCACAGGTGGTCTC 294
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 41 LeuAsnSerGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpValVal 59
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 295 ACAGCGGCTCACTGACGGGCGAGCAGAGTACTGGGTGGCTGGGGGAACACAGCCTCAGC 354
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 SerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluTyrAsnIleAla 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 355 CAGCTCGACTGACCGCAGAGATCCGGCAGCAGCGGCTTCTGTGACCATCCCGGTAC 414
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ValSerGluGlyGlyGlnPheIleAsnAlaAlaLysIleIleArgHisProArgTyr 99
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 415 CTGGGAGCTCGACGAGCCACGACGACGACCTCCGGCTGCTGGCTGGCTGGCTGGCTG 474
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 ---AsnAlaAsnThrIle---AspAsnAspIleMetLeuIleLysLeuSerSerProAla 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 475 CCGCTAACACGACGAGCGGTTCACCCCTGCGCCCTGCGCAATGACTGTGCAACCGCTGGCACC 534
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 ThrLeuAsnSerArgValSerAlaIleAlaLeuProLysSerCysProAlaAlaGlyThr 137
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 535 GAGTCCAGCTCTAGCTGGGGGTACACCAACACCCAGCAACCCATTCCTCGGATCTG 594
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 GlnCysLeuIleSerGlyTyrGlyAsnThrGlnSerIleGlyGlnAsnTyrProAspVal 157
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 595 CTCAGTGCCTCACTCTCCATCTCTCCATGCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 654
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 LeuGlnCysLeuLysAlaProIleLeuSerAspSerValCysArgAsnAlaTyrProGly 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 655 AGAATCAGCAGCAACATGTGTGTGTCAGCGCGCTCCCG---GGGACGATCCCTGCCAG 711
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 GlnIleSerSerAsnMetMetCysLeuGlyTyrMetGluGlyGlyLysAspSerCysGln 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 712 GGTGATTCCTGGGGGCCCCCTGTGTGTGGGGAGATCTTCAAGTCTGTGTCTTGGGG 771
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 GlyAspSerGlyGlyProValValCysAsnGlyGluLeuGlnGlyValValSerTrpGly 217
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 772 TCTGTGGGGCCCTGGGCAAGATGCATCCCTGGAGTCTACACCTATATTTCGAAGTAT 831
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 Ala-----GlyCysAlaGlnLysGlyLysProGlyValSerProLysValCysLysTyr 235
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 832 GTGGACTGGATCCGGATGATCATGTAGGAACAAC 864
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 ValSerTrpIleGlnThrIleAlaAlaAsn 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 12

A27547  
trypsin (EC 3.4.21.4) precursor, cationic - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004  
C:Accession: A27547  
Rifletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.  
Biochemistry 26, 3081-3086, 1987

A:Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.  
A:Reference number: A27547; MUID:87271609; PMID:3607011

A:Accession: A27547

A:Molecule type: mRNA

A:Residues: 1-247 <FL>

A:Cross-references: UNIPROT:P08426; GB:M16624; MID:g206498; PIDN:AAA41985.1; PID:g206499  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase

F:25-240/Domain: trypsin homology <TRY>

F:31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted

F:64,108,201/Active site: His, Asp, Ser #status predicted

F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

## Alignment Scores:

Pred. No.: 1.79e-28 Length: 247  
Score: 544.50 Matches: 109  
Percent Similarity: 60.32% Conservatives: 43  
Best Local Similarity: 43.25% Mismatches: 89  
Query Match: 26.36% Indels: 11  
DB: 2 Gaps: 5

US-10-015-385A-193 (1-1091) x A27547 (1-247)

```
QY 127 CTCAGCATCTTTTCTCTCTGTGTCTTCTGGGCTCAGCCAGGCA----- 174
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 1 MetLysAlaLeuIlePheLeuAlaPheLeuGlyAlaAlaValAlaLeuProLeuAspAsp 20
   ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||

QY 175 ---ACACCGAAGATTTTCAATGGCACTGAGTGGGGCTAACTACACCGTGGGAGTGG 231
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 AspAspLysIleValGlyGlyThrCysGlnLysAsnSerLeuProTyrGlnVal 40
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 232 GGGCTGTTTGGGGCACCAGCCTGGCTGGCGGGGTGCTTATTGACACAGGTGGTGC 291
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 41 SerLeuAsnAlaGlyTyrHisPhe---CysGlyGlySerLeuIleAsnSerGlnTrpVal 59
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 292 CTCAGCGGCTCACTGACGGCGGACGAGTACTGGGTGGCTGGGGGAACACAGCCTC 351
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 ValSerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIle 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 352 AGCCAGCTCGACTGGACCGCAGCATCCGGCAGCAGCGGTCTCTGTGACCATCCCGCG 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 AspValValGluGlyGlyGlnPheIleAspAlaAlaLysIleIleArgHisProSer 99
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 412 TACCTGGGAGCTCGACGAGCCACGACGACCTCCCGGCTGCTGGCTGGCTGGCTGGCTG 471
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 Tyr-----AsnAlaAsnThrPheAspAsnAspIleMetLeuIleLysLeuAsnSerPro 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 472 GTCCGCGTAAACGACGAGCTTCAACCCCTGCCCCCTGCCCCAATGACTGTGCAACCGCTGCG 531
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 AlaThrLeuAsnSerArgValSerThrValSerLeuProArgSerCysGlySerSerGly 137
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 532 ACCGAGTCCACGCTCTCAGGCTGGGGCATCACCAACACCCAGCAACCCATTCCTCCGGAT 591
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 ThrLysCysLeuValSerGlyTyrGlyAsnThrLeuSerSerGlyThrAsnTyrProSer 157
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 592 CTGCTCCAGTGCCTCAACCTCTCCATGCTGCCATGCCACTGCTGCTGCTGCTGCTGCTGCTG 651
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 LeuLeuGlnCysLeuAspAlaProValLeuSerAspSerSerCysLysSerSerTyrPro 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 652 GGGAGAAATCAGAGCAACATGTGTGTGTCAGCGCGCTCCCG---GGGACGATCCCTGC 708
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 GlyLysIleThrSerAsnMetPheCysLeuGlyPheLeuGluGlyGlyLysAspSerCys 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 709 CAGGTGTATTCTGGGGGCCCCCTGTGTGTGGGGAGTCTTCAAGTCTGTGTGCTGCTG 768
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 GlnGlyAspSerGlyProValValCysAsnGlyGlnLeuGlnGlyValValSerTrp 217
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 769 GGGTCTGTGGGGCCCTGTGGCAAGATGCATCCCTGGAGTCTACACCTATATTTCGAAG 828
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 GlyTyr-----GlyCysAlaGlnLysGlyLysProGlyValTyrThrLysValCysAsn 235
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 829 TATGTGGACTGGATCCGGATGATCATGTAGGAACAAC 864
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 236 TyrValAsnTrpIleGlnGlnThrValAlaAlaAsn 247

RESULT 13

TRRT1

trypsin (EC 3.4.21.4) I precursor - rat

N:Alternate names: trypsinogen I

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004

C:Accession: B22657; A00948

R:Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.

J. Biol. Chem. 259, 14255-14264, 1984

A:Title: Structure of two related rat pancreatic trypsin genes.

A:Reference number: A22657; MUID:85054880; PMID:6094547

A:Accession: B22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

A:Cross-references: UNIPROT:P00762; GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508

A:Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17

R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00948

A:Molecule type: mRNA

A:Residues: 1-246 <MAC>

A:Cross-references: GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508

C:Genetics:

A:Introns: 14/1; 67/2; 152/1; 197/3

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-23/Domain: activation peptide #status predicted <APT>

F:24-246/Product: trypsin I #status predicted <ENZ>

F:24-239/Domain: trypsin homology <TRY>

F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted

F:63, 107, 200/Active site: His, Asp, Ser #status predicted

F:75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:

Pred. No.: 2,256-28 Length: 246

Score: 543.00 Matches: 110

Percent Similarity: 63.56% Conservative: 47

Best Local Similarity: 44.53% Mismatches: 76

Query Match: 26.28% Indels: 14

DB: 1 Gaps: 7

US-10-015-385A-193 (1-1091) x TRRT1 (1-246)

QY 127 CTCAGCATCTTTGCTCTCTGTGTCTTGGGCTCAGCCAGGCA-----GCC 174

Db 1 MetSerAlaLeuIleLeuAlaLeuValGlyAlaAlaValAlaPheProLeuGluAsp 20

QY 175 ACACCGAAGATTTCAATGCGACTGAGTGTGGGGCTCACTCAGCGTGGCAGGTGGGG 234

Db 21 AspAspLysIleValGlyGlyThrCysProGluHisSerValProGlnValSer 40

QY 235 CTGTTTGGAGGCGACCGCTCGCGTGGGGGGTGTCTTTATTGACACAGTGGGTCCTC 294

Db 41 LeuAsnSerGlyThrHisPhe---CysGlyGlySerLeuIleAsnAspGlnTrpValVal 59

QY 295 ACAGCGGCTACTGAGCGGAGCAGGTACTGGGTGGCGCTGGGGGAAACACAGCTCAGC 354

Db 60 SerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIleAsn 79

QY 355 CAGCTCGACTGGACCGAGATCCGGCACAGCGGCTTCTGTGACCCATCCCGGCTAC 414

Db 80 ValLeuGluGlyAspGlnGlnPheIleAsnAlaAlaLysIleIleLysHisProAsnTyr 99

QY 415 CTGGGAGCCTTCGACGAGCAGCAGCAGCAGCTCCGCGCTGCGGTGGCGCTGCCCGTC 474

Db 100 -----SerSerTrpThrLeuAsnAsnAspIleMetLeuIleLysLeuSerSerProVal 117

QY 475 CCGGTAAACAGCAGCGGTTCACCCCTGCGCCCTGCGCCCAATGACTGTGTGCAACCGCTGGCACC 534

Db 118 LysLeuAsnAlaArgValAlaProValAlaLeuProSerAlaCysAlaProIleGlyThr 137

QY 535 GAGTCCACAGTCTCAGGCTGGGG-----ATCACCAACACCCACGGAAACCATTCCTCCG 588

Db 138 GlnCysLeuIleSerGlyTrpGlyAsnThrLeuSerAsnGlyValAsnAsn-----Pro 155

QY 599 GATCTGCTCCAGTGGCTCAACCTCTCCATCGTCTCCATGCCACCTGCCATGGTGTGTAT 648

Db 156 AspLeuLeuGlnCysValAspAlaProValLeuSerGlnAlaAspCysGluAlaIleVal 175

QY 649 CCGGGAGAAATCACAGCAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 705

Db 176 ProGlyGluIleHisSerSerMetIleCysValGlyPheLeuGluGlyGlyLysAspSer 195

QY 706 TGCCAGGTGTATTTGGGGGCCCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765

Db 196 CysGlnGlyAspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleValSer 215

QY 766 TGGGGGTGTGTGGGGCCCTGT 825

Db 216 TrpGlyTyr-----GlyCysAlaLeuProAspAsnProGlyValThrThrLysValCys 233

QY 826 AAGTATGTGACTGATCGATCCGG 846

Db 234 AsnPheValGlyTrpIleGln 240

RESULT 14

S31779

trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C>Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004

C:Accession: S66657; S31779

R:Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.

Eur. J. Biochem. 232, 677-685, 1995

A:Title: Molecular cloning and characterization of anionic and cationic variants of tryp

A:Reference number: S66657; MUID:96035908; PMID:7556223

A:Accession: S66657

A:Molecule type: mRNA

A:Residues: 1-238 <MAL>

A:Cross-references: UNIPROT:P35033; EMBL:X70074; NID:G64387; PIDN:CAA49679.1; PID:G64388

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-15/Domain: activation peptide #status predicted <APT>

F:16-238/Product: trypsin III #status predicted <MAT>

F:16-231/Domain: trypsin homology <TRY>

F:22-152, 40-56, 124-225, 131-198, 163-177, 188-212/Disulfide bonds: #status predicted

F:55, 99, 192/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.: 3,556-28 Length: 238

Score: 540.00 Matches: 108

Percent Similarity: 63.32% Conservative: 37

Best Local Similarity: 47.16% Mismatches: 78

Query Match: 26.14% Indels: 6

DB: 2 Gaps: 4

US-10-015-385A-193 (1-1091) x S31779 (1-238)

QY 181 AAGATTTTCAATGGACACTGAGTGTGGGGCTAACTACAGCCGTGGCAGGTGGGGCTGTTT 240

Db 15 LysIleValGlyGlyThrGluCysArgLysAsnSerAlaSerTrpGlnAlaSerLeuGln 34

QY 241 GAGGCGACCGCTCGGCTGGGGGGTGTCTTTATTGACACAGGTGGGTCTTCACAGCG 300

Db 35 SerGlyThrHisPhe---CysGlyGlySerLeuIleSerSerThrTrpValSerAla 53

QY 301 GCTCACTGCGCGCAGCAGGTACTGGGTGGCGCTGGGGGAAACACAGCTCAGCCAGCTC 360

Db 54 AlaHisCysTyrLysSerArgIleGlnValArgLeuGlyGluHisAsnIleAlaValAsn 73

QY 361 GACTGGACCGAGCATCGGGCACAGCGGCTTCTGTGTGACCCATCCCGGCTACCTGGGA 420



Db		:::      :::	74	GluglyThrGluGlnPheIleAaspSerVallysValIleMethHisProSerTyr----	91
Qy	421	GCTCCAGCAGCACACACACCTCCGGGTGCTGGCGGTGCCTCCGGTCGCCGTA	480		
Db	92	AasnSerArgAsnLeuAspAsnAspIleMetIleullelYsLeuSerLysProAlaSerLeu	111		
Qy	481	ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGCACCCGATGC	540		
Db	112	AasnSerTyrValSerThrValAlaLeuProSerSerCysAlaSerSerGlyThrArgCys	131		
Qy	541	CACGTCCTCAGGCTGGGCATCACCAACACCCACGGAAACCATTCCCGGATCTGCTCCAG	600		
Db	132	LeuValSerGlyTrpGlyAsnLeuSerGlySerSerSerAsnTyrProAspThrLeuArg	151		
Qy	601	TGCCTCAACCTCTCCATCTCCCATCCACCTGCCATCGTGATCCCGGAGAATC	660		
Db	152	CysLeuAspLeuProIleLeuSerSerSerSerCysAsnSerAlaTyrProGlyGlnIle	171		
Qy	661	ACGAGCAACATGGTGTGTGCAGGGCGGCTCCG---GGGCAGGATGCCTGCCAGGTGAT	717		
Db	172	ThrSerAsnMetPheCysAlaGlyPheMetGluGlyGlyAspSerCysGlnGlyAsp	191		
Qy	718	TCTGGGGCCCCCTGGTGTGTGGGGAGTCTCTCAAGGTCGTGGTCTCGGGGGTCTGTG	777		
Db	192	SerGlyGlyProValVaICysAsnGlyGlnLeuGlnGlyValValSerTrpGlyTyr---	210		
Qy	778	GGGCCCTTGGGAAGATGGCATCCCTCGAGTCTACACCTATATTTCAGATGATGGAC	837		
Db	211	--GlyCysAlaGlnArgAsnLysProGlyValTyrThrlYsValCysAsnTyrArgSer	229		
Qy	838	TGATCCGGATGATCATGAGGAACAAC	864		
Db	230	TrpIleSerSerThrMetSerSerAsn	238		

RESULT 15  
S05494  
trypsin (EC 3.4.21.4) IV precursor - rat  
N;Altein name: 23K protein; trypsinogen IV precursor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: S05494  
R;Luettcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.  
Nucleic Acids Res. 17, 6736, 1989  
A;Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.  
A;Reference number: S05494; MUID:89386010; PMID:2780302  
A;Accession: S05494  
A;Molecule type: mRNA  
A;Residues: 1-247 <LUE>

A/Residues: 1-247 <LUE>  
A/Cross-references: UNIPROT:P12788; EMBL:X15679; NID:G56813; PIDM:CAA33718.1; PID:G95618  
C/Superfamily: trypsin; trypsin homolog  
C/Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen

```
F;24-240/Domain: trypsin homology <TRY>
F;30-168,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,101,201/Active site: His, Asp, Ser #status predicted
F;76,78,81.86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
```

Alignment Scores:		
Pred. No.:	9.54e-28	Length:
Score:	53.50	Matches:
Percent Similarity:	59.76%	Conservative:
Best Local Similarity:	43.43%	Mismatches:
Query Match:	25.82%	Indels:
DB:	2	Gaps:
		247
		109
		41
		94
		7
		4

US-10-015-385A-193 (1-1091) x S05494 (1-247)

QY 121 ATGGGGCTCAGCATCTTT-----TTGCTCCTGTGTGTCTTGGGCTCAGCCAGGCAGCC 174  
||| :|||:||||| ||| :||| :|||  
Db 1 MetvsiIteSerItePhePheAlaPheLeuGlyAlaAlaValAlaLeuProValAsnAsp 20

Db  
1 MetLysIleSerIlePhePheAlaPheLeuGluValAlaValAlaLeuProValAsnAsp 20

Qy	175	ACACCGAAGATTTCAATGGCATGAGTGTGGGCGTAACATCACACCGTGGCAGGTGGGG	234
Db	21	AspAspLysIleValGlyGlyThrCysProLysHisLeuValProTyrGlnValSer	40
Qy	235	CTGTTTCAGGGCACACAGCTCGCTGGGGGGTGTCTATTATGACACACAGTGGGTCTCTC	294
Db	41	LeuHisAspGlyIleSerHisGlnCysGlySerLeuIleSerAspGlnTrpValLeu	60
Qy	295	ACAGCGCTCTCACTCAGCGGCAGCAGGTACTGGGTGCGCCTGGGGAAACACACGCTCAGC	354
Db	61	SerAlaAlaHisCysTyrLysArgLysLeuGlnValArgLeuGlyGluHisAsnIleHis	80
Qy	355	CAGCTCGACTGGACCGAGCAGATCCGGCACACGGGCTCTCTGTGACCCATCCCGGCTAC	414
Db	81	ValLeuGluGlyGlyGluGlnPheIleAspAlaGluLysIleIleArgHisProGluTyr	100
Qy	415	CTGGGAGCCTCGACGACGACGACGACGACTCCGGCTGCTGCGGCTGCGCTGCCCGTC	474
Db	101	-----AsnLysAspThrLeuAspAsnAspIleMetLeuIleLysLeuLysSerProAla	118
Qy	475	CGCGTAACGACGACGGTTCAACCCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACC	534
Db	119	ValLeuAsnSerGlnValSerThrValSerLeuProArgSerCysAlaSerThrAspAla	138
Qy	535	GAGTGCCACGCTCTCAGGTGGGGGATCACCAACCAACCCACCGAACCCTATCCCGGATCTG	594
Db	139	GlnCysLeuValSerGlyTyrGlyAsnThrValSerIleGlyGlyLysTyrProAlaLeu	158
Qy	595	CTCAGTGCTCAACCTCTCATCGTCTCCATGCCACTGCCATGGTGTGTATCCCGGG	654
Db	159	LeuGlnCysLeuGluAlaProValLeuSerAlaSerSerCysLysLysSerTyrProGly	178
Qy	655	AGAATCACGACCAACATGGTGTGTGACGGCGGCTCCCG--GGCAGGATCCCTGCCAG	711
Db	179	GlnIleThrSerAsnMetPheCysLeuGlyPheLeuGluGlyLysAspSerCysasp	198
Qy	712	GGTGATTTCTGGGGGCCCTCGTGTGTGTGGGGGAGTCTTCAAGGTCTGGTCTCTGGGGG	771
Db	199	GlyAspSerGlyGlyProValValCysAsnGlyGluIleGlnGlyIleValSerTrpGly	218
Qy	772	TCTGTGGGGCCCTGTGGACAAAGATGGCATCCCTGGAGTCTACACCTATATTGGCAAGTAT	831
Db	219	SerVal-----CysAlaMetArgLysProGlyValTyrThrLysValCysAsnTyr	236
Qy	832	GTGACTGGATTCGGATGATCATGAGGAACAAC	864
Db	237	LeuSerTrpIleGlnGluThrMetAlaAsnAsn	247

Search completed: March 5, 2005, 23:10:05  
Job time : 60 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 5, 2005, 23:00:39 ; Search time 221 Seconds

(without alignments)  
5055.913 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 2066

Sequence: 1 caagcaggtcatccctctgg.....aggggcaaaaaaaaaa 1091

Scoring table:

BLASUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=klp  
-O=/cn2.1/USPTO spool\_p/US10015385/runat\_05032005\_173554\_17304/app\_query.fasta\_1.1287  
-DB=Uniprot\_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-OCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10015385 @CN 1.1.244 @runat\_05032005\_173554\_17304 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Uniprot 03:.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1374	66.5	248 1	KLXC HUMAN
2	952.5	46.1	234 2	Q9CV76
3	632.5	30.6	260 1	KLX8 HUMAN
4	629.5	30.5	260 2	Q8IW69
5	625.5	30.3	260 1	NRPN RAT
6	622.5	30.1	260 1	NRPN MOUSE
7	618.5	29.9	250 1	KLX8 HUMAN
8	611	29.6	255 2	Q7JIG6
9	610	29.5	250 2	Q632F2
10	608	29.4	254 2	Q8CGR4
11	601	29.1	275 2	Q8IXD7
12	599	29.0	255 2	Q6IS10
13	599	29.0	256 1	KLXF HUMAN
14	597.5	28.9	249 2	Q9QYN4
15	597.5	28.9	276 2	Q9QYN3
16	595	28.8	255 2	Q96RQ0

Q9D140	mus musculus	293	2	Q9D140
Q8CGR6	mus musculus	276	2	Q8CGR6
Q8CGR5	mus musculus	250	2	Q8CGR5
Q80VS4	mus musculus	242	2	Q80VS4
Q6P3Z0	mus musculus	246	2	Q6P3Z0
Q90629	gallus gall	248	1	TRY3_CHICK
Q9P093	homo sapien	251	1	KLX8_HUMAN
Q90809	homo sapien	251	2	Q6B089
Q9UK99	homo sapien	250	1	KLK9_HUMAN
Q9UKR3	homo sapien	277	1	KLKD_HUMAN
Q90628	gallus gall	248	1	TRY2_CHICK
Q90627	gallus gall	248	1	TRY1_CHICK
Q9Y337	homo sapien	293	1	KLK5_HUMAN
Q43240	homo sapien	276	1	KLKA_HUMAN
P70059	xenopus lae	244	1	TRY2_XENLA
Q6GNU2	xenopus lae	255	2	Q6GNU2
P00761	sus scrofa	231	1	TRYP_PIG
P00760	bos taurus	243	1	TRY1_BOVIN
Q92876	homo sapien	244	1	KLK6_HUMAN
Q6GYJ5	struthio ca	237	2	Q6GYJ5
Q9UKR2	homo sapien	111	2	Q9UKR2
P19799	xenopus lae	243	1	TRY1_XENLA
P78206	xenopus lae	243	2	Q7SZ06
P49862	homo sapien	253	1	KLK7_HUMAN
Q91Y82	mus musculus	253	2	Q91Y82
O88301	mus musculus	246	2	O88301
P07146	mus musculus	246	1	TRY2_MOUSE
O54854	rattus norv	251	2	O54854
Q9D7Y7	mus musculus	247	2	Q9D7Y7
Q9CPN9	mus musculus	247	1	TRY2_BOVIN
Q29463	bos taurus	247	2	Q9CPN9
P06872	canis fami	246	2	Q6IE66
P06871	canis fami	246	1	TRY1_CANFA
P06826	rattus norv	247	1	TRY3_RAT
Q8NSN9	homo sapien	253	2	Q8NSN9
P00762	rattus norv	246	1	TRY1_RAT
Q79221	mus musculus	246	2	Q79221
Q9CPN7	mus musculus	247	2	Q9CPN7
P35033	salmo salar	238	1	TRY3_SALSA
Q792Y8	mus musculus	246	2	Q792Y8
Q91VE3	m thymopsin	249	2	Q91VE3
Q7T442	mus musculus	246	2	Q7T442
Q9R0T7	m pancreati	246	2	Q9R0T7
Q6R670	oreochromis	245	2	Q6R670
Q6H320	bos taurus	261	2	Q6H320
Q6R671	oreochromis	245	2	Q6R671
Q792Y9	mus musculus	245	2	Q792Y9
P12788	rattus norv	247	1	TRY4_RAT
P00763	rattus norv	246	1	TRY2_RAT
Q921R9	mus musculus	246	2	Q921R9
Q9QUK9	mus musculus	246	2	Q9QUK9
Q792Z0	mus musculus	246	2	Q792Z0
Q6H319	sus scrofa	263	2	Q6H319
P36373	rattus norv	261	1	KLK7_RAT
Q98H00	engraulis j	240	2	Q98H00
Q7M754	mus musculus	246	2	Q7M754
Q8QGW3	anguilla ja	244	2	Q8QGW3
P00752	sus scrofa	246	1	KLK_PIG
P15947	mus musculus	261	1	KLK6_MOUSE
Q632F4	rattus norv	258	2	Q632F4
P32821	rattus norv	246	1	TRYA_RAT
P32822	rattus norv	246	1	TRYB_RAT
P36374	rattus norv	261	1	KLK8_RAT
Q7T1R8	pangasius h	242	2	Q7T1R8
P35375	rattus norv	239	2	Q63275
P35032	salmo salar	231	1	TRY2_SALSA
P12323	cavia porce	239	1	KLK2_CAVPO
Q8AV83	brachydanio	261	2	Q8AV83
Q9N1Q1	saguinus oe	243	2	Q9N1Q1
Q99M20	mus musculus	278	2	Q99M20
Q61E55	rattus norv	279	2	Q61E55

90	511.5	24.8	261	2	Q29474	Q29474	canis famil	163	476.5	23.1	675	2	Q9W6J8	Q9W6J8	dissostrichu
91	510.5	24.7	238	2	Q9W7Q6	Q9W7Q6	paralichthy	164	475.5	22.9	219	2	Q91036	Q91036	gadus morhu
92	510.5	24.7	261	1	KLK3_MOUSE	Q9W7Q6	mus musculu	165	475.5	22.9	235	2	Q66PG8	Q66PG8	fugu rubrip
93	509.5	24.7	222	2	Q9AV11	Q9W7Q6	mus musculu	166	471	22.8	249	2	Q6DIW2	Q6DIW2	Q6DIW2 xenopus tro
94	509.5	24.7	235	2	Q63274	Q9W7Q6	Q63274 rattus norv	167	470.5	22.8	261	1	Q6LDS3	Q6LDS3	Q6LDS3 homo sapien
95	508	24.6	242	1	Q63274	Q9W7Q6	Q63274 rattus norv	168	470.5	22.8	261	1	KLK3_HUMAN	KLK3_HUMAN	P07286 homo sapien
96	508	24.6	242	1	Q63274	Q9W7Q6	Q63274 rattus norv	169	470	22.7	258	2	Q71QI1	Q71QI1	P07286 mus musculu
97	507	24.5	244	2	Q9W7Q7	Q9W7Q6	Q9W7Q7 paralichthy	170	469.5	22.7	261	1	KLK8_MOUSE	KLK8_MOUSE	Q8C232 mus musculu
98	507	24.5	244	2	Q9W7Q7	Q9W7Q6	Q9W7Q7 paralichthy	171	469.5	22.7	261	1	Q8C232	Q8C232	Q8C232 mus musculu
99	506	24.5	245	2	Q632F5	Q9W7Q6	Q632F5 rattus norv	172	468	22.7	259	1	KLK2_RAT	KLK2_RAT	P00759 rattus norv
100	505	24.4	242	2	Q632F5	Q9W7Q6	Q632F5 rattus norv	173	467.5	22.6	261	1	KLK2_MOUSE	KLK2_MOUSE	P36369 mus musculu
101	505	24.4	242	2	Q632F5	Q9W7Q6	Q632F5 rattus norv	174	467	22.6	258	2	Q71QI6	Q71QI6	Q71QI6 trimeresuru
102	505	24.4	249	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	175	464	22.5	258	2	Q8AY80	Q8AY80	Q8AY80 trimeresuru
103	505	24.4	260	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	176	464	22.5	258	2	Q8AY80	Q8AY80	Q8AY80 trimeresuru
104	504.5	24.4	269	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	177	461.5	22.4	261	2	Q8K0C6	Q8K0C6	Q8K0C6 mus musculu
105	503	24.3	241	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	178	458.5	22.2	250	1	KLK9_RAT	KLK9_RAT	P07647 rattus norv
106	503	24.3	263	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	179	458.5	22.2	261	1	TRYP_PLRPL	TRYP_PLRPL	P07647 rattus norv
107	502	24.3	249	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	180	452	21.9	260	2	KLK2_HUMAN	KLK2_HUMAN	P30151 homo sapien
108	502	24.3	259	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	181	451	21.8	260	2	Q71QJ4	Q71QJ4	P30151 homo sapien
109	501.5	24.3	237	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	182	450	21.8	258	1	VSP1_TRIST	VSP1_TRIST	Q71QJ4 trimeresuru
110	501	24.2	242	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	183	450	21.8	260	2	Q71QJ4	Q71QJ4	Q71QJ4 trimeresuru
111	501	24.2	247	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	184	448	21.7	258	2	Q8AY78	Q8AY78	Q8AY78 trimeresuru
112	501	24.2	247	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	185	447.5	21.7	258	1	VSP2_AKAC	VSP2_AKAC	Q8AY78 trimeresuru
113	499.5	24.2	241	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	186	446.5	21.6	257	2	VSP3_TRIMU	VSP3_TRIMU	Q8AY78 trimeresuru
114	499	24.2	239	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	187	446.5	21.6	257	2	Q71QI5	Q71QI5	Q8AY78 trimeresuru
115	498	24.1	249	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	188	446	21.6	258	1	VSP3_BOTJA	VSP3_BOTJA	Q8AY78 trimeresuru
116	498	24.1	254	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	189	444.5	21.5	249	2	Q8JFQ7	Q8JFQ7	Q8JFQ7 gadus morhu
117	497	24.1	257	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	190	441	21.3	257	1	VSP4_TRIMU	VSP4_TRIMU	Q8JFQ7 gadus morhu
118	497	24.1	258	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	191	439.5	21.2	257	2	VSP7_TRIMU	VSP7_TRIMU	Q8JFQ7 gadus morhu
119	497	24.1	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	192	439	21.2	279	2	Q9YQJ8	Q9YQJ8	Q9YQJ8 agkistrodon
120	496.5	24.0	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	193	438.5	21.2	257	1	VSP2_TRIMU	VSP2_TRIMU	Q9YQJ8 agkistrodon
121	496	24.0	242	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	194	438	21.2	259	1	VSP1_VIPLE	VSP1_VIPLE	Q9YQJ8 agkistrodon
122	496	24.0	247	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	195	437.5	21.2	257	1	VSP1_TRIMU	VSP1_TRIMU	Q9YQJ8 agkistrodon
123	496	24.0	262	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	196	436.5	21.1	250	2	Q03955	Q03955	Q03955 praomys nat
124	496	24.0	262	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	197	436.5	21.1	257	2	VSP5_TRIMU	VSP5_TRIMU	Q03955 praomys nat
125	495.5	24.0	257	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	198	436.5	21.1	257	2	Q71QI7	Q71QI7	Q71QI7 trimeresuru
126	495.5	24.0	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	199	435.5	21.1	257	2	Q71QI7	Q71QI7	Q71QI7 trimeresuru
127	495	24.0	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	200	435	21.0	258	1	VSP2_TRIJE	VSP2_TRIJE	Q9DF67 trimeresuru
128	495	24.0	261	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	201	434	21.0	258	1	VSP3_TRIJE	VSP3_TRIJE	Q9DF67 trimeresuru
129	494.5	23.9	247	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	202	434	21.0	260	2	VSPB_TRIGA	VSPB_TRIGA	Q13061 trimeresuru
130	493.5	23.9	248	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	203	434	21.0	260	2	Q71QI9	Q71QI9	Q13061 trimeresuru
131	493	23.9	262	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	204	433.5	21.0	257	2	Q71QJ0	Q71QJ0	Q71QJ0 trimeresuru
132	492	23.8	262	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	205	433	21.0	260	1	VSP1_AKHP	VSP1_AKHP	Q9YQJ2 agkistrodon
133	491.5	23.8	241	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	206	432	20.9	236	1	VSPA_DABRU	VSPA_DABRU	P18964 dabola ruse
134	491	23.8	256	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	207	432	20.9	257	2	Q9PTL3	Q9PTL3	Q9PTL3 agkistrodon
135	490.5	23.7	229	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	208	432	20.9	260	1	VSP2_AKHP	VSP2_AKHP	Q9YQI6 agkistrodon
136	490.5	23.7	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	209	432	20.9	260	2	Q73800	Q73800	Q73800 agkistrodon
137	489.5	23.7	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	210	431.5	20.9	205	2	Q96JEO	Q96JEO	Q96JEO homo sapien
138	489	23.7	244	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	211	431.5	20.9	257	2	Q71QJ1	Q71QJ1	Q71QJ1 trimeresuru
139	488	23.6	247	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	212	431.5	20.9	261	1	KLK2_HORSE	KLK2_HORSE	Q6H321 equus cabal
140	488	23.6	265	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	213	431.5	20.9	261	1	KLK3_MOUSE	KLK3_MOUSE	P04071 mus musculu
141	487.5	23.6	251	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	214	431	20.9	260	1	VSPA_TRIGA	VSPA_TRIGA	Q13060 trimeresuru
142	486	23.5	242	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	215	431	20.9	262	1	Q8AY81	Q8AY81	Q8AY81 trimeresuru
143	485.5	23.5	234	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	216	429.5	20.8	205	2	VSP1_AKCA	VSP1_AKCA	Q91053 agkistrodon
144	485.5	23.5	261	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	217	429.5	20.8	205	2	Q96JED	Q96JED	Q96JED homo sapien
145	485	23.5	304	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	218	429	20.8	176	2	Q8K5D7	Q8K5D7	Q8K5D7 mus musculu
146	484.5	23.5	251	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	219	429	20.8	258	1	VSP3_TRIGA	VSP3_TRIGA	Q13063 trimeresuru
147	484.5	23.5	259	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	220	429	20.8	260	2	Q8QHK3	Q8QHK3	Q8QHK3 crotalus at
148	484	23.4	255	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	221	428.5	20.7	262	2	Q8QHK3	Q8QHK3	Q8QHK3 crotalus at
149	483.5	23.4	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	222	427	20.7	234	2	Q9YGS1	Q9YGS1	Q9YGS1 agkistrodon
150	482	23.3	255	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	223	427	20.7	260	2	Q93502	Q93502	Q93502 agkistrodon
151	481.5	23.3	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	224	426.5	20.6	257	1	VSPC_TRIGA	VSPC_TRIGA	Q13062 trimeresuru
152	481	23.3	254	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	225	425	20.6	260	1	VSP1_AKAC	VSP1_AKAC	Q13062 agkistrodon
153	480.5	23.3	263	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	226	424.5	20.5	204	2	Q71QJ3	Q71QJ3	Q71QJ3 trimeresuru
154	479	23.2	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	227	423	20.5	257	2	Q96JED	Q96JED	Q96JED homo sapien
155	479	23.2	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	228	423	20.5	238	1	VSP1_AKCA	VSP1_AKCA	Q91053 agkistrodon
156	478.5	23.2	248	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	229	422.5	20.5	259	2	Q8UUK2	Q8UUK2	Q8UUK2 crotalus ad
157	478.5	23.2	250	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	230	422	20.4	256	2	Q7SYF1	Q7SYF1	Q7SYF1 cerastes ce
158	477.5	23.1	256	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	231	421.5	20.4	163	2	Q66H01	Q66H01	Q66H01 xenopus lae
159	477.5	23.1	261	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	232	420.5	20.4	257	2	Q71QI8	Q71QI8	Q71QI8 trimeresuru
160	477.5	23.1	263	1	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	233	420	20.3	234	2	Q8QHK2	Q8QHK2	Q8QHK2 crotalus at
161	477	23.1	247	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	234	419.5	20.3	234	2	Q8UUK1	Q8UUK1	Q8UUK1 agkistrodon
162	476.5	23.1	344	2	Q7SX90	Q9W7Q6	Q7SX90 brachydanio	235	418.5	20.3	257	2	Q71QI6	Q71QI6	Q71QI6 trimeresuru

236	418	20.2	260	2	Q8AV82	Q8AV82 trimeresuru	309	372.5	18.0	270	2	Q8I9P2	Q8I9p2 aplysina fi
237	417	20.2	236	1	VSPG_DABRU	P18965 daboia russ	310	371.5	18.0	855	2	Q7Z410	Q7Z410 homo sapien
238	415.5	20.1	178	2	O93594	O93594 dicentrarch	311	371.5	18.0	1059	2	Q7Z411	Q7Z411 homo sapien
239	415.5	20.1	237	2	Q7UJOH8	Q7UJH8 trimeresuru	312	371	18.0	234	1	VSP1_AGKRH	P26324 agkistrodon
240	414	20.0	257	2	Q8UUJ2	Q8UUJ2 agkistrodon	313	371	18.0	259	1	CFAD_PIG	P51779 sus scrofa
241	414	20.0	258	1	VSP1_TRIGA	O13059 trimeresuru	314	371	18.0	263	1	CTR2_CANFA	P04813 canis famli
242	414	20.0	260	1	VSP1_TRIFL	P05620 trimeresuru	315	371	18.0	271	1	EL2_RAT	P00774 rattus norv
243	413	20.0	258	2	Q7SZE1	Q7szel gloydus sa	316	370.5	17.9	204	2	Q86VI7	Q86vi7 homo sapien
244	413	20.0	260	1	VSP2_VIPLE	Q9PT40 vipera lebe	317	370.5	17.9	638	1	KAT_HUMAN	P03952 homo sapien
245	412	19.9	258	2	Q7UJOH7	Q7UJH7 trimeresuru	318	368	17.8	418	1	HATT_HUMAN	O60235 homo sapien
246	411.5	19.9	228	1	VSPA_LACMU	P33589 lachesis sh	319	367	17.8	267	2	Q640E1	Q640e1 xenopus lae
247	411	19.9	239	2	Q6T5L0	Q6t5l0 gloydus mu	320	366	17.7	258	1	VSP2_AGKRH	P47797 agkistrodon
248	411	19.9	260	2	Q7SZC3	Q7szc3 gallus gall	321	366	17.7	260	2	Q9W7Q3	Q9W7q3 paralicthy
249	408.5	19.8	257	2	Q8JH62	Q8Jh62 vipera lebe	322	366	17.7	307	2	Q6ZND6	Q6Znd6 homo sapien
250	408	19.7	235	1	VSP2_AGKBI	Q9PEN3 agkistrodon	323	365.5	17.7	245	2	Q8XI60	Q9xy60 ctenocephal
251	408	19.7	232	2	Q8AY79	Q8AY79 trimeresuru	324	365	17.7	263	2	Q7SX97	Q7sx97 brachydanio
252	407.5	19.7	258	1	VSP1_BOTJA	P81824 bothrops ja	325	364.5	17.6	265	2	Q6P326	Q6p326 xenopus tro
253	407	19.7	237	2	O93421	Q93421 agkistrodon	326	364.5	17.6	387	2	Q9XY57	Q9xy57 ctenocephal
254	407	19.7	257	1	VSP2_AGKCA	O43207 agkistrodon	327	363.5	17.6	314	1	TEST_HUMAN	Q9Y6M0 homo sapien
255	407	19.7	260	1	VSP2_TRIFL	O13057 trimeresuru	328	363.5	17.6	339	2	Q9JL44	Q9Jl44 mus musculus
256	406.5	19.7	231	1	VSP1_AGKCO	P09872 agkistrodon	329	363	17.6	340	2	Q8BJV6	Q8bjv6 mus musculus
257	406.5	19.7	257	2	Q7UJOH5	Q7UJH5 trimeresuru	330	363	17.6	342	1	PS8_MOUSE	Q9ead1 mus musculus
258	405.5	19.6	257	2	Q7UJOI3	Q7UJi3 trimeresuru	331	362.5	17.5	246	1	MCT1_MERUN	P50340 meriones un
259	405	19.6	234	2	Q7SZE2	Q7sze2 agkistrodon	332	361.5	17.5	267	2	Q7SZ51	Q7sz51 brachydanio
260	405	19.6	260	1	VSP1_TRIFE	Q9df68 trimeresuru	333	361.5	17.5	344	2	Q640F8	Q640f8 xenopus lae
261	403.5	19.5	257	2	Q6IWF1	Q6Iwfl bothrops al	334	361	17.4	255	2	Q6WGR1	Q6wgr1 ictalurus p
262	402.5	19.5	233	2	Q9YVJ9	Q9Yvj9 agkistrodon	335	360	17.4	331	2	Q8RIA6	Q8ria6 mus musculus
263	402	19.5	255	1	VSPA_BOTAT	P04971 bothrops at	336	360	17.4	331	2	Q8OX17	Q8ox17 mus musculus
264	402	19.5	260	1	VSP6_TRIMU	Q9dg83 trimeresuru	337	359.5	17.4	259	2	Q6AZC2	Q6azc2 brachydanio
265	401.5	19.4	257	2	Q8OG86	Q8OG86 bothrops in	338	359.5	17.4	269	2	O6ISU5	Q6isau5 homo sapien
266	401	19.4	234	1	VSP2_AGKCO	P83981 agkistrodon	339	359.5	17.4	277	1	TRY2_ANOGA	P35036 anopheles g
267	401	19.4	235	2	Q9OZ47	Q9oz47 agkistrodon	340	359.5	17.4	1019	1	LFC_TACTR	P28175 tachyples
268	400	19.4	258	2	Q8O2F0	Q8O2f0 agkistrodon	341	359.5	17.4	1019	2	Q8T9S1	Q8t9s1 tachyples
269	399	19.3	260	2	Q7UJOJ2	Q7UJj2 trimeresuru	342	359	17.4	311	2	Q8OXZ3	Q8oxz3 rattus norv
270	397.5	19.2	257	1	VSP2_BOTJA	O13069 bothrops ja	343	359	17.4	430	2	Q6GNK3	Q6gnk3 xenopus lae
271	397	19.2	260	1	Q7UJOI4	Q7UJi4 trimeresuru	344	359	17.4	245	1	Q804X0	Q804x0 fugu rubrip
272	396.5	19.2	260	1	VSP4_AGKAC	Q918w9 agkistrodon	345	358.5	17.4	263	1	MCT1_SHEEP	P00931 ovis aries
273	395.5	19.1	264	2	Q9ER05	Q9er05 mus musculus	346	358.5	17.4	263	1	CTRB_HUMAN	P17538 homo sapien
274	395	19.1	260	2	Q7UJOH9	Q7UJh9 trimeresuru	347	358.5	17.4	444	1	FA7_RABIT	P98139 oryctolagus
275	393.5	19.0	264	2	Q9D7P8	Q9d7p8 mus musculus	348	358	17.3	277	2	Q7T0T6	Q7tt06 xenopus lae
276	392	19.0	258	2	Q7UJOI2	Q7UJi2 trimeresuru	349	358	17.3	318	2	Q7RTY9	Q7rtY9 homo sapien
277	391.5	18.9	257	1	VSP3_TRIFL	O13058 trimeresuru	350	358	17.3	812	1	PLMN_BOVIN	P06868 bos taurus
278	391.5	18.9	264	2	Q9EQZ6	Q9eqz8 rattus norv	351	357.5	17.3	232	2	Q9XY45	Q9xy45 ctenocephal
279	391	18.9	253	2	Q8WZB4	Q8wzb4 homo sapien	352	357.5	17.3	321	1	TRYG_HUMAN	Q9nr12 homo sapien
280	391	18.9	258	2	Q98TT5	Q98tt5 agkistrodon	353	357.5	17.3	321	2	Q96RZ8	Q96rZ8 homo sapien
281	390	18.9	258	2	Q8JH85	Q8Jh85 vipera lebe	354	357.5	17.3	371	2	Q8MS52	Q8ms52 drosophila
282	390	18.9	258	2	O9I961	Q9I961 agkistrodon	355	357.5	17.3	643	2	Q97506	Q97506 sus scrofa
283	389	18.8	253	1	CFAD_HUMAN	P00746 homo sapien	356	357	17.3	262	1	GRAA_HUMAN	P12544 homo sapien
284	388	18.8	232	1	VSPA_BOTJA	P81661 bothrops ja	357	357	17.3	271	1	CTR1_PENVA	Q00871 penaeus van
285	388	18.8	257	1	VSP3_AGKAC	Q918x0 agkistrodon	358	357	17.3	806	1	PLMN_MACEU	O18783 macropus eu
286	388	18.8	269	1	EL2_PIG	P08419 sus scrofa	359	356.5	17.3	260	2	Q9V7G4	Q9v7G4 drosophila
287	387	18.7	181	2	Q8NFV7	Q8nfV7 homo sapien	360	356.5	17.3	261	2	Q9W7Q4	Q9W7q4 paralicthy
288	387	18.7	243	2	Q8GVJ5	Q8gvj5 homo sapien	361	355.5	17.2	276	1	MCT6_MOUSE	P21845 mus musculus
289	386.5	18.7	1524	2	Q91674	Q91674 xenopus lae	362	355	17.2	311	2	Q8WZM5	Q8wzm5 trichodema
290	386	18.7	258	2	Q9W7S1	Q9w7s1 agkistrodon	363	355	17.2	342	1	PS8_RAT	Q9es87 rattus norv
291	386	18.7	260	2	Q6T6S7	Q6t6s7 bitis gabon	364	354.5	17.2	249	2	Q6QX59	Q6qx59 lepeophthei
292	385.5	18.7	188	1	CTRL3_RAT	P15950 rattus norv	365	354.5	17.2	263	1	CTRA_GADMO	P47796 gadus morhu
293	385.5	18.7	264	1	CTRL3_RAT	P40313 homo sapien	366	354	17.1	260	1	GRAA_MOUSE	P11032 mus musculus
294	385.5	18.7	264	2	Q9D950	Q9d960 mus musculus	367	354	17.1	260	2	Q9W7P9	Q9W7p9 paralicthy
295	385.5	18.7	269	2	Q8IUW0	Q8Iuw0 mus musculus	368	354	17.1	271	1	EL2_MOUSE	P05208 mus musculus
296	385	18.6	263	1	CFAD_RAT	P32038 rattus norv	369	354	17.1	558	2	QL6711	Q6l711 rattus norv
297	384.5	18.6	195	2	Q7Z277	Q07277 homo sapien	370	353.5	17.1	263	2	Q6PGS4	Q6pgs4 xenopus lae
298	381	18.4	256	1	TRP3_PSEAM	Q93267 pseudopleur	371	353.5	17.1	270	1	TRYT_MERUN	P50342 meriones un
299	380.5	18.4	235	2	Q8N4E0	Q8n4e0 homo sapien	372	353.5	17.1	311	1	TRYG_MOUSE	Q9qu17 mus musculus
300	380	18.4	157	2	Q6B338	Q6b338 symphysodon	373	353.5	17.1	333	2	Q7O5Z6	Q7o5z6 anopheles g
301	380	18.4	455	2	Q63Y86	Q63y86 xenopus lae	374	353	17.1	505	2	Q966V4	Q966v4 halocynthia
302	379	18.3	220	2	Q8NCW4	Q8ncw4 homo sapien	375	353	17.1	274	1	MCT6_RAT	P50343 rattus norv
303	378	18.3	261	2	Q6DHD9	Q6dhd9 brachydanio	376	353	17.1	278	2	Q7PNF6	Q7pnf6 anopheles g
304	376	18.2	343	1	PS8_HUMAN	Q16651 homo sapien	377	353	17.1	456	1	PRTC_CANFA	Q28278 canis famli
305	374.5	18.1	259	1	CFAD_MOUSE	P03953 mus musculus	378	353	17.1	459	1	PRTG_PIG	Q9glp2 sus scrofa
306	374	18.1	261	2	Q8CJF4	Q8cjf4 rattus norv	379	352	17.0	304	1	DISP_RAT	P83748 rattus norv
307	373.5	18.1	330	2	Q6NVR7	Q6nv7 xenopus tro	380	352	17.0	1130	2	Q9DIW7	Q9dIw7 anopheles g
308	372.5	18.0	228	2	Q6FWH3	Q6fhw3 homo sapien	381	351.5	17.0	317	2	Q9DGR3	Q9dgr3 xenopus lae

382	351.5	17.0	460	1	PTC_MOUSE	P33587	mus musculus	455	342.5	16.6	437	1	ACRO_RAT	P23293	rattus norv
383	351.5	17.0	719	2	Q6DJ90	Q6DJ90	xenopus tro	456	342.5	16.6	624	1	FAII_MOUSE	Q91y47	mus musculus
384	351.5	17.0	1019	1	LFC_CARRO	Q26422	carcinoscor	457	342.5	16.6	810	1	PLMN_HUMAN	P00747	homo sapien
385	351.5	17.0	1083	2	Q6423	Q26423	carcinoscor	458	342.5	16.6	811	1	TMS6_HUMAN	Q81u80	homo sapien
386	351	17.0	310	1	DISP_MOUSE	Q9gyz9	mus musculus	459	342	16.6	275	1	TRB1_HUMAN	Q15661	homo sapien
387	351	17.0	328	2	Q80Z40	Q80Z40	rattus norv	460	342	16.6	335	2	Q8VIF2	Q8vif2	mus musculus
388	351	17.0	456	1	PTC_BOVIN	P00745	bos taurus	461	342	16.6	355	2	Q7PQR9	Q7PQR9	anopheles g
389	350.5	17.0	265	2	Q804G1	Q804G1	brachydanio	462	342	16.6	812	1	PLMN_MOUSE	P20918	mus musculus
390	350.5	17.0	274	2	Q16133	Q16133	anopheles s	463	341.5	16.5	258	1	GRAK_RAT	P49864	rattus norv
391	350.5	17.0	274	2	Q17086	Q17086	anopheles s	464	341.5	16.5	455	1	TMS5_MOUSE	Q9er04	mus musculus
392	350.5	17.0	434	2	Q7T3B6	Q7T3B6	brachydanio	465	341.5	16.5	573	2	Q9V516	Q9v516	drosophila
393	350.5	17.0	503	2	Q8AYE4	Q8aye4	brachydanio	466	341	16.5	251	2	Q9GLN2	Q9glN2	bos taurus
394	350	16.9	263	2	Q6GP11	Q6gp11	homo sapien	467	341	16.5	263	1	GRAK_MOUSE	Q3s205	mus musculus
395	350	16.9	268	2	Q6QOE9	Q6qoe9	xenopus lae	468	341	16.5	271	2	Q803Z4	Q803z4	brachydanio
396	350	16.9	268	2	Q642S8	Q642s8	xenopus tro	469	341	16.5	572	2	Q7RTY8	Q7rty8	homo sapien
397	350	16.9	271	2	Q18487	Q18487	penaeus van	470	341	16.5	704	1	CRAR_MOUSE	P90064	mus musculus
398	350	16.9	1134	2	Q7RTY7	Q7rty7	homo sapien	471	340.5	16.5	246	1	MCT4_MOUSE	P21812	mus musculus
399	349.5	16.9	261	2	Q66HW9	Q66hw9	brachydanio	472	340.5	16.5	274	1	TRY1_ANOGA	P35035	anopheles g
400	349.5	16.9	269	1	EL2A_HUMAN	P08217	homo sapien	473	340.5	16.5	329	2	Q42272	Q42272	xenopus lae
401	349.5	16.9	269	2	Q61CV2	Q61cv2	homo sapien	474	340.5	16.5	418	2	Q7PGU3	Q7pgu3	anopheles g
402	349.5	16.9	277	2	Q96899	Q96899	scolopendra	475	340.5	16.5	432	2	Q6UX37	Q6ux37	homo sapien
403	349.5	16.9	371	2	Q8CJ16	Q8cj16	rattus norv	476	340.5	16.5	437	1	TMS4_HUMAN	Q9nrs4	homo sapien
404	349.5	16.9	445	2	Q8CJ17	Q8cj17	rattus norv	477	340.5	16.5	446	1	FA7_RAT	Q8k3u6	rattus norv
405	349	16.9	467	2	Q967X8	Q967x8	panulirus a	478	340.5	16.5	624	2	Q9DRT3	Q9dat3	mus musculus
406	348.5	16.9	429	2	Q8AVB0	Q8avb0	brachydanio	479	340	16.5	273	2	Q9KSM1	Q9xsm1	ovis aries
407	348.5	16.9	799	2	Q6PF94	Q6pf94	mus musculus	480	340	16.5	360	2	Q17489	Q17489	anopheles g
408	348.5	16.9	811	1	TMS6_MOUSE	Q9dbi0	mus musculus	481	340	16.5	458	1	PRTC_RABIT	Q28661	oryctolagus
409	348.5	16.9	818	2	Q6PBA6	Q6pba6	brachydanio	482	339.5	16.4	247	2	Q08732	Q08732	mesocricetu
410	348	16.8	267	1	TRY7_ANOGA	P35041	anopheles g	483	339.5	16.4	253	1	TRYB_DROER	P54625	drosophila
411	348	16.8	269	2	Q61SN8	Q61sn8	homo sapien	484	339.5	16.4	258	1	GRAM_RAT	Q03238	rattus norv
412	347	16.8	275	2	Q6FHB8	Q6fhb8	homo sapien	485	339.5	16.4	263	2	Q9D8X8	Q9d8x8	mus musculus
413	347	16.8	284	2	Q8NFF6	Q8nff6	homo sapien	486	339.5	16.4	333	1	PLMN_CANFA	P80009	canis fami
414	347	16.8	457	1	TMS5_HUMAN	Q9h3s3	homo sapien	487	339	16.4	321	2	Q61E60	P00740	rattus norv
415	347	16.8	461	1	PTC_HUMAN	P04070	homo sapien	488	339	16.4	461	1	FA9_HUMAN	Q01777	rattus norv
416	346.5	16.8	263	2	Q63ZK0	Q63zk0	xenopus lae	489	339	16.4	461	1	FA9_PANTR	Q95nd7	pan troglod
417	346.5	16.8	267	2	Q9BK47	Q9bk47	luidia foli	490	339	16.4	556	2	Q903D5	Q803d5	brachydanio
418	346.5	16.8	269	1	EL2_BOVIN	Q29461	bos taurus	491	339	16.4	625	1	FAII_HUMAN	P03951	homo sapien
419	346.5	16.8	334	2	Q46507	Q46507	papio hanad	492	339	16.4	812	1	PLMN_RAT	Q01177	rattus norv
420	346.5	16.8	351	2	Q81E60	Q81e60	holotrichia	493	338.5	16.4	256	2	O18599	Q18599	drosophila
421	346.5	16.8	435	1	TMS4_MOUSE	Q8vca5	mus musculus	494	338.5	16.4	258	1	EL1_HUMAN	Q9unil	homo sapien
422	346.5	16.8	435	2	Q9NFY2	Q9nfy2	anopheles g	495	338.5	16.4	258	2	Q867B0	Q867b0	canis fami
423	346.5	16.8	446	1	FA7_MOUSE	P70375	mus musculus	496	338.5	16.4	260	2	Q8P2V9	Q8p2v9	xenopus tro
424	346.5	16.8	456	2	Q7QC30	Q7qc30	anopheles g	497	338.5	16.4	263	2	Q9CR35	Q9cd86	mus musculus
425	346.5	16.8	461	1	PTC_RAT	P31394	rattus norv	498	338.5	16.4	264	2	Q0DC86	Q0dc86	mus musculus
426	346.5	16.8	612	2	Q68FY8	Q68fy8	rattus norv	499	338.5	16.4	264	2	Q02569	O02569	culex quing
427	346.5	16.8	612	2	Q804W7	Q804w7	fugu rubrip	500	338.5	16.4	402	2	Q7QB73	Q7qb73	anopheles g
428	346	16.7	282	2	Q6NZY1	Q6nzy1	homo sapien	501	338.5	16.4	455	2	Q8CDR0	Q8cdr0	mus musculus
429	346	16.7	322	2	Q920S2	Q920s2	mus musculus	502	338.5	16.4	562	2	Q7PN85	Q7pn85	anopheles g
430	346	16.7	389	2	Q9VPX7	Q9vpX7	xenopus lae	503	338.5	16.4	802	2	Q6UXD8	Q6uxd8	homo sapien
431	345.5	16.7	454	2	Q46506	Q46506	papio hanad	504	338	16.4	210	2	Q63Z11	Q63z11	xenopus lae
432	345	16.7	253	1	TRYD_DROER	P54626	drosophila	505	338	16.4	365	2	Q97366	Q97366	holotrichia
433	345	16.7	328	2	Q61RA4	Q61ra4	xenopus lae	506	338	16.4	388	2	O44330	O44330	manduca sex
434	344.5	16.7	117	2	Q9PUF3	Q9puf3	bothrops ja	507	338	16.4	625	1	THRB_BOVIN	P00735	bos taurus
435	344.5	16.7	187	2	Q6FK75	Q6fk75	homo sapien	508	338	16.4	701	2	Q9JUS9	Q9jjs9	rattus norv
436	344.5	16.7	275	2	Q6B0S1	Q6b0s1	homo sapien	509	338	16.4	733	2	Q8CHN8	Q8chn8	rattus norv
437	344	16.7	257	2	Q8BZ04	Q8bz04	mus musculus	510	337.5	16.3	208	1	TRY5_AEDAE	P29787	aedes aegypt
438	344	16.7	265	2	Q6QXG1	Q6qxg1	lepeopthei	511	337.5	16.3	261	2	Q6QX60	Q6qx60	lepeopthei
439	344	16.7	275	1	TRB2_HUMAN	P20231	homo sapien	512	337.5	16.3	264	1	GRAK_HUMAN	P49863	homo sapien
440	344	16.7	280	2	Q8N171	Q8n171	homo sapien	513	337.5	16.3	282	2	Q9D4I3	Q9d4i3	mus musculus
441	344	16.7	297	2	Q8S781	Q8s781	rattus ratt	514	337.5	16.3	432	2	Q6GNA2	Q6gna2	xenopus lae
442	344	16.7	417	2	Q8BZ10	Q8bz10	mus musculus	515	337.5	16.3	471	2	Q8CFE0	Q8cfe0	mus musculus
443	343.5	16.6	266	2	Q8HYJ2	Q8hyj2	bos taurus	516	337	16.3	247	2	Q17039	Q17039	anopheles g
444	343.5	16.6	271	2	Q8HYJ2	Q8hyj2	macaca fasc	517	337	16.3	256	2	Q9R0K0	Q9r0k0	mus musculus
445	343.5	16.6	273	1	MCT7_MOUSE	Q02844	mus musculus	518	337	16.3	275	2	Q96RZ6	Q96rZ6	homo sapien
446	343.5	16.6	273	2	Q921N4	Q921n4	mus musculus	519	337	16.3	434	1	UROK_CHICK	P15120	gallus gall
447	343.5	16.6	517	2	Q8K0D2	Q8k0d2	mus musculus	520	336.5	16.3	247	1	MCT1_PAPHA	P52195	papio hamad
448	343	16.6	275	1	TRYT_CANFA	P15944	canis fami	521	336.5	16.3	251	1	MCT3_SHEEP	Q46683	ovis aries
449	342.5	16.6	248	2	O16126	O16126	boltenia vi	522	336.5	16.3	318	2	Q8MNY6	Q8mny6	niilaparvaca
450	342.5	16.6	248	2	Q9XY52	Q9xy52	ctenoccephal	523	336.5	16.3	428	2	Q8WPM7	Q8wpm7	oikopleura
451	342.5	16.6	273	1	MCT7_RAT	P27435	rattus norv	524	336.5	16.3	581	2	Q9BYE2	Q9bye2	homo sapien
452	342.5	16.6	273	2	Q6P6W8	Q6p6w8	rattus norv	525	336.5	16.3	638	2	KAL_MOUSE	P26262	mus musculus
453	342.5	16.6	433	2	Q80HD0	Q80hd0	brachydanio	526	336	16.3	227	1	Q8IX14	Q8ixi4	homo sapien
454	342.5	16.6	433	2	Q90YK1	Q90yk1	brachydanio	527	336	16.3	273	1	TRYT_SHEEP	Q9xsm2	ovis aries

528	336	16.3	280	2	Q64ID5	Q64id5 anthonomus	601	329.5	15.9	253	1	TRYD_DROME	P42276 drosophila
529	336	16.3	416	1	FA9_BOVIN	P00741 bos taurus	602	329.5	15.9	262	2	Q72ID6	Q8w10 lepeophthei
530	336	16.3	485	1	Q7PRK0	P07k0 anopheles g	603	329.5	15.9	266	2	Q8WR10	Q8w10 paralithode
531	336	16.3	654	2	Q6GNF4	Q6gnf4 canis faml	604	329.5	15.9	269	1	EL2B_HUMAN	P08218 homo sapien
532	336	16.3	790	1	PLMN_PIG	P06867 sus scrofa	605	329.5	15.9	270	2	Q64ID1	Q64id1 anthonomus
533	336	16.3	1303	2	Q6GS84	Q66884 oikopleura	606	329.5	15.9	283	2	Q6UWY2	Q6uwY2 homo sapien
534	335.5	16.2	258	2	Q6ISM6	Q6ism6 homo sapien	607	329.5	15.9	320	2	Q7PEV6	Q7peV6 anopheles g
535	335.5	16.2	266	1	ELJ_BOVIN	Q28153 bos taurus	608	329.5	15.9	324	1	TEST_MOUSE	Q9jfy7 mus musculus
536	335.5	16.2	275	1	TRYT_PIG	Q9n2d1 sus scrofa	609	329.5	15.9	336	2	Q8OYD8	Q8OyD8 mus musculus
537	335.5	16.2	558	2	Q86YM4	Q86ym4 homo sapien	610	329.5	15.9	578	2	Q6QO17	Q6qo17 bos taurus
538	335	16.2	216	2	Q9UD19	Q9ud19 homo sapien	611	329.5	15.9	1420	1	AP0A_WACMU	P14417 macaca mula
539	335	16.2	433	2	Q804X5	Q804x5 gallus gall	612	329	15.9	216	1	VSPP_LACMU	P84036 lachezia mu
540	334.5	16.2	247	2	Q70500	Q70500 rattus norv	613	329	15.9	264	2	Q08643	Q08643 mus musculus
541	334.5	16.2	275	2	Q7YS62	Q7y862 equus cabal	614	329	15.9	279	2	Q99MS4	Q99ms4 mus musculus
542	334.5	16.2	537	2	Q9BYE1	Q9bye1 homo sapien	615	329	15.9	306	1	BSS4_MOUSE	Q99r10 mus musculus
543	334	16.2	234	2	Q15096	Q15096 homo sapien	616	329	15.9	572	2	Q8BIK6	Q8bik6 mus musculus
544	334	16.2	245	1	CTRA_BOVIN	P00766 bos taurus	617	329	15.9	575	2	Q7O9W3	Q7q9w3 anopheles g
545	334	16.2	264	2	Q8QGF6	Q8qgf6 xenopus lae	618	329	15.9	681	2	Q7ZT70	Q7zt70 lampetra ja
546	334	16.2	320	2	Q7TOX2	Q7tox2 xenopus lae	619	329	15.9	722	2	Q6NUF5	Q6nuf5 xenopus lae
547	333.5	16.1	253	2	Q8MKZ1	Q8mkz1 drosophila	620	328.5	15.9	239	2	Q8T4P3	Q8t4p3 lepeophthei
548	333.5	16.1	253	2	Q8SXZ4	Q8sxz4 drosophila	621	328.5	15.9	245	1	CTRB_GADMO	P80646 gadus morhu
549	333.5	16.1	263	1	CTRB_RAT	P07338 rattus norv	622	328.5	15.9	253	1	TRYG_DROME	P42277 drosophila
550	333.5	16.1	275	2	Q7PNE7	Q7pnf7 anopheles g	623	328.5	15.9	260	1	MCT1_RAT	P09650 rattus norv
551	333.5	16.1	290	1	PR27_HUMAN	Q9bqr3 homo sapien	624	328.5	15.9	261	2	Q8T4P1	Q8t4p1 lepeophthei
552	333.5	16.1	824	2	Q6ICC2	Q6icc2 homo sapien	625	328.5	15.9	275	2	Q86TM8	Q86cm8 homo sapien
553	333	16.1	285	1	FA9_CAYPO	P16295 cavia porce	626	328.5	15.9	276	2	Q86UA5	Q86ua5 homo sapien
554	333	16.1	355	2	Q7PEW0	Q7pew0 anopheles g	627	328.5	15.9	338	1	PLMN_HORSE	P80010 equus cabal
555	333	16.1	360	2	Q7PEV7	Q7pev7 anopheles g	628	328.5	15.9	432	2	Q7QXK4	Q7qxl4 anopheles g
556	333	16.1	391	2	Q9V3Z2	Q9v3z2 drosophila	629	328.5	15.9	524	2	Q7SKH8	Q7sxh8 brachydanio
557	333	16.1	810	1	PLMN_ERIEU	Q29485 erinaceus e	630	328.5	15.9	615	2	Q6GNK4	Q6gnk4 xenopus lae
558	332.5	16.1	247	2	Q35342	Q35342 mesocricetu	631	328.5	15.9	683	2	Q8MRH5	Q8mrh5 drosophila
559	332.5	16.1	254	2	Q87637	Q8t637 aedes aegyp	632	328.5	15.9	786	1	STUB_DROME	Q05319 drosophila
560	332.5	16.1	260	2	Q8T4P6	Q8t4p6 lepeophthei	633	328.5	15.9	787	2	Q9VEY6	Q9vey6 drosophila
561	332.5	16.1	262	2	Q8T4P7	Q8t4p7 lepeophthei	634	328	15.9	226	1	COGS_UCAPU	P00771 uca pugilat
562	332.5	16.1	263	2	Q721D5	Q7z1d5 lepeophthei	635	328	15.9	270	2	Q278Z4	Q278z4 uca pugilat
563	332.5	16.1	264	2	Q7Y8S9	Q7y8s9 lepeophthei	636	328	15.9	328	2	Q6BEA2	Q6bea2 rattus norv
564	332.5	16.1	307	2	Q7TMD0	Q7tmd0 mus musculus	637	328	15.9	452	1	FA5_CANFA	P19540 canis faml
565	332.5	16.1	490	1	TMS2_MOUSE	Q9j1q8 mus musculus	638	328	15.9	699	1	CRAR_HUMAN	P48740 h complemen
566	332.5	16.1	638	1	KAL_RAT	P14272 rattus norv	639	328	15.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
567	332.5	16.1	810	1	PLMN_WACMU	P12545 macaca mula	640	327.5	15.9	247	1	MCT1_MACFA	P56435 macaca fasc
568	332	16.1	247	2	Q70T74	Q70t74 equus cabal	641	327.5	15.9	263	2	Q9TV16	Q9ty16 penaeus van
569	332	16.1	251	2	Q7Q9W2	Q7q9w2 anopheles g	642	327.5	15.9	266	2	Q27761	Q27761 penaeus van
570	332	16.1	258	2	Q97399	Q97399 phaeton coc	643	327.5	15.9	269	2	Q96QV5	Q96qv5 homo sapien
571	332	16.1	266	2	Q92077	Q92077 gadus morhu	644	327.5	15.9	269	2	Q6ISM5	Q6ism5 homo sapien
572	332	16.1	277	2	Q8SQ44	Q8sq44 sus scrofa	645	327.5	15.9	269	2	Q6GN82	Q6gn82 xenopus lae
573	332	16.1	355	2	Q9NFM1	Q9nf1 anopheles g	646	327.5	15.9	277	2	Q80WM7	Q80wm7 mus musculus
574	332	16.1	364	2	Q917V4	Q9i7v4 drosophila	647	327	15.8	259	1	DEF3_DERFA	P49275 dermatophag
575	331.5	16.0	250	2	Q8T4P4	Q8t4p4 lepeophthei	648	327	15.8	263	2	Q7SY84	Q7sy84 xenopus lae
576	331.5	16.0	254	2	Q8MMK9	Q8mmk9 aedes aegyp	649	327	15.8	466	2	Q6SA95	Q6sa95 felis silve
577	331.5	16.0	256	1	TRYA_DROME	P04814 drosophila	650	327	15.8	600	2	Q7ZTR2	Q7ztr2 xenopus lae
578	331.5	16.0	260	2	Q8T4P5	Q8t4p5 lepeophthei	651	326.5	15.8	248	1	GRAC_MOUSE	P08882 mus musculus
579	331.5	16.0	263	2	Q9PWQ6	Q9pwq6 gadus morhu	652	326.5	15.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
580	331.5	16.0	264	2	Q6GPY5	Q6gpy5 xenopus lae	653	326.5	15.8	266	1	EL1_PIG	Q6gnf7 xenopus lae
581	331.5	16.0	275	1	TRY3_ANOGA	P35037 anopheles g	654	326.5	15.8	266	2	Q91X79	Q91x79 mus musculus
582	331.5	16.0	679	2	Q96PQ8	Q96pq8 homo sapien	655	326.5	15.8	369	2	Q7QK11	Q7qk11 anopheles g
583	331	16.0	622	1	THRB_HUMAN	P00734 homo sapien	656	326.5	15.8	490	2	Q7TNO4	Q7tn04 mus musculus
584	331	16.0	722	2	Q8AW90	Q8aw90 lampetra ja	657	326	15.8	248	1	GR21_RAT	Q06605 rattus norv
585	331	16.0	722	2	Q9P8Z5	Q9p8z5 lampetra ja	658	326	15.8	268	2	Q46151	Q46151 pacifastacu
586	331	16.0	722	2	Q9P8Z5	Q9p8z5 lampetra ja	659	326	15.8	271	1	CTR2_PENVA	Q36178 penaeus van
587	330.5	16.0	237	2	Q29464	Q29464 bos taurus	660	326	15.8	329	2	Q7PEV8	Q7pev8 anopheles g
588	330.5	16.0	247	1	MCT1_HUMAN	P23946 homo sapien	661	325.5	15.8	259	2	Q8IRE0	Q8ire0 drosophila
589	330.5	16.0	256	1	TRYA_DROER	P54624 drosophila	662	325.5	15.8	261	1	DER3_DERPT	P39675 dermatophag
590	330.5	16.0	269	2	Q61SP9	Q6isp9 homo sapien	663	325.5	15.8	492	1	FA10_BOVIN	P00743 bos taurus
591	330.5	16.0	560	2	Q14520	Q14520 homo sapien	664	325.5	15.8	891	2	Q9VV38	Q9vv38 drosophila
592	330.5	16.0	638	2	Q8R0P5	Q8r0p5 mus musculus	665	324.5	15.7	146	2	Q9DDE1	Q9dde1 brachydanio
593	330	16.0	236	2	Q7SIG3	Q7sig3 salmo salar	666	324.5	15.7	228	2	Q7Q153	Q7q153 anopheles g
594	330	16.0	253	2	Q9V5Y3	Q9v5y3 drosophila	667	324.5	15.7	258	2	Q7YRZ7	Q7yrz7 bos taurus
595	330	16.0	266	2	Q81916	Q8i916 blomia trop	668	324.5	15.7	263	2	Q7PUB9	Q7pub9 anopheles g
596	330	16.0	282	1	FA9_RAT	P16296 rattus norv	669	324.5	15.7	275	1	TRYA_HUMAN	P15157 homo sapien
597	330	16.0	364	2	Q9N8S9	Q9nas9 anopheles g	670	324.5	15.7	312	2	Q7M755	Q7m755 mus musculus
598	330	16.0	365	2	Q7Q1D1	Q7q1d1 anopheles g	671	324.5	15.7	466	1	FA7_HUMAN	P08709 homo sapien
599	330	16.0	4548	1	AP0A_HUMAN	P08519 homo sapien	672	324	15.7	253	1	TRYB_DROME	P35004 drosophila
600	329.5	15.9	248	2	Q8T4P2	Q8t4p2 lepeophthei	673	324	15.7	257	1	GRAM_HUMAN	P51124 homo sapien

674	324	15.7	266	2	Q9W7Q0	Q9w7q0 paralichthy
675	324	15.7	459	1	FA9_MOUSE	P16294 mus musculus
676	324	15.7	1019	1	ENTK_HUMAN	P98073 homo sapien
677	323.5	15.7	299	2	Q9V8S7	Q9v8s7 drosophila
678	323.5	15.7	328	2	Q8BJR6	Q8bjr6 mus musculus
679	323.5	15.7	490	2	Q6P7D7	Q6p7d7 rattus norv
680	323.5	15.7	608	2	Q9PTW7	Q9ptw7 struthio ca
681	323.5	15.7	875	1	NETR_HUMAN	P56730 homo sapien
682	323	15.6	281	2	Q46137	Q46137 lumbricus r
683	323	15.6	296	2	Q9VDV1	Q9vdv1 drosophila
684	323	15.6	540	2	Q800Y7	Q800y7 meleagris g
685	323	15.6	653	1	HGFA_MOUSE	Q9r0s4 mus musculus
686	323	15.6	653	1	Q9VCS4	Q9vcs4 mus musculus
687	322.5	15.6	249	2	Q9QX62	Q9qx62 lepeophthei
688	322.5	15.6	258	2	Q9W5U8	Q9w5u8 drosophila
689	322.5	15.6	343	1	PLMN_SHEEP	P81286 ovis aries
690	322.5	15.6	372	2	Q9Y1K6	Q9y1k6 anopheles g
691	322.5	15.6	581	2	Q9XZM7	Q9xzm7 strongyloce
692	322	15.6	210	2	Q8AD88	Q8ads2 homo sapien
693	322	15.6	265	2	Q81848	O18488 penaeus van
694	322	15.6	320	2	Q8CIR7	Q8cir7 rattus norv
695	321.5	15.6	263	2	Q62562	Q62562 penaeus van
696	321.5	15.6	265	2	Q7SYX8	Q7syx8 xenopus lae
697	321.5	15.6	266	2	Q9D936	Q9d936 mus musculus
698	321.5	15.6	436	1	ACRO_MOUSE	P23578 mus musculus
699	321	15.5	226	1	DNLI_BOVIN	P80219 bos taurus
700	321	15.5	230	2	Q6IE13	Q6iel3 rattus norv
701	321	15.5	247	1	MCT2_MERUN	P50341 meriones un
702	321	15.5	248	1	NKP1_RAT	P18291 rattus norv
703	321	15.5	269	1	TRYM_CANFA	P19236 canis famli
704	321	15.5	411	2	Q9VUF0	Q9vuf0 drosophila
705	321	15.5	655	1	HGFA_HUMAN	Q04756 homo sapien
706	320.5	15.5	247	1	GRAB_MOUSE	P04187 mus musculus
707	320	15.5	249	2	Q9W7Q1	Q9w7q1 paralichthy
708	320	15.5	430	2	Q6RUQ3	Q6ruj3 trichinella
709	320	15.5	431	1	ACRO_RABIT	P48038 oryctolagus
710	320	15.5	465	1	Q9BJL7	Q9bjl7 trichinella
711	320	15.5	489	2	Q7Q432	Q7q432 anopheles g
712	320	15.5	536	2	Q7PX72	Q7px72 anopheles g
713	319.5	15.5	265	2	Q6NGG0	Q6ngg0 xenopus lae
714	319.5	15.5	374	2	Q9VUG2	Q9vug2 drosophila
715	319.5	15.5	453	2	Q812A6	Q812a6 mus musculus
716	319.5	15.5	559	2	Q6P7U0	Q6p7u0 mus musculus
717	319.5	15.5	607	2	Q6DFJ5	Q6dfj5 xenopus lae
718	319	15.4	241	2	Q7PFF7	Q7pff7 anopheles g
719	319	15.4	264	2	Q8IPY7	Q8ipy7 drosophila
720	319	15.4	461	2	Q95ND6	Q95nd6 pan troglod
721	319	15.4	1034	1	ENTK_PIG	P98074 sus scrofa
722	318.5	15.4	418	2	Q6IE15	Q6iel5 rattus norv
723	318.5	15.4	453	1	TMS3_MOUSE	Q8kit0 mus musculus
724	318.5	15.4	490	2	Q920K3	Q920k3 rattus norv
725	318	15.4	232	2	Q94508	Q94508 dermatophag
726	318	15.4	261	2	Q962G7	Q962g7 culex pipie
727	318	15.4	263	2	O02570	O02570 culex quinq
728	318	15.4	271	1	FA9_PIG	P16293 sus scrofa
729	318	15.4	274	1	FA9_SHEEP	P16291 ovis aries
730	318	15.4	295	2	Q69E28	Q69ez8 homo sapien
731	318	15.4	618	1	THRB_MOUSE	P19221 mus musculus
732	317.5	15.4	245	1	CTRB_BOVIN	P00767 bos taurus
733	317.5	15.4	246	1	GRAH_HUMAN	P20718 homo sapien
734	317.5	15.4	248	2	Q9AXY9	Q9axy9 rhizoperttha
735	317.5	15.4	256	1	TYPE_DROER	P54627 drosophila
736	317.5	15.4	559	1	TPA_MOUSE	P11214 mus musculus
737	317.5	15.4	604	1	CPAI_RAT	Q9wtw3 rattus norv
738	317.5	15.4	617	2	Q8J1S1	Q8jis1 triakis scy
739	317	15.3	248	2	Q63636	Q63636 rattus norv
740	317	15.3	624	2	Q95ME7	Q95me7 oryctolagus
741	316.5	15.3	246	1	MCT1_MOUSE	P11034 mus musculus
742	316.5	15.3	321	2	Q80Y38	Q8oy38 mus musculus
743	316.5	15.3	326	2	Q9D9M0	Q9d9m0 mus musculus
744	316.5	15.3	433	1	UROK_BOVIN	Q05589 bos taurus
745	316.5	15.3	441	2	Q81917	Q81917 manduca sex
746	316.5	15.3	607	2	Q91001	Q91001 gallus gall

747	316	15.3	246	2	Q9XY46	Q9xy46 ctenocephal
748	316	15.3	259	2	Q69E27	Q69ez7 homo sapien
749	316	15.3	269	2	Q9CQ52	Q9cq52 m mus muscu
750	316	15.3	289	2	Q9D7T9	Q9d7t9 mus musculus
751	316	15.3	336	2	Q8CIR9	Q8cir9 mus musculus
752	316	15.3	482	1	FA10_RAT	Q83207 rattus norv
753	316	15.3	697	2	Q8CG43	Q8cg43 rattus norv
754	316	15.3	733	2	Q8CD27	Q8cd27 mus musculus
755	316	15.3	733	2	Q8CD27	Q8cd27 mus musculus
756	315.5	15.3	254	1	TRY3_AEDAE	P29786 aedes aegyp
757	315.5	15.3	264	2	Q62561	Q62561 penaeus van
758	315.5	15.3	265	2	Q66KR6	Q66kr6 anopheles lae
759	315.5	15.3	266	1	EL1_RAT	P00773 rattus norv
760	315.5	15.3	314	2	Q9VR15	Q9vr15 drosophila
761	315.5	15.3	374	2	Q7QCS5	Q7qcs5 anopheles g
762	315.5	15.3	392	1	EAST_DROME	P13582 drosophila
763	315	15.2	248	2	Q63224	Q63224 rattus norv
764	315	15.2	275	1	TRY4_ANOGA	P35038 anopheles g
765	315	15.2	280	2	Q7Q494	Q7q494 anopheles g
766	315	15.2	280	2	Q66NX6	Q66nx6 canis famli
767	315	15.2	323	2	Q96QG4	Q96qg4 homo sapien
768	315	15.2	617	1	THRB_RAT	P18292 rattus norv
769	315	15.2	686	1	MAS2_HUMAN	O00187 homo sapien
770	314.5	15.2	256	1	TRYE_DROME	P35005 drosophila
771	314.5	15.2	261	2	Q6IDF4	Q6idf4 drosophila
772	314.5	15.2	609	2	Q7M761	Q7m761 mus musculus
773	314.5	15.2	680	2	Q868H7	Q868h7 branchiosto
774	314	15.2	280	2	Q66NX5	Q66nx5 canis famli
775	314	15.2	422	2	Q8WVC1	Q8wvc1 homo sapien
776	314	15.2	629	2	Q6AZS7	Q6azs7 xenopus lae
777	314	15.2	645	2	Q7PWE4	Q7pwe4 anopheles g
778	314	15.2	855	1	ST14_HUMAN	Q9y5y6 homo sapien
779	313.5	15.2	261	1	EUM3_EURMA	Q97370 euroglyphus
780	313.5	15.2	425	2	Q804X7	Q804x7 gallus gall
781	313	15.2	234	2	Q9HC80	Q9hc80 homo sapien
782	313	15.2	241	2	Q917L2	Q917l2 drosophila
783	313	15.2	420	2	Q90504	Q90504 eptatretus
784	313	15.2	483	2	Q8TX4	Q8tx4 drosophila
785	313	15.2	483	2	Q9VK10	Q9vk10 drosophila
786	313	15.2	613	2	Q93711	Q93711 xenopus lae
787	313	15.2	855	2	Q93J17	Q93j17 rattus norv
788	312.5	15.1	241	2	Q81YP2	Q81yp2 homo sapien
789	312.5	15.1	271	2	Q8T9B6	Q8t9r6 culex pipie
790	312.5	15.1	274	1	TRY5_ANOGA	P35039 anopheles g
791	312.5	15.1	300	2	Q96EF3	Q96ef3 homo sapien
792	312.5	15.1	390	2	Q9Y157	Q9y157 drosophila
793	312.5	15.1	615	1	FA12_HUMAN	P00748 homo sapien
794	312.5	15.1	680	2	Q868H5	Q868h5 branchiosto
795	312.5	15.1	1234	2	Q7PIQ7	Q7piq7 anopheles g
796	312.5	15.1	1322	2	Q7PNR7	Q7pnr7 anopheles g
797	312.5	15.1	1322	2	Q9NJS5	Q9njs5 anopheles g
798	312	15.1	295	2	Q8CIP7	Q8cip7 rattus norv
799	312	15.1	404	2	Q81862	Q81862 dermacerator
800	312	15.1	597	2	Q35727	Q35727 anopheles g
801	312	15.1	597	2	Q8PER0	Q8per0 mus musculus
802	312	15.1	609	2	Q80YCS	Q80ycs mus musculus
803	311.5	15.1	255	2	Q9Y7A9	Q9y7a9 metarhizium
804	311.5	15.1	255	2	Q25227	Q25227 lucilia cup
805	311.5	15.1	255	2	Q25227	Q25227 lucilia cup
806	311.5	15.1	255	2	Q7TN10	Q7tn10 mus musculus
807	311.5	15.1	293	2	Q23528	Q23528 caenorhabdi
808	311.5	15.1	566	1	TPA_BOVIN	Q28198 bos taurus
809	311.5	15.1	761	1	NETR_MOUSE	O08762 mus musculus
810	311.5	15.1	1322	2	Q9NAT0	Q9nat0 anopheles g
811	311	15.1	249	2	Q6IE11	Q6iel1 rattus norv
812	311	15.1	250	2	Q9V514	Q9v514 drosophila
813	311	15.1	261	1	CATG_MOUSE	P28293 mus musculus
814	311	15.1	421	2	Q60491	Q60491 cavia porce
815	311	15.1	559	1	TPA_RAT	P19637 rattus norv
816	311	15.1	1035	1	ENTK_BOVIN	P98072 bos taurus
817	311	15.1	1042	1	CORI_HUMAN	Q9y5q5 homo sapien
818	310.5	15.0	247	1	MCT2_RAT	P00770 rattus norv
819	310.5	15.0	259	2	Q7PF17	Q7pf17 anopheles g

820	310.5	15.0	371	2	Q8MRV3	Q8mry3 drosophila	893	304.5	14.7	271	2	Q7Q820	Q7q820 anopheles g
821	310.5	15.0	473	2	Q7P6V63	Q7p6v63 anopheles g	894	304.5	14.7	384	2	Q9XY63	Q9xy63 ctenocephal
822	310.5	15.0	1374	2	Q9VSU0	Q9vsu0 drosophila	895	304.5	14.7	492	1	TMS2 HUMAN	O15393 homo sapien
823	310.5	15.0	1449	2	Q8UI12	Q8ui12 drosophila	896	304.5	14.7	492	2	Q96T73	Q96t73 homo sapien
824	310.5	15.0	1450	2	Q8UIQ8	Q8uiq8 drosophila	897	304.5	14.7	685	2	Q92338	Q92338 mus musculus
825	310.5	15.0	1462	2	Q9UII3	Q9uii3 drosophila	898	304	14.7	268	1	CLCR_HUMAN	Q99895 homo sapien
826	310.5	15.0	2382	2	Q9BII19	Q9bii19 drosophila	899	304	14.7	375	2	Q8I7W8	Q8i7w8 dermacerator
827	310.5	15.0	2409	2	Q96G06	Q96g06 drosophila	900	304	14.7	393	2	Q6RX66	Q6rx66 armligeres s
828	310.5	15.0	2786	2	Q9VSU2	Q9vsu2 drosophila	901	304	14.7	400	2	Q9VCJ8	Q9vcj8 drosophila
829	310	15.0	275	1	FA9 RABIT	P16292 oryctolagus	902	304	14.7	423	2	Q8BM10	Q8bm10 mus musculus
830	310	15.0	315	2	Q8I7R3	Q8i7r3 drosophila	903	304	14.7	449	2	Q9VDU8	Q9vdu8 drosophila
831	310	15.0	327	2	Q7Q530	Q7q530 anopheles g	904	304	14.7	543	2	Q9BU99	Q9bu99 homo sapien
832	310	15.0	532	2	Q7P6T73	Q7p6t73 anopheles g	905	304	14.7	562	1	TPA_HUMAN	P00750 homo sapien
833	310	15.0	1111	2	Q80YN4	Q80yn4 rattus norv	906	304	14.7	589	2	Q6PJA5	Q6pia5 homo sapien
834	310	15.0	1379	2	Q9V4N6	Q9v4n6 gallus gall	907	303.5	14.7	240	2	Q7SYQ8	Q7syq8 xenopus lae
835	310	15.0	1397	2	Q7KQ9	Q7kq9 drosophila	908	303.5	14.7	244	1	MCT2_MOUSE	P15119 mus musculus
836	309.5	15.0	246	2	Q9EP90	Q9ep90 mus musculus	909	303.5	14.7	246	1	MCT4_MOUSE	P97592 rattus norv
837	309.5	15.0	265	2	Q9VVT3	Q9vvt3 drosophila	910	303.5	14.7	259	2	Q6JPG5	Q6jpg5 neodiprion
838	309.5	15.0	284	2	Q7Q493	Q7q493 anopheles g	911	303.5	14.7	309	2	Q27083	Q27083 tachyples
839	309.5	15.0	468	2	Q9U0G3	Q9u0g3 pacifastacu	912	303.5	14.7	352	2	Q6UWB4	Q6uwb4 homo sapien
840	309.5	15.0	471	2	Q804X6	Q804x6 gallus gall	913	303.5	14.7	603	1	CFAI_MOUSE	Q61129 mus musculus
841	309.5	15.0	698	2	Q6GPF9	Q6gpf9 xenopus lae	914	303.5	14.7	761	2	Q99JC8	Q99jc8 rattus norv
842	309.5	15.0	868	2	Q9Y1V3	Q9y1v3 polyandroca	915	303	14.7	255	1	CATG_HUMAN	P08311 homo sapien
843	309	15.0	285	2	Q8CG42	Q8cg42 rattus norv	916	302.5	14.6	119	2	Q9NR68	Q9nr68 homo sapien
844	308.5	14.9	240	2	Q6IE06	Q6ie06 rattus norv	917	302.5	14.6	223	2	Q9VBV4	Q9vby4 drosophila
845	308.5	14.9	260	1	MCT9_MOUSE	O35164 mus musculus	918	302.5	14.6	273	1	TRY6_ANOGA	P35040 anopheles g
846	308.5	14.9	260	2	Q6VPJ6	Q6vpj6 sarcoteles s	919	302.5	14.6	394	2	P91817	P91817 tachyples
847	308.5	14.9	272	2	Q9XYV6	Q9xyv6 rhizopertha	920	302.5	14.6	394	2	P91817	P91817 tachyples
848	308.5	14.9	317	1	BS4_HUMAN	Q9gzv4 homo sapien	921	302	14.6	1113	1	CORI_MOUSE	Q92319 mus musculus
849	308.5	14.9	334	2	Q6UXE0	Q6uxe0 homo sapien	922	302	14.6	247	2	Q6T376	Q6t376 eisenia foe
850	308.5	14.9	1004	2	P79953	P79953 xenopus lae	923	302	14.6	255	1	TRY4_LUCCU	P35044 lucilia cup
851	308	14.9	125	2	Q804G0	Q804g0 sphoeroides	924	302	14.6	268	2	Q9W7Q2	Q9w7q2 paralichthy
852	308	14.9	301	2	Q8I9P4	Q8i9p4 aurelia aur	925	302	14.6	269	2	Q7PW17	Q7pw17 anopheles g
853	308	14.9	321	2	Q6WZL2	Q6wzl2 homo sapien	926	302	14.6	270	2	Q8WR11	Q8wr11 paralithode
854	308	14.9	335	2	Q86PB3	Q86pb3 drosophila	927	302	14.6	281	2	Q76898	Q76898 drosophila
855	308	14.9	377	2	Q9VB68	Q9vb68 drosophila	928	302	14.6	284	2	Q8IRX5	Q8irx5 drosophila
856	308	14.9	408	2	Q8MR95	Q8mr95 drosophila	929	302	14.6	291	2	Q8IQ89	Q8iq89 drosophila
857	308	14.9	417	1	HEPS_HUMAN	P05981 homo sapien	930	302	14.6	394	1	URTQ_DESRO	P49150 desmodus ro
858	307.5	14.9	255	2	Q7PFI6	Q7pfi6 anopheles g	931	302	14.6	424	2	Q9VA88	Q9va88 drosophila
859	307.5	14.9	676	2	Q6DUJ6	Q6duj6 cyprinus ca	932	301.5	14.6	477	1	URT2_DESRO	P15638 desmodus ro
860	307	14.9	135	2	Q6Z284	Q6z284 mus musculus	933	301.5	14.6	241	2	Q8BW11	Q8bw11 m mus muscu
861	307	14.9	250	2	Q6Z284	Q6z284 mus musculus	934	301.5	14.6	257	2	O19023	O19023 macaca mulla
862	307	14.9	862	1	CTR1_ANOGA	Q17036 anopheles g	935	301.5	14.6	273	2	Q7JYN3	Q7jyn3 drosophila
863	307	14.9	318	2	Q7Q9W4	Q7q9w4 anopheles g	936	301.5	14.6	433	2	Q8MHY7	Q8mhy7 oryctolagus
864	307	14.9	726	2	Q7QB84	Q7qbp4 anopheles g	937	301.5	14.6	433	2	Q8MIL0	Q8mil0 oryctolagus
865	307	14.9	728	2	Q96RS4	Q96rs4 homo sapien	938	301.5	14.6	505	2	Q7QCV2	Q7qcv2 anopheles g
866	306.5	14.8	308	2	Q9W454	Q9w454 drosophila	939	301	14.6	698	2	Q9PU71	Q9pu71 xenopus lae
867	306.5	14.8	362	2	Q9W453	Q9w453 drosophila	940	301	14.6	255	2	O34289	O34289 salvelinus
868	306.5	14.8	365	2	Q7QGL1	Q7qgl1 anopheles g	941	301	14.6	268	2	Q7F030	Q7f030 anopheles g
869	306.5	14.8	375	1	PCE TACTR	P21902 tachyples	942	301	14.6	279	2	Q7PX39	Q7px39 anopheles g
870	306.5	14.8	418	2	Q8SZK2	Q8szk2 drosophila	943	301	14.6	279	2	Q7TNX3	Q7tnx3 mus musculus
871	306.5	14.8	685	2	Q91WP0	Q91wp0 mus musculus	944	301	14.6	283	2	Q9SV22	Q9sv22 lumbricus b
872	306	14.8	162	2	Q6UBM2	Q6ubm2 homo sapien	945	301	14.6	417	2	Q8VHK8	Q8vbk8 mus musculus
873	306	14.8	247	2	Q8NID2	Q8nid2 homo sapien	946	301	14.6	417	2	Q8VDV1	Q8vdl1 mus musculus
874	306	14.8	266	2	Q6AZC0	Q6azc0 brachydanio	947	301	14.6	431	1	URTB_DESRO	P98121 desmodus ro
875	306	14.8	433	2	Q9QWF2	Q9qwf2 rattus sp.	948	300.5	14.5	442	1	URTK_PIG	P04185 sus scrofa
876	305.5	14.8	228	2	Q9XY49	Q9xy49 ctenocephal	949	300.5	14.5	239	2	Q7T2H1	Q7t2h1 xenopus lae
877	305.5	14.8	246	1	MCT2_SHEEP	P79204 ovis aries	950	300.5	14.5	276	2	P91894	P91894 arenicola m
878	305.5	14.8	246	2	Q91VB1	Q91vb1 mus musculus	951	300.5	14.5	278	2	Q68FN6	Q68fn6 brachydanio
879	305.5	14.8	256	1	HYPA_HYPLI	P35587 hypoderma l	952	300.5	14.5	314	2	Q8RUT2	Q8rut2 mus musculus
880	305.5	14.8	274	2	Q6GNF0	Q6gnf0 xenopus lae	953	300.5	14.5	318	2	Q8OUR4	Q8our4 mus musculus
881	305.5	14.8	278	2	Q7Q492	Q7q492 anopheles g	954	300.5	14.5	369	2	Q6AXZ6	Q6axz6 rattus norv
882	305.5	14.8	383	2	Q7Q102	Q7q102 manduca sex	955	300.5	14.5	386	2	Q8I924	Q8i924 bombyx mori
883	305.5	14.8	418	2	Q9VA87	Q9va87 drosophila	956	300	14.5	562	2	Q8SQ23	Q8sq23 sus scrofa
884	305.5	14.8	435	1	SNAK DROME	P05049 drosophila	957	300	14.5	245	1	GILX_HELHO	P43685 heloderma h
885	305.5	14.8	441	2	Q804X2	Q804x2 fugu rubrip	958	300	14.5	417	2	Q8VHJ4	Q8vhj4 rattus norv
886	305	14.8	247	1	GRAB_HUMAN	P10144 h granzyme	959	299.5	14.5	433	1	UROK_MOUSE	P08869 mus musculus
887	305	14.8	281	2	Q67BC3	Q67bc3 homo sapien	960	299.5	14.5	241	2	Q63637	Q63637 rattus norv
888	305	14.8	307	2	Q64ID2	Q64id2 anthonomus	961	299.5	14.5	246	1	MCTX_MOUSE	Q00356 mus musculus
889	305	14.8	391	2	Q7PXJ5	Q7pxj5 anopheles g	962	299.5	14.5	254	2	Q6DBS8	Q6db88 brachydanio
890	305	14.8	395	2	Q9BZW1	Q9bzw1 homo sapien	963	299.5	14.5	258	1	CTR2_ANOGA	Q17025 anopheles g
891	305	14.8	733	2	Q9VTX9	Q9vtx9 drosophila	964	299.5	14.5	272	2	Q7Q9W5	Q7q9w5 anopheles g
892	304.5	14.7	258	2	Q9XY53	Q9xy53 ctenocephal	965	299.5	14.5	282	2	Q7PT16	Q7pt16 anopheles g
										325	2	O15944	O15944 sarcophaga

966	299.5	14.5	372	2	Q9W2C8	Q9w2c8 drosophila	1039	293	14.2	246	2	Q9R2C8	Q9r2c8 rattus norv
967	299.5	14.5	615	2	Q8IZZ5	Q8izz5 homo sapien	1040	293	14.2	247	1	MCT3 RAT	P50339 rattus norv
968	299.5	14.5	974	2	Q9OWD8	Q9owd8 bufo japoni	1041	293	14.2	265	1	SER1_DROME	P17205 drosophila
969	299.5	14.5	1069	1	ENTK_MOUSE	P97435 mus musculu	1042	293	14.2	268	2	Q16900	Q16900 aedes aegyp
970	299	14.5	256	2	Q6VIQ1	Q6viq1 verticilliu	1043	293	14.2	268	2	Q8NUR8	Q8n0r8 aedes aegyp
971	299	14.5	421	1	ACRO HUMAN	P10323 homo sapien	1044	293	14.2	277	2	Q9VFN8	Q9vfn8 drosophila
972	299	14.5	519	2	Q8T3A3	Q8t3a3 ciona intes	1045	293	14.2	278	2	Q8MQQ2	Q8mq02 drosophila
973	298.5	14.4	235	2	Q91004	Q91004 gecko gecko	1046	293	14.2	301	2	Q7Q6U2	Q7q6u2 anopheles g
974	298.5	14.4	248	2	Q9VQ98	Q9vq98 drosophila	1047	293	14.2	427	2	Q6Y2X4	Q6y2x4 manduca sex
975	298.5	14.4	249	1	MCT1_CANFA	P21842 canis famil	1048	293	14.2	433	1	UROK_PAPCY	P16227 papio cynoc
976	298.5	14.4	350	2	Q7QKY0	Q7qky0 anopheles g	1049	293	14.2	777	2	Q8CAN9	Q8can9 mus musculu
977	298.5	14.4	407	1	FAT BOVIN	P22457 bos taurus	1050	293	14.2	855	1	STI4_MOUSE	P56677 mus musculu
978	298.5	14.4	433	2	Q8T3A2	Q8t3a2 ciona intes	1051	292.5	14.2	235	2	Q90387	Q90387 cynops pyrr
979	298	14.4	235	2	Q28731	Q28731 oryctolagus	1052	292.5	14.2	236	2	Q9Z1H1	Q9z1h1 mus musculu
980	298	14.4	255	2	Q18435	Q18435 helicoverpa	1053	292.5	14.2	317	2	Q8K4D1	Q8k4d1 mus musculu
981	298	14.4	268	2	Q8T4T4	Q8t4t4 aedes aegyp	1054	292.5	14.2	390	2	Q8MP08	Q8mp08 bombyx mori
982	298	14.4	348	2	Q86WS5	Q86ws5 homo sapien	1055	292.5	14.2	469	2	Q8GMD9	Q8gmd9 ornithorhyn
983	298	14.4	421	2	Q86ICK2	Q86ick2 homo sapien	1056	292	14.1	257	2	Q8T639	Q8t639 aedes aegyp
984	297.5	14.4	254	2	Q76520	Q76520 stomoxys ca	1057	292	14.1	268	1	CLCR RAT	P55091 rattus norv
985	297.5	14.4	256	2	Q6WJY6	Q6wjy6 bdellovibri	1058	292	14.1	270	2	Q8T4A8	Q8t4a8 drosophila
986	297.5	14.4	269	2	Q8NZF9	Q8azf9 xenopus lae	1059	292	14.1	276	2	Q97398	Q97398 phaedon coc
987	297.5	14.4	277	2	Q8IQ10	Q8iq10 drosophila	1060	292	14.1	332	2	Q8SYS8	Q8sys8 drosophila
988	297.5	14.4	293	2	Q7Q8F9	Q7q8f9 anopheles g	1061	291.5	14.1	216	1	CTR2_VESOR	P00768 vespa orien
989	297.5	14.4	408	2	Q9VM19	Q9vm19 drosophila	1062	291.5	14.1	238	2	Q2Z1D3	Q2z1d3 rattus norv
990	297.5	14.4	472	2	Q7Q182	Q7q182 anopheles g	1063	291.5	14.1	255	2	Q9NBC9	Q9nbc9 glossina mo
991	297.5	14.4	486	2	Q7PX74	Q7px74 anopheles g	1064	291.5	14.1	264	2	Q7Q290	Q7q290 anopheles g
992	297.5	14.4	616	2	Q8Y507	Q8y507 sus scrofa	1065	291.5	14.1	270	2	Q7Q5A6	Q7q5a6 anopheles g
993	297	14.4	237	1	TRYP_ASTFL	P00765 astacus flu	1066	291.5	14.1	678	2	Q9JJS8	Q9jjs8 rattus norv
994	297	14.4	247	1	MCT5_MOUSE	P21844 mus musculu	1067	291	14.1	239	2	Q6LCU4	Q6lcu4 lumbricus r
995	297	14.4	256	2	Q9XY51	Q9xy51 ctenocephal	1068	291	14.1	271	2	Q54213	Q54213 streptomyce
996	297	14.4	268	2	Q9BIG0	Q9big0 aedes aegyp	1069	291	14.1	410	2	Q7QJ44	Q7qj44 anopheles g
997	297	14.4	454	1	TMS3_HUMAN	P57727 homo sapien	1070	291	14.1	415	1	ACRO_PIG	P08001 sus scrofa
998	297	14.4	477	1	URT1_DESRO	P98119 desmodus ro	1071	291	14.1	435	2	Q29015	Q29015 sus sp. pre
999	296.5	14.4	248	1	GRAP_MOUSE	P08883 mus musculu	1072	291	14.1	436	1	HEPS_MOUSE	Q35453 mus musculu
1000	296.5	14.4	270	1	EL3B_HUMAN	P08861 homo sapien	1073	291	14.1	730	2	Q5Q1Q8	O6qlq8 gallus gall
1001	296.5	14.4	272	2	Q9V5X6	Q9v5x6 drosophila	1074	290.5	14.0	483	2	Q7PKJ7	Q7pkj7 anopheles g
1002	296.5	14.4	279	2	Q9QZ74	Q9qz74 rattus norv	1075	290	14.0	149	2	Q6DTY8	Q6dty8 hypophthalm
1003	296.5	14.4	283	2	Q25394	Q25394 lumbricus r	1076	290	14.0	256	1	HYPB_HYPLI	P35588 hypoderma l
1004	296.5	14.4	283	2	Q8ITU7	Q8itu7 lumbricus r	1077	290	14.0	257	2	Q27440	Q27440 aedes aegyp
1005	296.5	14.4	581	2	Q96015	Q96015 drosophila	1078	290	14.0	390	2	Q61G82	Q61g82 hyphantria
1006	296.5	14.4	1047	2	Q9VZH2	Q9vzh2 drosophila	1079	290	14.0	472	2	Q9BLI7	Q9bli7 drosophila
1007	296	14.3	265	2	Q74696	Q74696 phaenocphaer	1080	289.5	14.0	246	2	P13366	P13366 mus musculu
1008	296	14.3	553	2	Q6P719	Q6p719 xenopus lae	1081	289.5	14.0	248	1	GRAG_MOUSE	Q6r560 ostrinia nu
1009	295.5	14.3	239	2	Q9QME0	Q9qme0 ornithorhyn	1082	289.5	14.0	257	2	Q6R560	Q6r560 ostrinia nu
1010	295.5	14.3	239	2	Q91218	Q91218 oncorhynch	1083	289.5	14.0	339	2	Q9QX91	Q9qx91 rattus norv
1011	295.5	14.3	270	2	Q9VRS4	Q9vrs4 drosophila	1084	289.5	14.0	366	2	Q9QX85	Q9qx85 rattus norv
1012	295.5	14.3	453	2	Q6ZWC3	Q6zmc3 homo sapien	1085	289.5	14.0	541	2	Q9QX90	Q9qx90 rattus norv
1013	295	14.3	260	2	Q9V6P6	Q9v6p6 drosophila	1086	289.5	14.0	623	2	Q9JJP3	Q9jjp3 rattus norv
1014	295	14.3	267	2	Q6DGM4	Q6dgm4 brachydanio	1087	289.5	14.0	643	2	Q9QX84	Q9qx84 rattus norv
1015	295	14.3	268	2	Q8T4T5	Q8t4t5 aedes aegyp	1088	289	14.0	260	2	Q7RTY3	Q7rty3 homo sapien
1016	295	14.3	269	2	Q95KW7	Q95kw7 bos taurus	1089	289	14.0	278	2	Q7QHS0	Q7qhs0 anopheles g
1017	295	14.3	358	2	Q45029	Q45029 drosophila	1090	289	14.0	376	1	FA10_TROCA	P81428 trophidichis
1018	295	14.3	681	2	Q7Q554	Q7q554 anopheles g	1091	289	14.0	377	2	P79343	P79343 bos taurus
1019	295	14.3	688	2	Q868H6	Q868h6 branchiost	1092	289	14.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1020	294.5	14.3	244	2	Q816N3	Q816n3 eisenia foe	1093	288.5	14.0	583	1	CFAL_HUMAN	P05156 homo sapien
1021	294.5	14.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp	1094	288.5	14.0	255	2	Q9XY62	Q9xy62 ctenocephal
1022	294.5	14.3	575	2	Q81RB8	Q81rb8 drosophila	1095	288.5	14.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1023	294	14.2	247	2	Q61E57	Q61e57 rattus norv	1096	288.5	14.0	442	2	Q804X1	Q804x1 figu rubrip
1024	294	14.2	259	2	Q9X161	Q9xy61 ctenocephal	1097	288.5	14.0	1047	2	Q24019	Q24019 drosophila
1025	294	14.2	265	2	Q9VHF8	Q9vnh8 drosophila	1098	288	13.9	257	2	Q9NB49	Q9nb49 aedes aegyp
1026	294	14.2	271	2	Q9GTK2	Q9gtk2 cullex quinq	1099	288	13.9	261	2	Q8IRE1	Q8ire1 drosophila
1027	294	14.2	293	2	Q725A4	Q725a4 homo sapien	1100	288	13.9	405	2	Q8MZM7	Q8mzm7 anopheles g
1028	294	14.2	303	2	Q76900	Q76900 drosophila	1101	287.5	13.9	405	2	Q90244	Q90244 acipenser t
1029	293.5	14.2	246	2	Q61E10	Q61e10 rattus norv	1102	287.5	13.9	244	2	Q6T375	Q6t375 eisenia foe
1030	293.5	14.2	256	2	Q9XXY1	Q9xyy1 rhyzopertha	1103	287.5	13.9	244	2	Q7KR00	Q7krd0 drosophila
1031	293.5	14.2	257	2	Q7Z0G1	Q7z0g1 phlebotomus	1104	287.5	13.9	249	2	Q76HL1	Q76hl1 mus musculu
1032	293.5	14.2	302	2	Q8SYZ7	Q8syz7 drosophila	1105	287.5	13.9	382	2	Q76RQ6	Q76rq6 xenopus lae
1033	293.5	14.2	302	2	Q9W586	Q9w586 drosophila	1106	287.5	13.9	603	1	FA12_CAVPO	Q63206
1034	293.5	14.2	317	2	Q8K4I7	Q8k4i7 mus musculu	1107	287.5	13.9	845	2	Q6S9W8	Q6s9w8 homo sapien
1035	293.5	14.2	425	2	Q7P285	Q7p285 anopheles g	1108	287	13.9	204	2	Q61AM0	Q61am0 homo sapien
1036	293.5	14.2	431	1	UROK_HUMAN	P00749 homo sapien	1109	287	13.9	244	2	Q25081	Q25081 hypoderma l
1037	293.5	14.2	475	2	Q804W9	Q804w9 figu rubrip	1110	287	13.9	256	2	Q8T4T3	Q8t4t3 aedes aegyp
1038	293.5	14.2	845	2	Q6GR54	Q6gr54 xenopus lae	1111	287	13.9	268	2		



1112	287	13.9	273	2	Q9VEM5	Q9vem5 drosophila	1185	280	13.6	248	2	Q920S1	Q920s1 mus musculus
1113	287	13.9	291	2	Q8MLC5	Q8mlc5 drosophila	1186	280	13.6	254	1	TRYP_SARBU	P51588 sarcophaga
1114	287	13.9	416	2	Q8MT26	Q8mt26 homo sapien	1187	280	13.6	267	2	Q8SYK8	Q8syk8 drosophila
1115	287	13.9	422	1	DE51_HUMAN	Q9ul52 homo sapien	1188	280	13.6	271	2	Q9V4W5	Q9v4w5 drosophila
1116	287	13.9	423	2	Q6UW31	Q6uw31 homo sapien	1189	280	13.6	282	2	Q25395	Q25395 lumbricus r
1117	287	13.9	481	1	FA10_MOUSE	Q88947 mus musculus	1190	280	13.6	336	2	Q7RTY5	Q7rtty5 homo sapien
1118	287	13.9	581	2	Q81925	Q81925 hypanthria	1191	280	13.6	420	2	Q7Q235	Q7q235 anopheles g
1119	287	13.9	667	2	Q9BUM1	Q9bjm1 trichnella	1192	280	13.6	420	2	Q61E14	Q61e14 rattus norv
1120	286.5	13.9	218	1	CTR2_VESCR	P07669 vespa crabr	1193	279.5	13.5	330	2	Q61E62	Q61e62 rattus norv
1121	286.5	13.9	220	2	Q7QM61	Q7qtm61 anopheles g	1194	279.5	13.5	745	2	Q9PVY3	Q9pvy3 cyprinus ca
1122	286.5	13.9	375	2	Q7PTP7	Q7ptp7 anopheles g	1195	279	13.5	242	2	Q6T374	Q6t374 eisenia foe
1123	286	13.8	235	2	Q6XGZ4	Q6xgz4 homo sapien	1196	279	13.5	267	2	Q9VA67	Q9va67 drosophila
1124	286	13.8	254	1	CTPL_HALRU	P35003 halicoris ru	1197	279	13.5	280	1	TRYZ_DROME	P42280 drosophila
1125	286	13.8	272	2	Q7Q483	Q7q483 anopheles g	1198	279	13.5	280	2	Q9V5X8	Q9v5x8 drosophila
1126	286	13.8	398	2	Q8MKP4	Q8mkp4 drosophila	1199	279	13.5	385	2	Q25101	Q25101 herdmania m
1127	286	13.8	416	2	Q8BZ13	Q8bz13 mus musculus	1200	279	13.5	694	2	Q8R099	Q8r099 mus musculus
1128	286	13.8	416	2	Q8BZ30	Q8bz30 mus musculus	1201	279	13.5	694	2	Q6P6T1	Q6p6t1 rattus norv
1129	286	13.8	443	2	Q8JHC9	Q8jhc9 brachydanio	1202	279	13.5	717	2	Q8AXR1	Q8axr1 xenopus lae
1130	285.5	13.8	175	2	Q6PLJ9	Q6plj9 squilla ora	1203	279	13.5	721	2	Q7ZT69	Q7zt69 lampetra ja
1131	285.5	13.8	248	1	MCTR_RAT	P97594 rattus norv	1204	278.5	13.5	269	2	Q7PWT2	Q7pwt2 anopheles g
1132	285.5	13.8	270	1	ELJ3_HUMAN	P09093 homo sapien	1205	278.5	13.5	326	2	Q7ZZ80	Q7zz80 brachydanio
1133	285.5	13.8	270	2	Q96QL8	Q96ql8 homo sapien	1206	278.5	13.5	432	1	UROK_RAT	P29598 rattus norv
1134	285.5	13.8	270	2	Q91039	Q91039 gadus morhu	1207	278.5	13.5	593	1	FA12_BOVIN	P98140 bos taurus
1135	285.5	13.8	289	2	Q8MR67	Q8mr67 drosophila	1208	278	13.5	239	2	Q9NKC5	Q9nkc5 drosophila
1136	285.5	13.8	290	2	Q9VRT2	Q9vrt2 drosophila	1209	278	13.5	474	2	Q7PZH7	Q7pzh7 anopheles g
1137	285	13.8	424	2	Q6RS58	Q6rs58 ostrinia nu	1210	278	13.5	488	1	FA10_HUMAN	P00742 homo sapien
1138	285	13.8	470	2	Q8T3A1	Q8t3a1 ciona intes	1211	278	13.5	501	2	Q7QCVO	Q7qcvo anopheles g
1139	285	13.8	688	2	Q868H4	Q868h4 brachiosco	1212	277.5	13.4	245	2	Q8BLI8	Q8bli8 lumbricus r
1140	284.5	13.8	172	2	Q6T776	Q6t776 homo sapien	1213	277.5	13.4	266	2	Q24091	Q24091 drosophila
1141	284.5	13.8	245	2	Q6DKQ3	Q6dkq3 eisenia foe	1214	277.5	13.4	271	2	Q76519	Q76519 stomoxys ca
1142	284.5	13.8	253	1	CAC3_BOVIN	P05805 bos taurus	1215	277.5	13.4	272	2	Q82KG0	Q82kg0 streptomyce
1143	284.5	13.8	564	2	Q7RTZ1	Q7rtz1 homo sapien	1216	277.5	13.4	845	2	Q9DGR1	Q9dgr1 xenopus lae
1144	284.5	13.8	686	2	Q6Q1Q9	Q6qlq9 gallus gall	1217	277	13.4	252	2	Q76498	Q76498 diaprepes a
1145	284	13.7	235	2	Q6B4R4	Q6b4r4 bos taurus	1218	277	13.4	254	1	PRN3_MOUSE	Q61096 mus musculus
1146	284	13.7	243	2	O01309	O01309 botryllus s	1219	277	13.4	1629	2	Q9V513	Q9v513 drosophila
1147	284	13.7	247	1	TRYP_SIMVI	P35048 simulium vi	1220	277	13.4	1674	2	Q8SY35	Q8sy35 drosophila
1148	284	13.7	257	2	Q86FL8	Q86fl8 aedes aegy	1221	276.5	13.4	257	2	Q97099	Q97099 anopheles d
1149	283.5	13.7	268	2	Q9XY56	Q9xy56 ctenocephal	1222	276.5	13.4	262	2	Q9V5J2	Q9v5j2 drosophila
1150	283.5	13.7	707	2	Q8QGV0	Q8qgv0 cyprinus ca	1223	276	13.4	257	2	Q818E4	Q818e4 ochlerotatu
1151	283	13.7	258	2	Q9GME1	Q9gme1 ornithorhyn	1224	276	13.4	271	1	S24D_ANOGA	Q17004 anopheles g
1152	283	13.7	273	2	Q9VKA8	Q9vka8 drosophila	1225	276	13.4	300	2	Q7Q6U1	Q7q6u1 anopheles g
1153	283	13.7	320	2	Q7QKL3	Q7qkl3 anopheles g	1226	276	13.4	302	2	Q9VCJ0	Q9vcj0 drosophila
1154	283	13.7	424	2	Q6RS59	Q6rs59 ostrinia nu	1227	276	13.4	376	1	FA10_HOPST	P83370 hoptoccephal
1155	283	13.7	490	1	FA10_RABIT	O19045 oryctolagus	1228	275.5	13.3	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1156	282.5	13.7	245	2	Q7PJQ0	Q7pjq0 anopheles g	1229	275.5	13.3	256	2	Q818E5	Q818e5 ochlerotatu
1157	282.5	13.7	246	2	Q817P0	Q817p0 lumbricus b	1230	275.5	13.3	258	2	Q6NLM5	Q6nlm5 drosophila
1158	282.5	13.7	267	2	Q9VLF5	Q9vlf5 drosophila	1231	275.5	13.3	262	2	Q9V5X9	Q9v5x9 drosophila
1159	282.5	13.7	269	2	Q9V929	Q9v929 drosophila	1232	275.5	13.3	265	2	Q17800	Q17800 caenorhabdi
1160	282.5	13.7	319	2	Q9VR85	Q9vr85 drosophila	1233	275.5	13.3	296	2	Q8TF06	Q8tf06 aedes aegy
1161	282.5	13.7	687	2	Q69DK8	Q69dk8 sus scrofa	1234	275	13.3	237	2	Q17035	Q17035 anopheles g
1162	282	13.6	258	2	Q6JKF3	Q6jkf3 neodiprion	1235	275	13.3	256	2	Q25082	Q25082 hypoderma l
1163	282	13.6	259	2	O18600	O18600 drosophila	1236	275	13.3	260	2	Q9V5J1	Q9v5j1 drosophila
1164	282	13.6	263	2	Q9NB92	Q9nb92 agrotis ips	1237	275	13.3	262	2	Q7Z0G3	Q7z0g3 phlebotomus
1165	282	13.6	416	1	HERS_RAT	Q05511 rattus norv	1238	275	13.3	284	2	Q8AXQ8	Q8axq8 xenopus lae
1166	282	13.6	496	2	Q8CHP7	Q8chp7 cavia porce	1239	275	13.3	317	2	Q7Q619	Q7q619 anopheles g
1167	281.5	13.6	249	2	Q8C1Q8	Q8clq8 mus musculus	1240	275	13.3	467	2	Q6IT09	Q6it09 pseudonaja
1168	281.5	13.6	258	2	Q9BGY6	Q9bgy6 aedes aegy	1241	275	13.3	492	2	Q7Z155	Q7z155 chiromantes
1169	281.5	13.6	329	2	Q7QB72	Q7qb72 anopheles g	1242	275	13.3	688	1	C1S_HUMAN	P09871 homo sapien
1170	281.5	13.6	388	2	Q7Z1F0	Q7z1f0 cotesia rub	1243	275	13.3	707	2	Q7QW31	Q7qw31 oncorhynch
1171	281.5	13.6	430	2	Q7PNQ4	Q7pnq4 anopheles g	1244	275	13.3	717	2	Q8AXR0	Q8axr0 xenopus lae
1172	281	13.6	262	2	Q7Z0G5	Q7z0g5 phlebotomus	1245	274.5	13.3	695	1	CASP_MESAU	P15156 mesocricetu
1173	281	13.6	267	2	Q9VAG6	Q9vag6 drosophila	1246	274	13.3	87	2	Q9CQ78	Q9cq78 m mus muscu
1174	281	13.6	322	2	Q9AGI6	Q9agi6 rhizobium l	1247	274	13.3	254	2	Q8K597	Q8k597 rattus norv
1175	281	13.6	564	2	Q8MKB1	Q8mkb1 oryctolagus	1248	274	13.3	265	2	Q9VHF7	Q9vhf7 drosophila
1176	280.5	13.6	227	2	Q7PHB4	Q7phb4 anopheles g	1249	273	13.2	125	2	Q86VI8	Q86vi8 homo sapien
1177	280.5	13.6	255	2	Q97100	Q97100 anopheles d	1250	273	13.2	247	1	MCTR_MOUSE	P43430 mus musculus
1178	280.5	13.6	270	2	Q7Q0N6	Q7q0n6 anopheles g	1251	273	13.2	257	2	Q818E3	Q818e3 aedes polyn
1179	280.5	13.6	329	2	Q9GL10	Q9gl10 ovis aries	1252	273	13.2	258	1	TRYU_DROER	P54629 drosophila
1180	280.5	13.6	365	2	Q9Y1K7	Q9y1k7 anopheles g	1253	273	13.2	288	2	Q9VEM8	Q9vem8 drosophila
1181	280.5	13.6	366	2	Q7O170	Q7o170 mus musculus	1254	272.5	13.2	262	1	TRYU_DROME	P42279 drosophila
1182	280.5	13.6	439	2	Q8BHM9	Q8bhm9 m mus muscu	1255	272.5	13.2	282	2	Q7PX30	Q7px30 anopheles g
1183	280.5	13.6	494	2	Q9VJD7	Q9vjd7 drosophila	1256	272.5	13.2	287	2	Q9VTV2	Q9vtv2 drosophila
1184	280	13.6	241	2	Q7PQB3	Q7pqb3 anopheles g	1257	272.5	13.2	375	2	Q9NAS8	Q9nas8 anopheles g



1404	258	12.5	267	2	Q9GP27	Q9GP27 drosophila
1405	258	12.5	269	2	Q7Q515	Q7Q515 anopheles g
1406	258	12.5	277	2	Q7PG95	Q7PG95 anopheles g
1407	258	12.5	295	2	O18445	O18445 helicoverpa
1408	258	12.5	300	2	Q7Q6U0	Q7Q6U0 anopheles g
1409	258	12.5	352	2	Q7KVM3	Q7KVM3 drosophila
1410	258	12.5	387	2	Q7RTY4	Q7RTY4 homo sapien
1411	257.5	12.5	196	2	Q6VFC8	Q6VFC8 anopheles g
1412	257.5	12.5	248	2	Q6IE09	Q6IE09 rattus norv
1413	257.5	12.5	254	2	Q01136	Q01136 metarhizium
1414	257.5	12.5	255	2	Q961Y0	Q961Y0 galliera me
1415	257.5	12.5	259	2	Q97097	Q97097 anopheles a
1416	257.5	12.5	274	2	Q6DHC9	Q6DHC9 brachydanio
1417	257.5	12.5	418	2	Q7Q529	Q7Q529 anopheles g
1418	257	12.4	237	2	Q6LBN2	Q6LBN2 homo sapien
1419	257	12.4	256	2	O18441	O18441 helicoverpa
1420	257	12.4	284	2	Q8MLV8	Q8MLV8 drosophila
1421	257	12.4	417	2	Q6JE90	Q6JE90 homo sapien
1422	256.5	12.4	196	2	Q6VFD0	Q6VFD0 anopheles g
1423	256.5	12.4	235	1	TRXD_HUMAN	Q9BZJ3 homo sapien
1424	256.5	12.4	242	2	Q6NTB8	Q6NTB8 homo sapien
1425	256.5	12.4	827	2	Q7PZ88	Q7PZ88 anopheles g
1426	256	12.4	245	2	Q9XY47	Q9XY47 ctenocephal
1427	256	12.4	265	2	Q9XY55	Q9XY55 ctenocephal
1428	256	12.4	267	2	Q9VRU0	Q9VRU0 drosophila
1429	256	12.4	282	2	Q7QCX2	Q7QCX2 anopheles g
1430	256	12.4	403	2	Q9KSG6	Q9KSG6 vibrio chol
1431	256	12.4	421	2	Q6ZMR5	Q6ZMR5 homo sapien
1432	255.5	12.4	220	2	O6XI43	O6XI43 drosophila
1433	255.5	12.4	254	2	O18436	O18436 helicoverpa
1434	255.5	12.4	273	2	Q7Z163	Q7Z163 dermatophag
1435	255.5	12.4	324	2	Q6BD09	Q6BD09 drosophila
1436	255.5	12.4	334	2	Q9VEA0	Q9VEA0 drosophila
1437	255.5	12.4	431	2	Q7PVO5	Q7PVO5 anopheles g
1438	255	12.3	292	2	Q7PVO5	Q7PVO5 anopheles g
1439	255	12.3	367	2	Q7O169	Q7O169 mus musculu
1440	255	12.3	374	2	Q8OYD5	Q8OYD5 mus musculu
1441	255	12.3	405	2	Q7PNQ3	Q7PNQ3 anopheles g
1442	254.5	12.3	254	2	O18434	O18434 helicoverpa
1443	254.5	12.3	278	2	P91893	P91893 arenicola m
1444	254.5	12.3	357	2	Q7Q092	Q7Q092 anopheles g
1445	254.5	12.3	357	2	Q7QXK6	Q7QXK6 anopheles g
1446	254.5	12.3	392	2	Q9VMZ3	Q9VMZ3 drosophila
1447	254.5	12.3	493	2	Q7PVE2	Q7PVE2 anopheles g
1448	254	12.3	305	2	Q8MLR2	Q8MLR2 drosophila
1449	254	12.3	323	2	Q76920	Q76920 drosophila
1450	253.5	12.3	282	2	O641D4	O641D4 anthonomus
1451	253.5	12.3	405	2	Q8MQS8	Q8MQS8 apis mellif
1452	253	12.2	242	2	Q9XY59	Q9XY59 ctenocephal
1453	253	12.2	251	2	Q9VXC9	Q9VXC9 drosophila
1454	253	12.2	253	2	Q6W741	Q6W741 pediculus h
1455	253	12.2	258	2	Q9VS86	Q9VS86 drosophila
1456	253	12.2	272	1	SEB3_DROME	P17207 drosophila
1457	253	12.2	287	2	Q675S0	Q675S0 oikopleura
1458	253	12.2	288	2	Q8C9T5	Q8C9T5 aedes aegypt
1459	252.5	12.2	245	2	Q7Q2Q8	Q7Q2Q8 anopheles g
1460	252.5	12.2	254	2	Q76954	Q76954 lacanobia o
1461	252.5	12.2	291	2	Q6V1Y9	Q6V1Y9 lygus lineo
1462	252.5	12.2	401	2	O6LH17	O6LH17 photobacter
1463	252	12.2	235	2	Q7PRK6	Q7PRK6 anopheles g
1464	252	12.2	295	2	O18450	O18450 helicoverpa
1465	252	12.2	301	2	Q7Q6T0	Q7Q6T0 anopheles g
1466	252	12.2	400	2	Q27081	Q27081 tachypneus
1467	251.5	12.2	186	2	Q6X655	Q6X655 marmota mon
1468	251.5	12.2	266	2	Q8MLC2	Q8MLC2 drosophila
1469	251.5	12.2	267	2	Q9VGB8	Q9VGB8 drosophila
1470	251.5	12.2	276	2	O18443	O18443 helicoverpa
1471	251.5	12.2	291	2	Q8WPE4	Q8WPE4 lygus lineo
1472	251.5	12.2	291	2	Q6V1Y7	Q6V1Y7 lygus lineo
1473	251.5	12.2	291	2	O6V1Z0	Q6V1Z0 lygus lineo
1474	251.5	12.2	298	2	Q8T4N4	Q8T4N4 rhinipicephal
1475	251.5	12.2	305	2	Q7Q6S4	Q7Q6S4 anopheles g
1476	251.5	12.2	318	2	Q7QC37	Q7QC37 anopheles g
1477	251.5	12.2	520	2	Q8ING0	Q8ING0 drosophila
1478	251.5	12.2	556	2	Q8DEK7	Q8DEK7 brachydanio
1479	251	12.1	268	2	Q7Z0G0	Q7Z0G0 phlebotomus
1480	251	12.1	285	2	Q7Q5K4	Q7Q5K4 anopheles g
1481	251	12.1	716	1	HGFL_MOUSE	P26928 mus musculu
1482	250.5	12.1	226	2	O6XHU4	O6XHU4 drosophila
1483	250.5	12.1	240	2	Q7PYJ1	Q7PYJ1 anopheles g
1484	250.5	12.1	268	2	Q9VT24	Q9VT24 drosophila
1485	250	12.1	124	2	Q8C6G5	Q8C6G5 mus musculu
1486	250	12.1	203	2	Q9NB77	Q9NB77 heliothis z
1487	250	12.1	274	2	Q8MUQ0	Q8MUQ0 glossina fu
1488	249.5	12.1	253	2	O18442	O18442 helicoverpa
1489	249.5	12.1	254	2	O18447	O18447 helicoverpa
1490	249.5	12.1	258	2	Q7Q2P0	Q7Q2P0 anopheles g
1491	249.5	12.1	269	2	Q7PWL5	Q7PWL5 anopheles g
1492	249.5	12.1	274	2	Q9VRS7	Q9VRS7 drosophila
1493	249.5	12.1	282	2	O18655	O18655 plodia inte
1494	249.5	12.1	381	2	Q8MQY4	Q8MQY4 drosophila
1495	249.5	12.1	464	2	O6L7Z5	O6L7Z5 haemaphysal
1496	249.5	12.1	520	2	Q8SY93	Q8SY93 drosophila
1497	249	12.1	253	2	Q9NGY5	Q9NGY5 heliothis v
1498	249	12.1	388	2	Q966V2	Q966V2 halocynthia
1499	249	12.1	714	2	Q7PWE5	Q7PWE5 anopheles g
1500	249	12.1	716	2	Q91XG8	Q91XG8 mus musculu

## ALIGNMENTS

## RESULT 1

## KLKC\_HUMAN

ID KLKC\_HUMAN STANDARD; PRT; 248 AA.

AC Q9UKR0; Q9UKR1;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Kallikrein 12 precursor (EC 3.4.21.-) (kallikrein-like protein 5)

DE (KLK-LS) (UNQ669/PRO1303)

GN Homo sapiens (Human)

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]\_TaxID=9606;

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=20118156; PubMed=10652563;

RA Yousef G.M., Luo L.-Y., Diamandis E.P.;

RT "Identification of novel human kallikrein-like genes on chromosome

RT 19q13.3-q13.4."

RL Anticancer Res. 19:2843-2852(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RA Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;

RT "Cloning of new alternatively spliced forms of the kallikrein-like

RT gene 5 (KLK-LS)";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;

RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,

RT "Sequencing and expression analysis of the serine protease gene

RT cluster located in chromosome 19q13 region.";

RL Gene 257:119-130(2000).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Y., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Q., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieda J., Woods K., Xie M.-H., Yansura D.,



Qy	841	ATCCGATGATCATGAGGACAC	864	RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
Db	241	IleArgMetArgAsn	248	RA	-1- SIMILARITY: Belongs to peptidase family S1.	
RESULT 2				CC	EMBL; AK009217; BAB26143.1; -	
Q9CV76		PRELIMINARY;	234 AA.	DR	HSSP; P00760; 1EZX.	
ID	Q9CV76			DR	MEROPS; S01.020; -	
AC	Q9CV76;			DR	MGI; MGI:1916761; K1k12.	
DT	01-JUN-2001	(TrEMBLrel. 17, Created)		DR	GO; GO:0004263; F.chymotrypsin activity; IEA.	
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)		DR	GO; GO:0008233; F.peptidase activity; IEA.	
DE	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		DR	GO; GO:0004295; F.trypsin activity; IEA.	
DE	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:231008B01 product:similar to KALLIKREIN 12 (EC 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (K1K-15) (Fragment).			DR	GO; GO:0006508; P.proteolysis and peptidolysis; IEA.	
DE	3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (K1K-15) (Fragment).			DR	InterPro; IPR001254; Peptidase S1.	
GN	Name=K1k12;			DR	InterPro; IPR001314; Peptidase S1A.	
OS	Mus musculus (Mouse).			DR	InterPro; IPR009003; Pept_Ser_Cys.	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			DR	PFam; PF00089; Trypsin; 1.	
OX	NCB1_TaxID=10090;			DR	PRINTS; PR00722; CHYMOTRYPSIN.	
RN	SEQUENCE FROM N.A.			DR	SMART; SM00020; Tryp_SPC; 1.	
RP	STRAIN=C57BL/6J; TISSUE=Tongue;			DR	PROSITE; PS02440; TRYPSIN_DOM; 1.	
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
RX	Carninci P.; Hayashizaki Y.;			DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
RA	"High-efficiency full-length cDNA cloning.";			KW	Hydrolase; Protease; Serine protease.	
RT	Meth. Enzymol. 303:19-44(1999).			FT	NON_TER	
RL	[2]			SQ	SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;	
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=Tongue;			Alignment Scores:		
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			Pred. No.:	3,098-52	
RA	RIKEN FANTOM Consortium;			Score:	952.50	
RT	"Functional annotation of a full-length mouse cDNA collection.";			Percent Similarity:	82.13%	
RL	Nature 409:685-690(2001).			Best Local Similarity:	70.64%	
RN	[3]			Query Match:	46.10%	
RP	SEQUENCE FROM N.A.			DB:	2	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;			US-10-015-385A-193 (1-1091) x Q9CV76 (1-234)		
RX	The FANTOM Consortium;			Qy	160 CTGAGCCAGCCAGCCACCCAGAGATTTTCAATGGCACTGAGTGTGGCGTAACACAG 219	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			Db	1 LeuSerGlnAlaAspArgGluLysIleTyrHenglyValGluCysGlyValLeuValAsp 20	
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";			Qy	220 CGGTGCAGGTGGGCTGTTGAGGCGCCAGCCCTGCGCTGCGGGGGTGTCTTATTGAC 279	
RL	Nature 420:563-573(2002).			Db	21 ProTrpGlnValGlyLeuPheHisGlyIleTyrLeuArgCysGlyValLeuValAsp 40	
RP	SEQUENCE FROM N.A.			Qy	280 CACAGTGGGTCTCACAGCGGCTCAGTGCAGCGCAGCAGGACTGCGGTGGCGTGGGG 339	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;			Db	41 ArgLysTrpValLeuThrAlaAlaHisCysArg---AspLysTyrValValArgLeuGly 59	
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;			Qy	340 GAACACAGCTCAGCGAGCTCGACTGGAGCCAGCAGATCCCGCAGCGGCTTCTCTGTG 399	
RA	Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,			Db	60 GluHisSerLeuThrLysLeuAspTrpThrGluGlnLeuArgHisThrPheserile 79	
RT	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			Qy	400 ACCATPCCCGGTACTCGGAGCCTCGACGACCCAGCAGCAGCAGCTCCGCTGCTCGG 459	
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";			Db	80 ThrHisProSerTyrGlnGlyAlaTyrGlnAsnHisGluHisAspLeuArgLeuArg 99	
RP	Genome Res. 10:1617-1630(2000).			Qy	460 CTGCGCTCCCGTCCGGTAAACAGCAGCGCTTCAACCCCTGCGCCCTGCCAATGACTGT 519	
RC	SEQUENCE FROM N.A.			Db	100 LeuAsnArgProIleHisLeuThrArgAlaValArgProValAlaLeuProSerSerCys 119	
RX	STRAIN=C57BL/6J; TISSUE=Tongue;			Qy	520 GCACACGCTGGCAGCGAGTGCCACCTCTCAGGCTGGGGCATCACCACACCCAGCGAAC 579	
RA	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;			Db	120 valThrThrGlyAlaMetCysHisValSerGlyTrpGlyThrThrAsnLysProTrpAsp 139	
RT	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,			Qy	580 CCATTTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGTCTCCCATGCCATGCCAT 639	
RL	Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,			Db	140 ProPheProAspArgLeuGlnCysLeuAsnLeuSerThrValSerAsnGluThrCysArg 159	
RP	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,			Qy	640 GGTGTGTATCCCGGAGGAAATCAGAGCAACATGTGTGTGTGCGAGGGGGGTCCCGGGGCG 699	
RC	Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,			Db	160 AlaValPheProGlyArgValThrGluAsnMetLeuCysAlaGlyGlyGluAlaGlyLys 179	
RX	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,					
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,					
RT	Okaz					



KW Signal; Zymogen. 28  
FT SIGNAL 1  
FT PROPEP 29  
FT CHAIN 33  
FT ACT\_SITE 73  
FT ACT\_SITE 120  
FT ACT\_SITE 212  
FT ACT\_SITE 212  
FT DISULFID 39  
FT DISULFID 58  
FT DISULFID 145  
FT DISULFID 152  
FT DISULFID 184  
FT DISULFID 208  
FT DISULFID 223  
FT CARBOHYD 110  
FT VARSPLIC 23  
FT VARSPLIC 23  
SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C3B660 CRC64;

Alignment Scores:  
Pred. No.: 5.8e-32  
Score: 632.50  
Percent Similarity: 58.08%  
Best Local Similarity: 48.08%  
Query Match: 30.61%  
DB: 1  
Length: 260  
Matches: 125  
Conservative: 26  
Mismatches: 96  
Indels: 13  
Gaps: 4

US-10-015-385a-193 (1-1091) x KLK8\_HUMAN (1-260)

QY 88 CCTTTTCCCCAGACTTGGAGTGGACCCACCATGGGGCTCAGCATCTTTTGGCTCTG 147  
DB 6 ProArgAlaAlaLysThrTrp-----MetPheLeuLeuLeu 17  
QY 148 -----TGTGTCTTGGGCTCAGCAGGCGACCCACACCGAAGATTTCATGGCACT 198  
DB 18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyClyHis 37  
QY 199 GAGTGTGGCGPACTCAGCGGTGGAGTGGGGCTGTTTGGGGCAGCCAGCGCTGGCG 258  
DB 38 GluGlyGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGlnGlyGlnLeuLeu 57  
QY 259 TGGGGGGTGTCTTATGCACACAGTGGGTCTCAGCGGCTCAGCGGCTCAGCGGCGG 318  
DB 58 CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysLysPro 77  
QY 319 AGGTACTGGTGGCGCTGGGGAAACACAGCCCTCAGCGCTCAGCGTGGACCGCAGATC 378  
DB 78 LysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAspGlyProGluGlnGlu 97  
QY 379 CGGCACAGCGGCTTCTGTGACCCATCCCGGCTACCTGGGAGCGCTCGACG---AGCCAC 435  
DB 98 IleProValValGlnSerIleProHisProCysTyrAsnSerSerAspValGluAspHis 117  
QY 436 GAGCAGCAGCTCCGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGCA 495  
DB 118 AsnHisAspLeuMetLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLys 137  
QY 496 CCCCTGCCCTGCCAATGACTGTGCAACCGCTGCACCGAGTGCACGCTCTCAGCGCTGG 555  
DB 138 ProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTrp 157  
QY 556 GGCATCACCACCCACCGAACCCATCTCCCGGATCTGCTCCAGTGCCTCAACCTCC 615  
DB 158 GlyThrValThrSerProArgGluAsnPheProAspThrLeuAsnCysAlaGluValLys 177  
QY 616 ATCGTCTCCATGCCACCTGCCATGGTGTATCCCGGAGAGATCAGCAGCAGCATGGTG 675  
DB 178 IlePheProGlnLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal 197  
QY 676 TGTGAGCGGGCTCCCGGCGAGCATGCTGCCAGGTGATCTCTGGGGCCCTCGGTGG 735  
DB 198 CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal 217

QY 736 TGTGGGGAGTCTCTCAAGGTCTGTGCTGTGGGGCTGTGTGGGGCCCTGTGGACAAGAT 795  
DB 218 CysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer---AspProCysGlyArgSer 236  
QY 796 GGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGACTGCGATCGGATCATG 855  
DB 237 AspLysProGlyValThrAsnIleCysArgTyrLeuAspIleLysLysIleIle 256

RESULT 4  
Q8IW69 PRELIMINARY; PRT; 260 AA.  
AC Q8IW69  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Kallikrein 8, isoform 1 preproprotein.  
GN Name=KLK8;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; BC040887; AAH40887.1; -!  
DR HSSP; P00760; 1EXZ.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 260 AA; 28050 MW; EF5934EB96295660 CRC64;

Alignment Scores:  
Pred. No.: 8.99e-32  
Score: 629.50  
Percent Similarity: 58.08%  
Length: 260  
Matches: 125  
Conservative: 26







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QY 280 CACAGTGGTCTCTCACAGCGGCTCACTGCGCCGCGCAGCAGTACTGGGTGGCTCGCTGGGG 339
Db 65 AspArgTrpValLeuThraAlaHisCysLysAspLysTySerValArgLeuGly 84
QY 340 GAACACGCTCAGCAGCTCGACTCGAGCGGCGCAGCAGAGATCCGCGCAGCGGCTTCTCTGG 399
Db 85 AspHisSerLeuGlnIlyArgAspGluProGluGlnGluIleGlnValAlaArgSerIle 104
QY 400 ACCATCCCGGCTACCTCGGAGCTCG---ACGAGCCACGAGCAGCAGCTCCGGCTGGT 456
Db 105 GlnHisProCysPheAsnSerSerAsnProGluAspHisSerHisAspIleMetLeuIle 124
QY 457 CGGCTGGCGCTCGCGTCCGCTACACGACGCGTTCACCCCTCCCTCCCTCGCCCAATGAC 516
Db 125 ArgLeuGlnAsnSerAlaAsnLeuGlyAspLysValLysProIleGluLeuAlaAsnLeu 144
QY 517 TGTGCAACCGCTGGCCAGCGAGTCCAGCTCTCAGGCTGGGCGATCACCAACCCACCGG 576
Db 145 CysProLysValGlnLysCysIleIleSerGlyTrpGlyThrValThrSerProGln 164
QY 577 AACCCATTCCCGGATCTGCTCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGC 636
Db 165 GluAsnPheProAsnThrLeuAsnCysAlaGluValLysIleTyrSerGlnAsnLysCys 184
QY 637 CATGTGTGTATCCCGGAGATCAGCAGCAACATGTTGTGTGTGCGAGCGGCTCCCGGGG 696
Db 185 GluArgAlaTyrProGlyLysIleThrGluGlyMetValCysAlaGlySerSerAsnGly 204
QY 697 CAGGATGCTCCGCGGTGATCTCGGGGCGCCCTGTGTGTGGGGAGTCTTCAAGT 756
Db 205 AlaAspThrCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlyValLeuGlnGly 224
QY 757 CTGGTGTCTGGGGTCTGTGGGGCGCTGTGGACAGATGCGATCCCTGGAGTCTACACC 816
Db 225 IleThrThrTrpGlySer---AspProCysGlyLysProGluLysProGlyValThr 243
QY 817 TATATTCAAGTATGTGACTGATCCGGATCCGGATGATCATG 855
Db 244 LysIleCysArgTyrThrAsnTrpIleLysLysThrMet 256

RESULT 6
NRPN_MOUSE STANDARD; PRT; 260 AA.
AC Q61955;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
GN Name=Klk8; Synonyms=Nrpn, Prss19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neuropilin gene, Prss19 to chromosome
RT 7B4.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Grewen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=9825202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropilin, a plasticity-
RT related serine protease.";
RL J. Biol. Chem. 273:11189-11196 (1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropilin, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224 (1999).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
CC fluorophosphate, leupeptin and (4-aminodiphenyl)methanesulfonyl 1-
CC fluoride.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
CC mouse brain and is localized at highest concentration in pyramidal
CC neurons of the hippocampal CA1-3 subfields.
CC -!- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
CC NOTE=Ref.4.
CC -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
CC NOTE=Ref.4.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC
CC EMBL; D30785; BAA06451.1; -.
CC EMBL; AB032202; BAA92435.1; -.
CC EMBL; BC055895; AAB55895.1; -.
CC PIR; I56559; I56559.
CC PDB; INPM; X-ray; A/B=33-256.
CC MEROPS; S01.244; -.
CC MGD; MGI:892018; Klk8.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
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RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=hippocampus, and prostate;  
RX MEDLINE=20329229; PubMed=10872828; DOI=10.1006/bbrc.2000.2761;  
RA Mitui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;  
RT "A novel isoform of a kallikrein-like protease, TLSP/hike proteasin,  
RL (PRSS20), is expressed in the human brain and prostate.";  
RN Biochem. Biophys. Res. Commun. 272:205-211 (2000).  
[3]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;  
RA Yousef G.M., Scorilas A., Diamandis E.P.;  
RT "Genomic organization, mapping, tissue expression, and hormonal  
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new member  
RT of the human kallikrein gene family.";  
RL Genomics 63:88-96 (2000).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
RA Moss P., Paepfer B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene  
RT cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130 (2000).  
[5]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270 (2003).  
[6]  
RN SEQUENCE FROM N.A.  
RX PubMed=15057824; DOI=10.1038/nature02399;  
RA Grinwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,  
RA Lamerdin J.E., Heilstein A., Goodstein D., Couronne O., Tran-Gyamfi M.,  
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,  
RA Caenepeel S., Carrano A.V., Caiole C., Chan Y.M., Christensen M.,  
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,  
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
RA Slezak T., Solovvey V., Thayer N., Tice H., Tsai M., Ustaszewska A.,  
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535 (2004).  
[7]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves  
CC bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and  
CC weakly cleaves other substrates for kallikrein and trypsin.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9UBX7-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UBX7-2; Sequence=VSP\_005402;  
CC -!- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform  
CC 1 is expressed preferentially in brain; isoform 2 in prostate.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
CC subfamily.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; AB012917; BAA33404.1; ALT\_INIT.  
CC EMBL; AB013730; BAA88713.1; -.  
CC EMBL; AB041036; BAA96797.1; -.  
CC EMBL; AF164623; AAD47815.1; -.  
CC EMBL; AF243527; AAG33364.1; -.  
CC EMBL; AY359014; AAG39373.1; -.  
CC EMBL; AC011473; AAG23257.1; -.  
CC EMBL; BC022068; AAG22068.1; -.  
CC HSSP; P00760; 1EZX.  
CC MEROPS; S01.257; -.  
CC Genew; HGNC:6359; KLK11.  
CC H-InvDB; HIX0015375; -.  
CC MIM; 604434; -.  
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.  
CC InterPro; IPR009003; Pept Ser Cys.  
CC InterPro; IPR001254; Peptidase S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC Pfam; PF00089; Trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC PROSITE; PS02040; TRYPSIN\_DOM; 1.  
CC PROSITE; PS00134; TRYPSIN\_SER; 1.  
CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal; Zymogen.  
FT SIGNAL 1 18 Potential.  
FT PROPEP 19 21 Activation peptide (Potential).  
FT CHAIN 22 250 Kallikrein 11.  
FT ACT\_SITE 62 62 Charge relay system (By similarity).  
FT ACT\_SITE 110 110 Charge relay system (By similarity).  
FT ACT\_SITE 203 203 Charge relay system (By similarity).  
FT DISULFID 28 163 By similarity.  
FT DISULFID 47 63 By similarity.  
FT DISULFID 135 237 By similarity.  
FT DISULFID 142 209 By similarity.  
FT DISULFID 174 188 By similarity.  
FT DISULFID 199 224 By similarity.  
FT CARBOHYD 99 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 165 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 181 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 210 N-linked (GlcNAc... ) (Potential).  
 FT VARSPLIC 1 M -> MORLRRLRDKWSSRGHGLTAAPKPGARSPLOAM  
 FT (in isoform 2).  
 FT /FTid=VSP\_005402.  
 SQ SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;

Alignment Scores:  
 Pred. No.: 4,46e-31 Length: 250  
 Score: 618.50 Matches: 120  
 Percent Similarity: 62.25% Conservative: 35  
 Best Local Similarity: 48.19% Mismatches: 89  
 Query Match: 29.94% Indels: 5  
 DB: 1 Gaps: 4

US-10-015-385A-193 (1-1091) x KLKB\_HUMAN (1-250)

QY	127	CTCAGCATCTTTTTCCTCTCTGTGTCTTCTGGGCTCAGCGAGCCACGCCGAAGATT	186
DB	4	LeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyGluThr---Argile	22
QY	187	TTCATGGCACTAGCTGTGGCGTAATCTACAGCCGTGGCAGGTGGGGCTGTTTGAGGC	246
DB	23	IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGluLys	42
QY	247	ACCAGCTCGCTGCGGGGGTCTCTATTACACAGGTGGGTCTCACAGCGGCTCAC	306
DB	43	ThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThralaHis	62
QY	307	TGCAGCGGACAGAGGTACTTGGGTGGCGCTGGGGAAACACAGCTCAGCCTCGACTCG	366
DB	63	CysLeuLysProArgTyrrileValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGly	82
QY	367	ACGAGCAGATCGGCACAGCGGCTTCTGTGACCATCCGGCTACCTGGGAGCC---	423
DB	83	CysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu	102
QY	424	---TGCAGGACGACGAGCAGACCTCCGGGTGTCTGGGCTGCGGCTGCCCTCCCGCT	480
DB	103	ProAsnLysAspHisArgAsnAspileMetLeuValLysMetAlaSerProValSerile	122
QY	481	ACCAGAGCGTTCAACCCCTGCCCCCTGCCCAATGACTGTGCACCCGTGGCAGCGATGC	540
DB	123	ThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCys	142
QY	541	CAGCTCTCAGGCTGGGGCATCACCAACACACAGAACCCATTCGCCGATCTGCTCCAG	600
DB	143	LeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArg	162
QY	601	TGCCTCAACCTTCCATCGTCTCCCATGCCCACCTGCGCATGTGTATCCCGGAGATC	660
DB	163	CysAlaAsnIlethrilelleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnile	182
QY	661	ACGAGCAACATGTTGTGTCAGGC---GGCGTCCCGGGCAGGATGCTGCCAGGGTGAT	717
DB	183	ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyasp	202
QY	718	TCTGGGGCCCCCTGTGTGTGGGGAGTCTCTTCAAGGTCTGGTCTCTGGGGTCTGTG	777
DB	203	SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyllelleSerTrpGlyGln---	221
QY	778	GGGCCCTGTGGACAAGATGGCATCCTTGAGTCTACACATATATTGCAAGTATGTGGAC	837
DB	222	AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp	241
QY	838	TGGATCCGGATGATCATGAGCAACAC	864
DB	242	TrpIleGlnGluThrMetLysAsnAsn	250

PRELIMINARY; PRT; 255 AA.

RESULT 8  
 Q7JIG6  
 ID O7JIG6

AC	Q7JIG6;	AC
05-JUL-2004	(TrEMBLrel. 27, Created)	
05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	KLK15.	
OS	Saguinus oedipus (Cotton-top tamarin).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.	
OX	NCBI_TaxID=9490;	
RN	[1]	
SEQUENCE FROM N.A.		
RP	MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080;	
RX	Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.;	
CC	-1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ databases.	
RL	EMBL; AF173845; AA545302.1; --	
DR	HSP; P00761; 1AKS	
DR	GO; GO:004263; F:chymotrypsin activity; IEA.	
DR	GO; GO:0008233; F:peptidase activity; IEA.	
DR	GO; GO:0004295; F:trypsin activity; IEA.	
DR	GO; GO:006508; P:proteolysis and peptidolysis; IEA.	
DR	InterPro; IPR001254; Peptidase S1.	
DR	InterPro; IPR001314; Peptidase S1A.	
DR	InterPro; IPR009003; Pept_Ser_Cys.	
DR	Pfam; PF00089; Trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	SMART; SM0020; Tryp_SPC; 1.	
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
KW	Hydrolase; Protease; Serine protease.	
SQ	SEQUENCE 255 AA; 28078 MW; A040914ABC8FEC8D CRC64;	
Alignment Scores:		
Pred. No.:	1.33e-30	Length: 255
Score:	611.00	Matches: 118
Percent Similarity:	62.34%	Conservative: 31
Best Local Similarity:	49.37%	Mismatches: 76
Query Match:	29.57%	Indels: 14
DB:	2	Gaps: 5
US-10-015-385A-193 (1-1091) x Q7JIG6 (1-255)		
QY	181 AAGATTTCATGGCACTGAGTGTGGCGCTAACTCACAGCGTGGCAGGTGGCGTGT 240	
DB	:	:
	20 LysLeuLeuGluGlyGluGlyCysAlaProHisSerGlnProTrpGlnValalaLeuTyr 39	
QY	241 GAGGGACACGAGCTGCCTGGGGGTGCTTATTGACACAGGTGGTCTCTCACGCG 300	
DB		
	40 GluArgGlyArgPheAsnCysGlyAlaSerLeuIleSerProHisTrpValLeuSerAla 59	
QY	301 GCTCAGTCAGCGGCACAGGACTAGTGTGGCTGGCGGGAACACAGCCTCAGCGCTC 360	
DB		
	60 AlaHisCysGlnSerArgPheMetArgValaArgLeuGlyGluHisAsnLeuArgLysArg 79	
QY	361 GACTGGACCGAGCAGATCCGCGACACAGCGGTCTCTGTGACCCATCCCGGTACTCTGGA 420	
DB	:	
	80 AspGlyProGluGlnLeuArgThrAlaSerArgValIleProHisProArgTyr----- 97	
QY	421 GCCTCGACGACCGACAGCAGCAGCTCCGCTGTGGGTGGCGCTCCCGTCCGCGTA 480	
DB		
	98 GluAlaArgSerHisArgHisAspIleMetLeuLeuArgLeuValGlnProAlaArgLeu 117	
QY	481 ACCAGCAGCGTTCAACCCCTCCCTGCCCAATGACTGTGCAACCGCTGCCACCGAGTGC 540	
DB		
	118 ThrProGlnValArgProValValLeuProThrArgCysProHisProGlyGluAlaCys 137	
QY	541 CAGCTCTCAGGCTGGGCATCACCAACAC-----CCACGG 576	

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||||| 138 ValSerGlyTrpGlyLeuValSerHisAsnGluProGlyThrThrGlyArgProGln 157
||||| 577 AAC-----CCATCCCGGATCTCCAGTCCCTCAACCTCTCCATCTCCATGCC 630
||| 158 SerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleSerIleSerAspAla 177
||| 631 ACTGTCATGGTGTATCCCGGAGATCAACAGCAACATGTTGTGTGTCAGCGCGTC 690
||| 178 SerCysAspIleAsnTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGlu 197
||| 691 ---CCGGGCGAGGATCCCTGCCAGGCTGATCTGGGGGCCCTGTGGAGCAAGATGCCATCCCTGGA 747
||| 198 GlyArgGlyAlaGluSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGlyIle 217
||| 748 CTTCAAGTCTGTGTCTCTGGGGGCTGTGGGGCCCTGTGGAGCAAGATGCCATCCCTGGA 807
||| 218 LeuGlnGlyIleValSerTrpGlyAspVal---ProCysAspAsnThrThrLysProGly 236
||| 808 GTCTACACCTATATTTGCAAGTATGTGACTGGATCCGATCGGATGATGAGGAACAAC 864
||| 237 ValTyrThrLysValCysArgTyrValLysTrpIleArgGluThrMetLysArgAsn 255

RESULT 9
Q63ZF2 PRELIMINARY; PRT; 250 AA.
ID Q63ZF2 AC Q63ZF2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Glandular kallikrein II precursor.
GN Name=Klik1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
RA Olsson A.Y., Lilja H., Lundwall A.;
RT "Taxon-specific evolution of glandular kallikrein genes and
RT identification of a progenitor of prostate-specific antigen.";
RL Genomics 84:147-156(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001364; DAA05600.1; --
KW Signal.
FT SIGNAL. 1 18 Potential.
FT CHAIN 22 250 Glandular kallikrein II.
SQ SEQUENCE 250 AA; 27630 MW; 247B29D3F0DEF8F1 CRC64;

Alignment Scores:
Pred. No.: 1,54e-30 Length: 250
Score: 610.00 Matches: 115
Percent Similarity: 61.79% Conservative: 37
Best Local Similarity: 46.75% Mismatches: 90
Query Match: 29.53% Indels: 4
DB: 2 Gaps: 3

US-10-015-385A-193 (1-1091) x Q63ZF2 (1-250)

QY 136 TTTTGTCTCTGTGTCTTCTGGGTCAGCCAGGCGCACCCAGAGATTTTCAATGGC 195
||| 6 PhelieAlaLeuAlaLeuValThrGlyHisValGlyGlyGluThrArgIleIleLysGly 25
||| 196 ACTGAGTGTGGCGGTAACACAGCGGTGGAGGTGGGCTGTTCAGGCGCACCGACCTGTG 255
||| 26 TyrGluCysArgProHisSerGlnProTrpGlnValAlaLeuPheGlnLysThrArgLeu 45
||| 256 CCCTGGGGGTGTCTTATTCACACAGGTGGTCTTCACAGCGGCTCACTGCGAGCGGC 315
||| 46 LeuCysGlyAlaThrLeuIleAlaProLysTrpLeuLeuThrAlaAlaHisCysArgLys 65

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QY 316 AGCAGGTACTGGTGGCGCTGGGGGAACACAGCCTCAGCAGCTCGACTCGACCGAGCAG 375
||| 66 ProHisTyrTrpGlyLeuGlyGluHisAsnGluLysThrAspGlyCysGluGln 85
||| 376 ATCCGCGCAGCGGCTTCTCTGTGACCCATCCGGCTACCTGGGAGCC-----TCGACG 429
||| 86 ArgArgMetAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLys 105
||| 430 AGCCAGCAGCAGCAGCCTCCGGCTGTCTGGCGCTGCCGCTGCCCTCCCGCTAAACAGCAGC 489
||| 106 AspHisArgAsnAspIleMetLeuValLysMetSerSerProAlaPheIleThrArgAla 125
||| 490 GTTCAACCCCTGCTGCCCAATGACTGTGCAACCGCTGGCAGCGAGTGCCAGCTCTCA 549
||| 126 ValArgProLeuThrLeuSerSerLeuCysValThrAlaGlyThrSerCysLeuIleSer 145
||| 550 GGCTGGGCGATCACCAACACACACGACCATTCCTCCGATCTGCTCCAGTGCCTCAAC 609
||| 146 GlyTrpGlyThrThrSerSerProGlnLeuArgLeuProHisSerLeuArgCysAlaAsn 165
||| 610 CTCTCCATCTCTCCCATGCCATGCCATGTGTGTATCCCGGAGAAATCACGAGCAAC 669
||| 166 ValSerIleIleGlyHisLysGluCysGluArgAlaTyrProGlyAsnIleThrAspThr 185
||| 670 ATGGTGTGTGACAGC---GGCGTCCCGGGGAGGATGCTCCAGGATGATCTGGGGGC 726
||| 186 MetLeuCysAlaSerValArgLysGluGlyLysAspSerCysGlnGlyAspSerGlyGly 205
||| 727 CCCTGGTGTGTGGGGAGTCTCTCAAGTCTGGTGTCTCTGGGGGTCTGTGGGGCCCTGT 786
||| 206 ProLeuValCysAsnGlySerLeuGlnGlyIleIleSerTrpGlyGln---AspProCys 224
||| 787 GGACAAGATGGCATCCCTCGAGTCTACACCTATATTGCAAGTATGTGAGTGGATCCGG 846
||| 225 AlaValThrArgLysProGlyValThrLysValCysLysTyrPheAspThrIleHis 244
||| 847 ATGATCATGAGGAACAAC 864
||| 245 GluValMetArgAsnAsn 250

RESULT 10
Q8CGR4 PRELIMINARY; PRT; 254 AA.
ID Q8CGR4 AC Q8CGR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ProstIn.
GN Name=Klik15; Synonyms=KLK15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AY152434; AAN78422.1; --
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.297; --
DR MGD; MGI:2447533; KLIK15.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Protease; Serine protease.  
SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEBDD01861 CRC64;

Alignment Scores:  
Pred. No.: 2,06e-30 Length: 254  
Score: 608.00 Matches: 124  
Percent Similarity: 60.8% Conservative: 30  
Best Local Similarity: 49.01% Mismatches: 77  
Query Match: 29.43% Indels: 22  
DB: 2 Gaps: 7

US-10-015-385A-193 (1-1091) x Q8CGR4 (1-254)

QY 133 AFCTTTTGTCTCTGTGTTCTTGGCTCAGCAGGAGCCACCA-----CCGAGATT 186  
Db 1 MetTrpLeuLeuAlaPheValLeuLeuValSerAlaAlaGlnAspGlyAspVal 20  
QY 187 TTCATGACACTGAGTGGGGGTAACACACAGCGTGGCAGTGGGCTGTTTCAGGGC 246  
Db 21 LeuGluGlyGluGluCysValProHisSerGlnProTrpGlnValAlaLeuPheGluArg 40  
QY 247 ACCAGCCTCGCTCGGGGGTGTCTCTATTGACACAGTGGGTGCTTCACAGCGCTCAC 306  
Db 41 GlyArgPheAsnCysGlyAlaPheLeuLeuLeuSerProArgTrpValLeuThrAlaAlaHis 60  
QY 307 TGCAGCGGAGCAGTACTGGTGGCGCTGGGGGACACAGCTCAGCAGCTCAGCTCAGTGG 366  
Db 61 CysGlnThrArgPheMetArgValArgLeuGluGlyGluHisAsnLeuArgLysPheAspGly 80  
QY 367 ACCGAGCAGATCCGACACAGCGGCTTCTGTGACCCATCCCGGCTACTCGGAGCCTCG 426  
Db 81 ProGluGlnLeuArgSerValSerArgLeuLeuProHisProGlyTyr-----GluAla 98  
QY 427 ACGAGCCAGCAGCAGCTCCGGTGTCTGGCGGTGGCGCTCGCGCTCCGCTCCGTAACACAGC 486  
Db 99 ArgThrHisArgHisAspLeuMetLeuLeuArgLeuPheLysProAlaArgLeuThrAla 118  
QY 487 ACCGTTCAACCTCGCTCGCGCTCCCAATGACTGTGTGCAACCGTGGCAGCAGTGGCAGCTC 546  
Db 119 TyrValArgProValAlaLeuProArgArgCysProLeuLeuGlyGluAspCysValVal 138  
QY 547 TCAGGCTGGGGCATCACCAACACCCAGCAACCA-----582  
Db 139 SerGlyTrpGlyLeuLeuSer---AspAsnProGlyAlaThrGlySerGlnLysSer 157  
QY 583 -----TTCGCGGATCTGCTCCAGTGCCTCAACCTCTCCATGCTTCCATGCCACC 633  
Db 158 HisValArgLeuProAspThrLeuHisCysAlaAsnLeuSerLeuLeuValCysGlyGly 177  
QY 634 TCCCATGTGTATCCCGGAGATATCAGCAACATGGTGTGTGCA-----GGC 684  
Db 178 CysAsnLysAspTyrProGlyArgValLeuProThrMetValCysAlaGlyValGluGly 197  
QY 685 GCGCTCCCGGGCAGATCCCTGCCAGGTGATTCTGGGGGCCCCCTGGTGTGGGGGA 744  
Db 198 Gly-----GlyThrAspSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGly 215  
QY 745 GTCCTTCAAGTCTGCTGTCTGGGGTCTGTGGGGCCCTGTGGGCAAGATGGCATCCCT 804  
Db 216 AlaLeuGlnGlyLeuValSerTrpGlyAspVal---ProCysAspThrThrThrLysPro 234  
QY 805 GGAGTCTACACCTATATTGCAAGTATGTGGACTGGATC 843  
Db 235 GlyValTyrThrLysValCysSerTyrLeuGluTrpIle 247

RESULT 11  
Q81XD7 PRELIMINARY; PRT; 275 AA.  
AC Q81XD7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Variant form hippostasin/KLK11.  
GN Name=KLK11;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;  
RL submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; AB078780; BAC54105.1; -.  
DR HSSP; P00760; 1EZX.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Protease; Serine protease.  
SQ SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;

Alignment Scores:  
Pred. No.: 5,76e-30 Length: 275  
Score: 601.00 Matches: 121  
Percent Similarity: 56.93% Conservative: 35  
Best Local Similarity: 44.16% Mismatches: 88  
Query Match: 29.09% Indels: 30  
DB: 2 Gaps: 5

US-10-015-385A-193 (1-1091) x Q81XD7 (1-275)

QY 127 CTCAGCATCTTTTGTCTCTCTGTGTTCTTGGCTCAGCAGGAGCCACACCGAGATT 186  
Db 4 LeuGlnLeuLeuLeuLeuAlaLeuAlaThrGlyLeuValGlyGluThr---Argile 22  
QY 187 TTCATGACACTGAGTGGGGGTAACCTCACAGCGTGGCAGTGGGCTGTTTCAGGGC 246  
Db 23 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLys 42  
QY 247 ACCAGCCTCGCTCGGGGGTGTCTCTATTGACACAGTGGGTGCTTCACAGCGCTCAC 306  
Db 43 ThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHis 62  
QY 307 TGCAGCGGC-----315  
Db 63 CysLeuLysProTrpValSerLeuThrSerProThrHisValSerProAspLeuSerSer 82  
QY 316 -----AGCAGGTACTGGGTGGCGCTCGGCGAACACACAGCTC 351  
Db 83 SerAsnTyrCysLeuSerHisLeuSerArgTrpIleValHisLeuGlyGlnHisAsnLeu 102  
QY 352 AGCCAGCTCGACTGGACCGCAGCAGATCCGGCAGCAGCGCTTCTCTGTGACCATCCCGGC 411  
Db 103 GlnLysGluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGly 122  
QY 412 TACCTGGGAGCC-----TCGACGAGCCACGAGCAGCTCCCGCTGCTGGGCTGGCG 465

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Db 123 PheAsnAenSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAla 142
Qy 466 CTGCCCGTCCGTAACACAGCAGCGCTTCAACCCCTGCGCCCTCCCACTGCTGCAACC 525
Db 143 SerProValSerIleThrTrpAlaValArgProLeuThrLeuSerArgCysValThr 162
Qy 526 GCTGGACCGAGTGCACGCTCTCAGCTGGGGATCACAACACCCAGCAACCCATTC 585
Db 163 AlaGlyThrSerCysLeuSerGlySerGlyThrSerSerProGlnLeuArgLeu 182
Qy 586 CGGATCTGCTCCAGTGCCTCAACCTCTCCATCGCTCCCATGCCACCTGCATGGTGTG 645
Db 183 ProHisThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAla 202
Qy 646 TATCCCGGAGCAATCACAGCAACATCGTGTGTGCGAGC--GGCGTCCCGGGCAGGAT 702
Db 203 TyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAsp 222
Qy 703 GCCTGCCAGGTGATCTGGGGGCCCTCGTGTGTGGGGAGTCTTCAAGTCTGTGTG 762
Db 223 SerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 242
Qy 763 TCCTGGGGTCTGTGGGGCCCTCTGGACAGATGCATCCCTGGAGTACACCTATATT 822
Db 243 SerTrpGlyGln--AspProCysAlaIleThrArgLysProGlyValThrLysVal 261
Qy 823 TGCAAGTATGTGGAGTGCATCGGATCGGATCATGAGGAACAAC 864
Db 262 CysLysTrpValAspTrpIleGlnGluThrMetLysAsnAsn 275

RESULT 12
Q61S10 PRELIMINARY; PRT; 255 AA.
AC Q61S10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 15, isoform 4 preproprotein.
GN Name=KLK15;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
```

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CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC069518; AAH69518.1; -.
DR EMBL; BC069480; AAH69480.1; -.
DR HSSP; P00761; 1AKS.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Peptidase S1A.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 255 AA; 28016 MW; 1581B784D4A39C4F CRC64;

Alignment Scores:
Pred. No.: 7.67e-30 Length: 255
Score: 599.00 Matches: 120
Percent Similarity: 59.38% Conservative: 32
Best Local Similarity: 46.88% Mismatches: 86
Query Match: 28.99% Indels: 18
DB: 2 Gaps: 6

US-10-015-385A-193 (1-1091) x Q61S10 (1-255)
Qy 142 CTCCTGTGTGTCTTGGGCTCAGCCAGCAGCCACA-----CCGAAGATTTC 189
Db 3 LeuLeuLeuThrLeuSerPheLeuLeuAlaSerThrAlaGlnAspGlyAspLysLeuLeu 22
Qy 190 AATGGCACTGAGTGTGGCGCTAACTCACAGCGCTGGCAGGTGGGCTGTGTTGAGGCGACC 249
Db 23 GluGlyAspGluCysAlaProHisSerGlnProTrpGlnValAlaLeuTyrGluArgGly 42
Qy 250 AGCTGCGCTGCGGGGTGTCTTATTGACACAGGTGGTCTCAGCGGCTACTGTC 309
Db 43 ArgPheAsnCysGlyAlaSerLeuIleSerProHisTrpValLeuSerAlaAlaHisCys 62
Qy 310 AGCGCAGCAGGTACTGGTGGCTGGCGTGGGGAACACAGCCTCAGCAGCTCCAGTGGACC 369
Db 63 GlnSerArgPheMetArgValArgLeuGlyGluHisAsnLeuArgLysArgAspGlyPro 82
Qy 370 GAGCAGATCCGCGCACAGCGGCTCTCTGTGTGCCCATCCCGCTACTGCGGAGCCCTGACG 429
Db 83 GluGlnLeuArgThrSerArgValIleProHisProArgTyr-----GluAlaArg 100
Qy 430 AGCACAGACGACCTCCGCTGCTGCGGTGCGCTGCGCTGCGCTGCGGTACACGACGACG 489
Db 101 SerHisArgAsnAspIleMetLeuLeuArgLeuValGlnProAlaArgLeuAsnProGln 120
Qy 490 GTTCNAACCCCTGCCCTGCCCAATGACTGTGCACCGCTGCAGCGGAGTGCACCTCTCA 549
Db 121 ValArgProAlaValLeuProThrArgCysProHisProGlyGluAlaCysValValSer 140
Qy 550 GCCTGGGGCATCAACCAACAC-----CCACGGGAAC-----579
Db 141 GlyTrpGlyLeuValSerHisAsnGluProGlyThrAlaGlySerProArgSerGlnVal 160
Qy 580 CCATTCCGGATGCTGCTCAGTGCCTCAACCTCTCCATGCTCCCATGCCACCTGCCAT 639
Db 161 SerLeuProAspThrLeuHisCysAlaAsnIleSerIleSerAspThrSerCysAsp 180
Qy 640 GGTGTGTATCCGGGAGATCACAGCAACATGGTGTGTGCGGGGGGCTC---CCGGGG 696
Db 181 LysSerTrpProGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGluGlyArgGly 200
Qy 697 CAGGATGCTCCAGGGTGATTCTGGGGGCCCTTGTGTGTGGGGAGTCTCTCAAGT 756
Db 201 AlaGluSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGlyIleLeuGlnGly 220
Qy 757 CTGGTGTCTCGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACC 816
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Db 221 ileValSerTrpGlyAspVal---ProCysAspaenthThrThrLysProGlyValThr 239
QY 817 TATATTGCAGTATGCGATCGGATCGGATGATCATGAGGACAC 864
Db 240 LysValCysHisTrpLeuGluTrpIleArgGluThrMetLysArgAsn 255
RESULT 13
KLKF HUMAN STANDARD; PRT: 256 AA.
AC Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9H2R9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
GN Name=KLK15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING AND TISSUE SPECIFICITY.
RX PubMed=11010966; DOI=10.1074/jbc.M005432007;
RA Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-
RT regulation in prostate cancer.";
RT J. Biol. Chem. 276:53-61(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RT Gene 257:119-130(2000).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
RA Dhanich M.E., Spiess M.;
RT "A novel serine proteinase-like sequence from human brain.";
RT Biochim. Biophys. Acta 1218:225-228(1994).
RN [4]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RC Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Protease whose physiological substrate is not yet known.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H2R5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2R5-2; Sequence=VSP_005405;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=3;
CC IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
CC Name=4;
CC IsoId=Q9H2R5-4; Sequence=VSP_005404;
CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
CC expressed in the prostate, salivary, and adrenal glands and in the
CC colon testis and kidney.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC
DR EMBL; AF242195; AAG09469.1; -
DR EMBL; AF242195; AAG09470.1; -
DR EMBL; AF242195; AAG09471.1; -
DR EMBL; AF242195; AAG09472.1; -
DR EMBL; AF243527; AAG33354.1; -
DR EMBL; X75363; AEX53145.1; ALT_SEQ.
DR HSSP; P00760; 1EXZ.
DR MEROPS; S01.081; -
DR Genew; HGNC:20453; KLK15.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 21 Activation peptide (Potential).
FT CHAIN 22 256 Kallikrein 15.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 106 106 Charge relay system (By similarity).
FT ACT_SITE 209 209 Charge relay system (By similarity).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 122 206 Missing (in isoform 4).
FT VARSPLIC 122 256 Missing (in isoform 2).
FT VARSPLIC 161 161 V -> G (in isoform 3).
FT VARSPLIC 162 256 Missing (in isoform 3).
FT CONFLICT 147 160 SHNPFPTAGSPRSQ -> PLSSP (in Ref. 2).
SQ SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;
Alignment Scores:
Pred. No.: 7,68e-30 Length: 256
Score: 599.00 Matches: 121
Percent Similarity: 59.53% Conservative: 32
Best Local Similarity: 47.08% Mismatches: 88
Query Match: 28.99% Indels: 16
DB: 1 Gaps: 6
US-10-015-385A-193 (1-1091) x KLKF_HUMAN (1-256)
QY 133 ATCTTTTGCTCTGTGTGTTCTTTGGGTACGCCAGGAGGCACACA-----CCGAAGATT 186
Db 3 LeuLeuLeuThrLeuSerPheLeuLeuAlaSerThrAlaGlnAspGlyAspLysLeu 22
QY 187 TTCATGGCACTAGTGTGGCGGTAACTACAGCGCTGGCAGTGGGGCTGTTTCAGGGC 246
Db 23 LeuGluGlyAspGluCysAlaProHisSerGlnProTrpGlnValAlaLeuTyrGluArg 42
QY 247 ACCAGCCTCGCTGGCGGGGTGTCCTATTACACACAGGTGGTCTCTCACAGCGGCTCAC 306
Db 43 GlyArgPheAsnCysGlyAlaSerLeuLeuSerProHisTrpValLeuSerAlaAlaHis 62
QY 307 TCAGCGGCACAGGATGCTGGGTGCGCTGGGGGAACACAGCCTCAGCGCTCAGCTGCG 366
Db 63 CysGlnSerArgPheMetArgValArgLeuGluHisAsnLeuArgLysArgSpGly 82
QY 367 ACCGAGCAGATCCGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACTCGGAGCCTCG 426

```







```
QY 595 CTCCAGTGCCTCAACCTCTCCATCGTCTCCATGCCACCTGCCATGGTGTGTATCCCGGG 654
Db |||:|||| |||:|||||:|||| ||| ||| ||| ||| ||| ||| ||| |||
187 LeuArgCysAlaAsnValSerIleIleGluHisLysGluCysGluLysAlaTyrProGly 206
QY 655 AGAATCACGAGCAACATGGTGTGTGCAGGC--GGCGTCCCGGGGCGAGGATGCTGCCAG 711
Db ||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
207 AsnIleThrAspThrMetLeuCysAlaSerValArgLysGluGlyLysAspSerCysGln 226
QY 712 GGTGATTCTGGGGCCCCCTGTGTGTGGGGAGTCTTCAAGGTCTGTGTCTCTGGGG 771
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
227 GlyAspSerGlyGlyProLeuValCysAsnGlySerLeuGlnGlyIleIleSerTrpGly 246
QY 772 TCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTCAGATAT 831
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
247 Gln---AspProCysAlaValThrArgLysProGlyValTyrThrLysValCysLysTyr 265
QY 832 GTGGACTGGATCCGGATGATCATGAGGAACAAC 864
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 PheAsnTrpIleHisGluValMetArgAsnAsn 276
```

Search completed: March 5, 2005, 23:17:52  
Job time : 251 secs



Run on: March 5, 2005, 23:40:21 ; Search time 183 Seconds  
(without alignments)  
4611.536 Million cell updates/sec

Title: US-10-015-385A-193  
Perfect score: 357  
Sequence: 1 caagcaggtcatcccttgg.....aggggcaaaaaaaaaa 1091  
Scoring table: OLIGO  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 3967864  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB21304	standard;	protein;	248	AA.	
DE	Human KIK-L5	protein #4.				
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN ) MOUNT SINAI HOSPITAL.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					
RESULT 2						
ID	AAB24428	standard;	protein;	248	AA.	
DE	Human PRO1303	protein sequence SEQ ID NO:203.				
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					
RESULT 3						
ID	AAB24032	standard;	protein;	248	AA.	
DE	Human PRO1303	protein sequence SEQ ID NO:33.				
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					
RESULT 4						
ID	AAY99393	standard;	protein;	248	AA.	
DE	Human PRO1303 (UNQ669)	amino acid sequence SEQ ID NO:194.				
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH ) GENENTECH INC.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					
RESULT 5						
ID	AAM231994	standard;	protein;	248	AA.	
DE	Human EST encoded	protein SEQ ID NO: 1519.				
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					
RESULT 6						
ID	AAB66142	standard;	protein;	248	AA.	
DE	Protein of the invention #54.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Best Local Similarity:	100.00%					
Query Match:	69.47%					
Mismatches:	0					
Indels:	0					

RESULT 7

ID ABO33635 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 8

ID ABO44488 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 9

ID ABO33512 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 10

ID ADC18063 standard; protein; 248 AA.  
DE Human PRO polypeptide #54.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 11

ID ADD70709 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 12

ID ADD39786 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 13

ID ADD70232 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 14

ID ADD38353 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 15

ID ADD39309 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0

RESULT 16

ID ADD39309 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0



PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0  
RESULT 35  
ID ADN10927 standard; protein; 248 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0  
RESULT 36  
ID ADL94713 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0  
RESULT 37  
ID ADT94373 standard; protein; 248 AA.  
DE Human PRO1303 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.47% Indels: 0  
RESULT 38  
ID AAB21303 standard; protein; 254 AA.  
DE Human KIK-L5 protein #3.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.83% Indels: 0  
RESULT 39  
ID ABG66676 standard; protein; 254 AA.  
DE Human novel polypeptide #11.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.83% Indels: 0  
RESULT 40  
ID ADN10926 standard; protein; 254 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.83% Indels: 0  
RESULT 41  
ID ADP56174 standard; protein; 254 AA.  
DE Human PRO protein sequence SEQ ID NO:2150.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.83% Indels: 0  
RESULT 42  
ID AAB21301 standard; protein; 184 AA.  
DE Human KIK-L5 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.54% Indels: 0  
RESULT 43  
ID AA029516 standard; protein; 248 AA.  
DE Human kallikrein-like protein 5 (18817).  
PN WO2003039475-A2.

PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 50.98% Indels: 0  
RESULT 44  
ID AAY28642 standard; protein; 162 AA.  
DE Human secreted protein from cDNA clone HKAFV61.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.05% Indels: 0  
RESULT 45  
ID AAB21302 standard; protein; 111 AA.  
DE Human KIK-L5 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 18.21% Indels: 0  
RESULT 46  
ID ADN10928 standard; protein; 111 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 18.21% Indels: 0  
RESULT 47  
ID ADR72141 standard; peptide; 16 AA.  
DE Common protein epitope tag, PET, for human kallikrein 4.  
PN US2004180380-A1.  
PD 16-SEP-2004.  
PA (ENGE-) ENGINEOS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.48% Indels: 0  
RESULT 48  
ID AAP70474 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen (TPA) analogue.  
PN WO8703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.92% Indels: 0  
RESULT 49  
ID AAB08953 standard; protein; 30 AA.  
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:110.  
PN WO200017222-A1.  
PD 30-MAR-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 50  
ID AAU76373 standard; protein; 70 AA.  
DE Human Marcov Model trypsin consensus protein sequence.  
PN WO200206455-A2.  
PD 24-JAN-2002.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 51  
ID ABP09500 standard; protein; 107 AA.  
DE Human ORFX protein sequence SEQ ID NO:18982.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 52  
ID ADC31388 standard; protein; 113 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1470.  
PN WO2003029271-A2.

PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 53  
ID AAP1986 standard; protein; 117 AA.  
DE Chain 2 of modified tissue plasminogen activator.  
PN EP253582-A.  
PD 20-JAN-1988.  
PA (NOVO) NOVO IND AS.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 54  
ID AAY72094 standard; protein; 187 AA.  
DE Human serine protease #5 encoded by clone HHFBJ67.  
PN WO200088247-A2.  
PD 16-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 55  
ID ABG30791 standard; protein; 187 AA.  
DE Human serine protease #4.  
PN US2002119925-A1.  
PD 29-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 56  
ID AAE17922 standard; protein; 187 AA.  
DE Human gene 4 encoded serine protease, HHFBJ67.  
PN WO200198476-A1.  
PD 27-DEC-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 57  
ID AAU7550 standard; protein; 199 AA.  
DE Membrane-type serine protease #1.  
PN WO200212461-A2.  
PD 14-FEB-2002.  
PA (FARB) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 58  
ID AAY28590 standard; protein; 212 AA.  
DE Human Factor D.  
PN WO9942133-A1.  
PD 26-AUG-1999.  
PA (TANO-) TANOX INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 59  
ID AAG79215 standard; protein; 214 AA.  
DE Consensus sequence of trypsin serine protease-like protein domain.  
PN WO200173074-A2.  
PD 04-OCT-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 60  
ID AD117277 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 813.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 61  
ID AD117269 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 805.  
PN WO200268649-A2.  
PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 62  
ID ABO00751 standard; protein; 217 AA.  
DE Polypeptide encoded by novel human contig #2.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 63  
ID AD121707 standard; protein; 217 AA.  
DE Novel human polypeptide #186.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 64  
ID ADJ83076 standard; protein; 217 AA.  
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SEK/) SEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 65  
ID ABE21442 standard; protein; 226 AA.  
DE Human trypsin domain consensus protein #2.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 66  
ID ABG75786 standard; protein; 226 AA.  
DE Trypsin domain consensus sequence, SMART.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 67  
ID AAE14342 standard; protein; 227 AA.  
DE Human protease PRTS-7 protein.  
PN WO200183775-A2.  
PD 08-NOV-2001.



PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 68  
ID ABG75785 standard; protein; 227 AA.  
DE Trypsin domain consensus sequence, PFAM.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPELER-LIBERMANN R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 69  
ID AAE39994 standard; protein; 228 AA.  
DE Human adipisin protein #3.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST) GENSET SA.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 70  
ID ADN04134 standard; protein; 228 AA.  
DE Antipsoriatic protein sequence #262.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 71  
ID ADP03097 standard; protein; 228 AA.  
DE Human insulin resistance-related adipisin protein.  
PN JF2004041208-A.  
PD 12-FEB-2004.  
PA (SANY) SANKYO CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 72  
ID ADP23853 standard; protein; 228 AA.  
DE PRO polypeptide SEQ ID NO:1031.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 73  
ID ADI17268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 74  
ID ADI17276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 75  
ID ADJ83075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERRHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 76  
ID AAE06932 standard; protein; 235 AA.  
DE Human membrane-type serine protease (WTSP) 4.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 77  
ID ADI10375 standard; protein; 235 AA.  
DE Human cell surface protease #3.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 78  
ID ADJ46899 standard; protein; 235 AA.  
DE Human transmembrane serine protease (WTSP) polypeptide #3.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 79  
ID AAB11695 standard; protein; 238 AA.  
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:2.  
PN WO200031272-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 80  
ID ADA50474 standard; protein; 238 AA.  
DE Human protease SEQ ID NO:72.  
PN WO2003040393-A2.  
PD 15-MAY-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 81  
ID AAR07241 standard; protein; 245 AA.  
DE t-PA(Del1296-302).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 82  
ID AAE21441 standard; protein; 249 AA.  
DE Human trypsin domain consensus protein #1.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 83  
ID AAR05772 standard; protein; 250 AA.  
DE Human adipisin gene product from the clone phg31.  
PN WO9006365-A.  
PD 14-JUN-1990.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
PA (DANA-) DANA-PARBER CANCER INST.  
PA (META-) METABOLIC BIOSYSTEMS INC.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 84  
ID AAR05421 standard; protein; 250 AA.  
DE Human adipisin/D encoded by a cDNA.  
PN WO9001540-A.  
PD 22-FEB-1990.  
PA (CALB-) CALIF BIOTECHN INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 85  
ID AAR07239 standard; protein; 252 AA.  
DE t-PA(R304->S).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 86  
ID AAR07240 standard; protein; 252 AA.  
DE t-PA(R304->E).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 87  
ID AAR07242 standard; protein; 252 AA.  
DE t-PA(R298->E).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 88  
ID AAR07244 standard; protein; 252 AA.  
DE t-PA(K296,R298,R299->E,E,E).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 89  
ID AAR07243 standard; protein; 252 AA.  
DE t-PA(R299->E).  
PN WO9010649-A.  
PD 20-SEP-1990.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 90  
ID AAY08025 standard; protein; 253 AA.  
DE Mouse protease-related protein (PVP).  
PN DE19736198-Cl.  
PD 24-DEC-1998.  
PA (DEXR-) DEUT KREBSFORSCHUNGSZENTRUM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 91  
ID AAB98506 standard; protein; 253 AA.  
DE Human tissue plasminogen activator serine protease catalytic domain.  
PN WO200129056-A1.

PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 92  
ID ADA50481 standard; protein; 253 AA.  
DE Human protease SEQ ID NO:79.  
PN WO2003040393-A2.  
PD 15-MAY-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 93  
ID AAE39993 standard; protein; 253 AA.  
DE Human adipisin protein #2.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST) GENSET SA.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 94  
ID AAE39992 standard; protein; 253 AA.  
DE Human adipisin protein #1.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST) GENSET SA.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 95  
ID ADE58223 standard; protein; 253 AA.  
DE Human Protein P00746, SEQ ID NO 4094.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 96  
ID AAY50873 standard; protein; 265 AA.  
DE Vampire bat saliva plasminogen activator protein fragment.  
PN WO9957251-A2.  
PD 11-NOV-1999.  
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 97  
ID AAY9592 standard; protein; 266 AA.  
DE Vampire bat salivary plasminogen activator DSPA.  
PN WO200032759-A1.  
PD 08-JUN-2000.  
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 98  
ID AAE24189 standard; protein; 268 AA.  
DE Human native K2S heterologous protein fragment (260-527).  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 99  
ID AAE24195 standard; protein; 268 AA.  
DE Human K2S heterologous protein fragment (260-527) mutant #2.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 100  
ID AAE25043 standard; protein; 268 AA.  
DE Human kringle 2 serine protease protein fragment (residues 260-527).  
PN WO200240650-A2.

PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 101  
ID AAE24194 standard; protein; 272 AA.  
DE Human K2S heterologous protein fragment (260-527) mutant #1.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 102  
ID AAB11696 standard; protein; 273 AA.  
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:4.  
PD WO200031272-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 103  
ID AAE24196 standard; protein; 274 AA.  
DE Human K2S heterologous protein fragment (260-527) mutant #3.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 104  
ID AAE24198 standard; protein; 308 AA.  
DE Human native K2S heterologous protein fragment (220-527).  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 105  
ID AAE24192 standard; protein; 308 AA.  
DE Human K2S heterologous protein fragment (220-527) mutant #2.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 106  
ID AAE25042 standard; protein; 308 AA.  
DE Human Kringle 2 serine protease protein fragment (residues 220-527).  
PD WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 107  
ID AAB11697 standard; protein; 311 AA.  
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:6.  
PD WO200031272-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 108  
ID AAE24191 standard; protein; 312 AA.  
DE Human K2S heterologous protein fragment (220-527) mutant #1.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 109  
ID AAE24193 standard; protein; 314 AA.  
DE Human K2S heterologous protein fragment (220-527) mutant #3.  
PD WO200240696-A2.  
PD 23-MAY-2002.

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 110  
ID AAB03159 standard; protein; 321 AA.  
DE Mouse trypsin family serine protease Tespec PRO-3.  
PD WO200026352-A1.  
PD 11-MAY-2000.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 111  
ID ADP29456 standard; protein; 324 AA.  
DE Human secreted protein SEQ ID #223.  
PD WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 112  
ID AAP70450 standard; protein; 329 AA.  
DE Human tissue plasminogen activator (tPA) analogue comprising the B domain  
DE of Protein A linked to a catalytic fragment of tPA.  
PD WO8705934-A.  
PD 08-OCT-1987.  
PA (CREA/) CREA R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 113  
ID AAE24198 standard; protein; 331 AA.  
DE Human K2S heterologous protein fragment (197-527) mutant #2.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 114  
ID AAE24183 standard; protein; 331 AA.  
DE Human native K2S heterologous protein fragment (197-527).  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 115  
ID AAE25037 standard; protein; 331 AA.  
DE Human Kringle 2 serine protease protein fragment (residues 197-527).  
PD WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 116  
ID AAE24197 standard; protein; 335 AA.  
DE Human K2S heterologous protein fragment (197-527) mutant #1.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 117  
ID AAE24185 standard; protein; 335 AA.  
DE Human K2S heterologous protein fragment (193-527) mutant #2.  
PD WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 118  
ID AAE25047 standard; protein; 335 AA.  
DE Human K2S protein fragment (residues 197-527) mutant #2.  
PD WO200240650-A2.  
PD 23-MAY-2002.

PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 119  
ID AAE25039 standard; protein; 335 AA.  
DE Human K2S protein fragment (residues 193-527) mutant #2.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 120  
ID AAE25046 standard; protein; 335 AA.  
DE Human K2S protein fragment (residues 197-527) mutant #1.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 121  
ID AAE24200 standard; protein; 337 AA.  
DE Human K2S heterologous protein fragment (197-527) mutant #4.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 122  
ID AAE24201 standard; protein; 337 AA.  
DE Human K2S heterologous protein fragment (191-527) mutant #3.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 123  
ID AAE24199 standard; protein; 337 AA.  
DE Human K2S heterologous protein fragment (197-527) mutant #3.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 124  
ID AAE25049 standard; protein; 337 AA.  
DE Human K2S protein fragment (residues 197-527) mutant #4.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 125  
ID AAE25048 standard; protein; 337 AA.  
DE Human K2S protein fragment (residues 197-527) mutant #3.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 126  
ID AAE24184 standard; protein; 339 AA.  
DE Human K2S heterologous protein fragment (193-527) mutant #1.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 127  
ID AAE25038 standard; protein; 339 AA.  
DE Human K2S protein fragment (residues 193-527) mutant #1.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 128  
ID AAE24187 standard; protein; 343 AA.  
DE Human K2S heterologous protein fragment (191-527) mutant #2.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 129  
ID AAE24186 standard; protein; 343 AA.  
DE Human K2S heterologous protein fragment (191-527) mutant #1.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 130  
ID AAE25041 standard; protein; 343 AA.  
DE Human K2S protein fragment (residues 191-527) mutant #2.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 131  
ID AAE25040 standard; protein; 343 AA.  
DE Human K2S protein fragment (residues 191-527) mutant #1.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 132  
ID AAP94414 standard; protein; 345 AA.  
DE Sequence of coding region in plasmid pUTtrp.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 133  
ID AAP94415 standard; protein; 345 AA.  
DE Sequence of coding region in plasmid pthTtrp.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 134  
ID AAR35404 standard; protein; 348 AA.  
DE tPA-8.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 135  
ID AAR35401 standard; protein; 348 AA.  
DE tPA-2.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 136  
ID AAP70641 standard; protein; 354 AA.  
DE Modified tissue plasminogen activator.  
PN AU8661804-A.  
PD 05-MAR-1987.  
PA (ELIL) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 3.64% Indels: 0
RESULT 137
ID AAR41024 standard; protein; 354 AA.
DE Modified tissue plasminogen activator #2.
PN US244806-A.
PD 14-SEP-1993.
PA (ELIL ) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 138
ID AAE24182 standard; protein; 354 AA.
DE Human native K2S heterologous protein fragment (174-527).
PN WO200240698-A2.
PD 23-MAY-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 139
ID AAE25036 standard; protein; 354 AA.
DE Human Kringle 2 serine protease protein fragment (residues 174-527).
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 140
ID ABU62712 standard; protein; 354 AA.
DE Human plasminogen activating enzyme.
PN CN1380416-A.
PD 20-NOV-2002.
PA (UYFU-) UNIV FUDAN.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 141
ID AAP94407 standard; protein; 355 AA.
DE Sequence encoded by plasmid pTRKPA delta trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 142
ID AAP94411 standard; protein; 355 AA.
DE Sequence of coding region in plasmid pSTTKtrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 143
ID AAR06417 standard; protein; 355 AA.
DE Tissue plasminogen activator deriv.
PN EP382174-A.
PD 16-AUG-1990.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 144
ID AAR44836 standard; protein; 355 AA.
DE Human truncated tPA-1 mutein.
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 145
ID AAR44835 standard; protein; 355 AA.
DE Human truncated tPA-6' mutein.
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 146
ID AAR35407 standard; protein; 355 AA.
DE tPA-13.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 147
ID AAR35409 standard; protein; 355 AA.
DE tPA-15.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 148
ID AAR35406 standard; protein; 355 AA.
DE tPA-12.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 149
ID AAR35400 standard; protein; 355 AA.
DE tPA-1.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 150
ID AAR35411 standard; protein; 355 AA.
DE tPA-17.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 151
ID AAR35413 standard; protein; 355 AA.
DE tPA-5.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 152
ID AAR35414 standard; protein; 355 AA.
DE tPA-6.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 153
ID AAR35408 standard; protein; 355 AA.
DE tPA-14.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 154
ID AAR35410 standard; protein; 355 AA.
DE tPA-16.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 155
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ID AAR35412 standard; protein; 355 AA.  
DE tPA-18.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 156  
ID AAR35402 standard; protein; 355 AA.  
DE tPA-6.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 157  
ID AAR35403 standard; protein; 355 AA.  
DE tPA-7.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 158  
ID AAR35405 standard; protein; 355 AA.  
DE tPA-11.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 159  
ID AAW34667 standard; protein; 355 AA.  
DE Thrombolytically active protein K1X2P, based on human t-PA.  
PN US5676947-A.  
PD 14-OCT-1997.  
PA (BOF ) BOEHRINGER MANNHEIM GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 160  
ID AAW28536 standard; protein; 355 AA.  
DE mt-PA6-E.  
PN US5658788-A.  
PD 19-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 161  
ID AAW14431 standard; protein; 355 AA.  
DE Tissue plasminogen activator derivative, mt-PA6-E.  
PN US5595736-A.  
PD 21-JAN-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 162  
ID ADN02588 standard; protein; 355 AA.  
DE Human recombinant tissue-type plasminogen activator (r-PA).  
PN CN1429909-A.  
PD 16-JUL-2003.  
PA (SHAN-) SHANGHAI XINGSHENGYUAN MEDICINE RES CO LT.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 163  
ID ADN02590 standard; protein; 355 AA.  
DE Recombinant tissue-type plasminogen activator (r-PA) Leu346Pro mutant.  
PN CN1429909-A.  
PD 16-JUL-2003.  
PA (SHAN-) SHANGHAI XINGSHENGYUAN MEDICINE RES CO LT.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 164  
ID AAW28537 standard; protein; 356 AA.  
DE mt-PA9.  
PN US5658788-A.  
PD 19-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 165  
ID AAW28535 standard; protein; 356 AA.  
DE mt-PA6-D.  
PN US5658788-A.  
PD 19-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 166  
ID AAW14430 standard; protein; 356 AA.  
DE Tissue plasminogen activator derivative, mt-PA6-D.  
PN US5595736-A.  
PD 21-JAN-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 167  
ID AAW1432 standard; protein; 356 AA.  
DE Tissue plasminogen activator derivative, mt-PA9.  
PN US5595736-A.  
PD 21-JAN-1997.  
PA (ELIL ) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 168  
ID ADF32668 standard; protein; 356 AA.  
DE Mutant tissue plasminogen activator.  
PN CN1381460-A.  
PD 27-NOV-2002.  
PA (AIRF-) AIR FORCE GEN HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 169  
ID AAR05123 standard; protein; 358 AA.  
DE Bat-PA(I).  
PN EP352119-A.  
PD 24-JAN-1990.  
PA (MERI ) MERCK & CO INC.  
PA (SCHD ) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 170  
ID AAR22502 standard; protein; 371 AA.  
DE [GARSYQ]-[Plasminogen 443-541]-[t-PA 262-527] hybrid.  
PN WO9204450-A.  
PD 19-MAR-1992.  
PA (BERC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 171  
ID AAW87770 standard; protein; 372 AA.  
DE Human tissue plasminogen activator.  
PN WO9854199-A1.  
PD 03-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 172  
ID AAE25034 standard; protein; 377 AA.  
DE OmpA-X2S fusion protein.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 173  
ID AAB11399 standard; protein; 378 AA.

DE E. coli expression plasmid pET20b(+) -rPA encoded protein.  
PN EP1048732-A1.  
PD 02-NOV-2000.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 174  
ID AAB74200 standard; protein; 378 AA.  
DE FeIB-rPA fusion protein.  
PN EP1077262-A1.  
PD 21-FEB-2001.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 175  
ID AAB70770 standard; protein; 378 AA.  
DE Expression plasmid pET20b(+) -rPA protein.  
PN EP1077263-A1.  
PD 21-FEB-2001.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 176  
ID AAY72021 standard; protein; 378 AA.  
DE E. carotovora FeIB-rPA fusion protein encoded by pET20b(+) -rPA.  
PN EP1054063-A2.  
PD 22-NOV-2000.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 177  
ID AAR41796 standard; protein; 383 AA.  
DE CD4/Tissue-type plasminogen activator (tPA) fusion protein.  
PN WO9318162-A1.  
PD 16-SEP-1993.  
PA (CREA-) CREAGEN INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 178  
ID AAY42788 standard; protein; 383 AA.  
DE Human CD4-tPA fusion protein.  
PN US5961973-A.  
PD 05-OCT-1999.  
PA (CREA/) CREA R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 179  
ID AAU10702 standard; protein; 383 AA.  
DE Human CD4-tPA fusion protein.  
PN US6287561-B1.  
PD 11-SEP-2001.  
PA (CREA/) CREA R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 180  
ID AAP70640 standard; protein; 387 AA.  
DE Modified tissue plasminogen activator.  
PN AU8661804-A.  
PD 05-MAR-1987.  
PA (ELIL) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 181  
ID AAR41023 standard; protein; 387 AA.  
DE Modified tissue plasminogen activator.  
PN US5244806-A.  
PD 14-SEP-1993.  
PA (ELIL) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 182  
ID AAP94417 standard; protein; 389 AA.  
DE Sequence of coding region in plasmid pmTTK.

PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 183  
ID AAP94418 standard; protein; 389 AA.  
DE Sequence of coding region in plasmid pmSTTK.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 184  
ID AAU75907 standard; protein; 389 AA.  
DE Human epidermis-specific serine protease #2.  
PN WO200200702-A2.  
PD 03-JAN-2002.  
PA (FARB) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 185  
ID AAP82587 standard; protein; 390 AA.  
DE Modified tissue plasminogen activator lacking F and G region and kringles  
DE region 2 and Q-96, I-98 and S-119 substd for N, T and M resp.  
PN JP63230084-A.  
PD 26-SEP-1988.  
PA (EISA) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 186  
ID AAP82588 standard; protein; 390 AA.  
DE Modified tissue plasminogen activator lacking F and G region and kringles  
DE region 1 and G-183 and S-186 substd for S and T resp.  
PN JP63230084-A.  
PD 26-SEP-1988.  
PA (EISA) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 187  
ID AAP70021 standard; protein; 393 AA.  
DE Sequence of tissue plasminogen activator (tPA) deriv. with AAs 45-179  
DE deleted.  
PN EP242836-A.  
PD 28-OCT-1987.  
PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 188  
ID AAP70019 standard; protein; 393 AA.  
DE Recombinant plasminogen-activator.  
PN EP242835-A.  
PD 28-OCT-1987.  
PA (MATT/) MATTES R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 189  
ID AAR06486 standard; protein; 394 AA.  
DE V-PA gamma.  
PN EP383417-A.  
PD 22-AUG-1990.  
PA (SCHD) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 190  
ID AAR05125 standard; protein; 395 AA.  
DE Modified Bat-PA(H).  
PN EP352119-A.  
PD 24-JAN-1990.  
PA (MERI) MERCK & CO INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

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Query Match: 3.64% Indels: 0
RESULT 191
ID AAG78109 standard; protein; 395 AA.
DE Human thrombolytic enzyme NTA.
PN CN1287174-A.
PD 14-MAR-2001.
PA (DOUD/) DOU D.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 192
ID AAR25190 standard; protein; 396 AA.
DE mt-PA6.
PN EP493037-A2.
PD 01-JUL-1992.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 193
ID ADA56816 standard; protein; 413 AA.
DE Human secreted protein #99.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 194
ID ADA57353 standard; protein; 413 AA.
DE Human secreted protein #99.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 195
ID ADC74423 standard; protein; 413 AA.
DE Human secreted protein - SEQ ID 1056.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 196
ID ADC74063 standard; protein; 413 AA.
DE Human secreted protein - SEQ ID 696.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 197
ID ADD37850 standard; protein; 413 AA.
DE Human secreted protein #33.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 198
ID ADD38017 standard; protein; 413 AA.
DE Human secreted protein #200.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 199
ID AAB08912 standard; protein; 414 AA.
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:69.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 200
ID ABG76907 standard; protein; 418 AA.
DE Human spinesin-like protein.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 201
ID ABR57427 standard; protein; 418 AA.
DE Human NOV11 protein SEQ ID NO:32.
PN WO200294870-A2.
PD 28-NOV-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 202
ID ADJ38447 standard; protein; 418 AA.
DE Human novel protein NOV10b.
PN US2003212256-A1.
PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MULL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERH/) ZERHUSEN B D.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (GORM/) GORMAN L.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 203
ID ABM84894 standard; protein; 422 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5143.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 204
ID AAR1922 standard; protein; 434 AA.
DE Delta(92-179) and delta(466-470) tPA variant.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 205
ID AAP94412 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pSTQktrp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 206
ID AAP94410 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pTOiPA delta trp.
PN EP302456-A.
```



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PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 207
ID AAP94413 standard; protein; 437 AA.
DE Sequence of coding region in plasmid pSTQ1trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 208
ID AAP94409 standard; protein; 438 AA.
DE Sequence of coding region in plasmid pTQkPA delta trp.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 209
ID AAR09259 standard; protein; 439 AA.
DE t-PA variant d92-179, I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 210
ID AAR09260 standard; protein; 439 AA.
DE t-PA variant d92-179, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 211
ID AAR09261 standard; protein; 439 AA.
DE t-PA variant d92-179, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 212
ID AAR09258 standard; protein; 439 AA.
DE t-PA variant d92-179, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 213
ID AAR68851 standard; protein; 439 AA.
DE Delta 2-89 tissue plasminogen activator.
PN US5376547-A.
PD 27-DEC-1994.
PA (AMHP ) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 214
ID AAP70643 standard; protein; 441 AA.
DE Modified tissue plasminogen activator.
PN AU8661804-A.
PD 05-MAR-1987.
PA (ELIL ) LILLY & CO ELI.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 215
ID AAB11698 standard; protein; 445 AA.
DE Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:8.
PN WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO ) FUSO PHARM IND LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 216
ID AAR08150 standard; protein; 446 AA.
DE Non-glycosylated tPA deriv. lacking finger- and EGF-domains.
PN EP400545-A.
PD 05-DEC-1990.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 217
ID AAB11699 standard; protein; 457 AA.
DE Human serine protease BSSP2 (hBSSP2), SEQ ID NO:10.
PN WO200031272-A1.
PD 02-JUN-2000.
PA (FUSO ) FUSO PHARM IND LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 218
ID AAU82752 standard; protein; 457 AA.
DE Amino acid sequence of novel human protease #51.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 219
ID AAR22499 standard; protein; 467 AA.
DE [GARSYQ]-[Plasminogen 347-541]-[t-PA 262-527] hybrid.
PN WO9204450-A.
PD 19-MAR-1992.
PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 220
ID AAP94416 standard; protein; 472 AA.
DE Sequence of coding region in plasmid pmTQk112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 221
ID ABG76906 standard; protein; 472 AA.
DE Human hepsin/plasma transmembrane serine protease-like protein.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00%
Query Match: 3.64%
Indels: 0
Mismatches: 0
RESULT 222
ID ADJ38445 standard; protein; 472 AA.
DE Human novel protein NOV10a.
PN US2003212256-A1.
PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERH/) ZERHUSEN B D.
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PA (KEKU/) KERUDA R.  
PA (SPVT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (PERN/) FERNANDES E R.  
PA (GORM/) GORMAN L.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 223  
ID ADH41503 standard; protein; 472 AA.  
DE Novel human protein NOV4b.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 224  
ID AAP70642 standard; protein; 473 AA.  
DE Modified tissue plasminogen activator.  
PN AU8661804-A.  
PD 05-MAR-1987.  
PA (ELIL) LILLY & CO ELI.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 225  
ID ADM99257 standard; protein; 475 AA.  
DE Environmentally sourced protease protein SeqID 140.  
PN WO2004033668-A2.  
PD 22-APR-2004.  
PA (DIVE-) DIVERSA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 226  
ID AAR03004 standard; protein; 476 AA.  
DE Tissue plasminogen activator (t-PA) deriv.  
PN EP352710-A.  
PD 31-JAN-1990.  
PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 227  
ID ADD05463 standard; protein; 476 AA.  
DE Desmodus rotundus urokinase protein.  
PN WO2003037363-A2.  
PD 08-MAY-2003.  
PA (PAIO-) PAION GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 228  
ID AAR05122 standard; protein; 477 AA.  
DE Bat-PA(H).  
PN EP352119-A.  
PD 24-JAN-1990.  
PA (MERI) MERCK & CO INC.  
PA (SCHD) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 229  
ID AAR06458 standard; protein; 477 AA.  
DE v-PA alpha2.  
PN EP383417-A.  
PD 22-AUG-1990.  
PA (SCHD) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 230  
ID AAR06457 standard; protein; 477 AA.  
DE v-PA alpha1.  
PN EP383417-A.  
PD 22-AUG-1990.  
PA (SCHD) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 231  
ID AAR09247 standard; protein; 482 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 910.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 237  
ID AAR09250 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 238  
ID AAR09246 standard; protein; 483 AA.  
DE t-PA variant d1-44, N184D, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 239  
ID AAR09248 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.

ID AAP81036 standard; protein; 479 AA.  
DE Modified tissue plasminogen activator lacking F and G region and with G-183 and S-186 substd for S and T resp.  
PN JP63230084-A.  
PD 26-SEP-1988.  
PA (EISA) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 232  
ID AAR05571 standard; protein; 479 AA.  
DE Glycosylated plasminogen activator.  
PN JP02049586-A.  
PD 19-FEB-1990.  
PA (KANF) KANEGAFUCHI CHEM KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 233  
ID AAR22714 standard; protein; 480 AA.  
DE t-PA variant MB1005.  
PN US5100666-A.  
PD 31-MAR-1992.  
PA (MONS) MONSANTO CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 234  
ID AAB08950 standard; protein; 480 AA.  
DE Human secreted protein sequence encoded by gene 22 SEQ ID NO:107.  
PN WO20017222-A1.  
PD 30-MAR-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 235  
ID AAP60613 standard; protein; 482 AA.  
DE Polypeptide with plasminogen activator activity.  
PN JP61139386-A.  
PD 26-JUN-1986.  
PA (TOYJ) TOYO SODA MFG CO LTD.  
PA (SAGA) SAGAMI CHEM RES CENTRE.  
PA (CENG) CENTRAL GLASS CO LTD.  
PA (HODO) HODOGAYA CHEM IND CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 236  
ID ADQ39247 standard; protein; 482 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 910.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 237  
ID AAR09250 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 238  
ID AAR09246 standard; protein; 483 AA.  
DE t-PA variant d1-44, N184D, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 239  
ID AAR09248 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 240
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210K, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 241
ID AAR09254 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 242
ID AAR09257 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 243
ID AAR09247 standard; protein; 483 AA.
DE t-PA variant d1-44, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 244
ID AAR09251 standard; protein; 483 AA.
DE t-PA variant d1-44, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 245
ID AAR09263 standard; protein; 483 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 246
ID AAR09252 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 247
ID AAR09233 standard; protein; 483 AA.
DE t-PA variant d1-44, I210K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 248
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, D184, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 249
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, K210, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 250
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, S184, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 251
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, K210, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 252
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, S184, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 253
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, R252, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 254
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 255
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N103, S184, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 256
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, K210, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 257
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44, N67, R252, E275, I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
```

ID	AAR70882 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,R252,E275).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 268			
ID	AAR70885 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,D184,E275,I277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 269			
ID	AAR70889 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,R252,E275,O277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 270			
ID	AAR70844 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N67,D184,E275).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 271			
ID	AAR70888 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 272			
ID	AAR70890 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,K210,E275,I277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 273			
ID	AAR70880 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N103,K213,E275).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 274			
ID	AAR70847 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 275			
ID	AAR70853 standard; protein; 483 AA.		
DE	Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275,I277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 276			
ID	ABW83143 standard; protein; 495 AA.		
DE	Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275,I277).		
PN	US5385732-A.		
PD	31-JAN-1995.		
PA	(GETH ) GENENTECH INC.	Mismatches: 0	
Best Local Similarity:	100.00%	Indels: 0	
Query Match:	3.64%		
RESULT 277			
ID	ABW83143 standard; protein; 495 AA.		

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3392.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 277  
ID ABM81142 standard; protein; 508 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3391.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 278  
ID ADH41501 standard; protein; 513 AA.  
DE Novel human protein NOV4a.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 279  
ID ADH41511 standard; protein; 513 AA.  
DE Novel human protein NOV4f.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 280  
ID ADH41517 standard; protein; 513 AA.  
DE Novel human protein NOV4i.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 281  
ID ADH41515 standard; protein; 513 AA.  
DE Novel human protein NOV4h.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 282  
ID ADH41507 standard; protein; 513 AA.  
DE Novel human protein NOV4d.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 283  
ID ADH41513 standard; protein; 513 AA.  
DE Novel human protein NOV4g.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 284  
ID ADH41505 standard; protein; 513 AA.  
DE Novel human protein NOV4c.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 285  
ID ADH41519 standard; protein; 513 AA.  
DE Novel human protein NOV4j.

PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 286  
ID ADH41509 standard; protein; 513 AA.  
DE Novel human protein NOV4e.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 287  
ID ADH41521 standard; protein; 513 AA.  
DE Novel human protein NOV4k.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 288  
ID AAP60614 standard; protein; 516 AA.  
DE Plasmid pDAP3 encoded sequence.  
PN JP61139386-A.  
PD 26-JUN-1986.  
PA (TOYJ) TOYO SODA MFG CO LTD.  
PA (SAGA) SAGAMI CHEM RES CENTRE.  
PA (CENG) CENTRAL GLASS CO LTD.  
PA (HODO) HODOGAYA CHEM IND CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 289  
ID AAP70257 standard; protein; 516 AA.  
DE Sequence of human tissue plasminogen activator (TPA) and leader.  
PN EP231883-A.  
PD 12-AUG-1987.  
PA (SAGA) SAGAMI CHEM RES CENTRE.  
PA (NIPS) NIPPON SODA CO.  
PA (CENG) CENTRAL GLASS CO LTD.  
PA (TOYJ) TOYO SODA MFG CO LTD.  
PA (NISC) NISSAN CHEM IND LTD.  
PA (NISC) NISSAN CHEMICAL INDS KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 290  
ID ADN03787 standard; protein; 516 AA.  
DE Antipsoaristic protein sequence #90.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 291  
ID ABM80985 standard; protein; 516 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 292  
ID ADQ39246 standard; protein; 516 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 293  
ID AAP91961 standard; protein; 518 AA.  
DE Sequence of des 1-44E275 t-PA mutant.  
PN WO8909266-A.

PD 05-OCT-1989.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 294  
 ID AAR09237 standard; protein; 518 AA.  
 DE t-PA deletion variant d297-305.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 295  
 ID AAR74684 standard; protein; 518 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by DPVDQ).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 296  
 ID AAR74681 standard; protein; 518 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by TSRNR).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 297  
 ID AAR74686 standard; protein; 518 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by DSSRW).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 298  
 ID AAR74679 standard; protein; 518 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by TIANK).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 299  
 ID AAR09236 standard; protein; 519 AA.  
 DE t-PA deletion variant d297-304.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 300  
 ID AAR74680 standard; protein; 519 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by KPIAEK).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 301  
 ID AAR74687 standard; protein; 519 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by DPHEAT).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 302  
 ID AAR68852 standard; protein; 519 AA.  
 DE Delta 55-62 tissue plasminogen activator.  
 PN US5376547-A.  
 PD 27-DEC-1994.

PA (AMHP ) AMERICAN HOME PROD CORP.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 303  
 ID AAR09235 standard; protein; 520 AA.  
 DE t-PA deletion variant d297-303.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 304  
 ID AAR74689 standard; protein; 520 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 305  
 ID AAR74688 standard; protein; 520 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by DNCRPPG).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 306  
 ID ADL00357 standard; protein; 520 AA.  
 DE Human tissue type plasminogen activator (h-TPA) mutant polypeptide.  
 PN CN1397564-A.  
 PD 19-FEB-2003.  
 PA (LIBB/) LI B.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 307  
 ID AAP50400 standard; protein; 521 AA.  
 DE TPA- (13-527).  
 PN JP60041697-A.  
 PD 05-MAR-1985.  
 PA (ASAH ) ASAH CHEM IND CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 308  
 ID AAR09242 standard; protein; 521 AA.  
 DE t-PA deletion variant d300-305.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 309  
 ID AAR09234 standard; protein; 521 AA.  
 DE t-PA deletion variant d297-302.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 310  
 ID AAR74682 standard; protein; 521 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHTSVQT).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 311  
 ID AAR74678 standard; protein; 521 AA.  
 DE t-PA mutetin (N117Q, N184Q, delta 296-302, 44-50 replaced by ESKPEAE).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 312  
 ID AAR09241 standard; protein; 522 AA.  
 DE t-PA deletion variant d300-304.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 313  
 ID AAR09233 standard; protein; 522 AA.  
 DE t-PA deletion variant d297-301.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 314  
 ID AAR13921 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with H432A and R434A substns.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 315  
 ID AAR13918 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with K416A, H417A and E418A substns.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 316  
 ID AAR14486 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with Y67N substitution.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 317  
 ID AAR13917 standard; peptide; 522 AA.  
 DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A substitutions.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 318  
 ID AAR13919 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 319  
 ID AAR13920 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with R339A and R342A substns.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 320  
 ID AAR74685 standard; protein; 522 AA.  
 DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QPLQTPSS).  
 PN CN1082111-A.  
 PD 16-FEB-1994.

PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 321  
 ID AAR74683 standard; protein; 522 AA.  
 DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by YAYSQRDQ).  
 PN CN1082111-A.  
 PD 16-FEB-1994.  
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 322  
 ID AAR09232 standard; protein; 523 AA.  
 DE t-PA deletion variant d297-300.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 323  
 ID AAR09240 standard; protein; 523 AA.  
 DE t-PA deletion variant d300-303.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 324  
 ID AAP82584 standard; protein; 524 AA.  
 DE Modified tissue plasminogen activator lacking the G region and with G-183 DE and S-186 substd for S and T resp.  
 PN JP63230084-A.  
 PD 26-SEP-1988.  
 PA (EISA ) EISAI CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 325  
 ID AAP82585 standard; protein; 524 AA.  
 DE Modified tissue plasminogen activator lacking F and G region and with S- DE 119 substd for M.  
 PN JP63230084-A.  
 PD 26-SEP-1988.  
 PA (EISA ) EISAI CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 326  
 ID AAR09231 standard; protein; 524 AA.  
 DE t-PA deletion variant d297-299.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 327  
 ID AAR09239 standard; protein; 524 AA.  
 DE t-PA deletion variant d300-302.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 328  
 ID AAR99136 standard; protein; 524 AA.  
 DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
 PN US5501853-A.  
 PD 26-MAR-1996.  
 PA (BEHR ) BEHRINGWERKE AG.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 329  
 ID AAR99138 standard; protein; 524 AA.  
 DE Mutant human tissue plasminogen activator for fibrin clot lysis.

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PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 330  
ID AAR99134 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 331  
ID AAR99137 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 332  
ID AAR99132 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 333  
ID AAR99135 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 334  
ID AAR99133 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 335  
ID AAR99131 standard; protein; 524 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 336  
ID AAP90175 standard; peptide; 525 AA.  
DE Tissue plasminogen activator mutant 2K2.  
PN W08907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 337  
ID AAP93540 standard; protein; 525 AA.  
DE Tissue plasminogen activator (t-PA) variant MB1018.  
PN EF311589-A.  
PD 12-APR-1989.

PA (MONS ) MONSANTO CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 338  
ID AAR09230 standard; protein; 525 AA.  
DE t-PA deletion variant d297-298.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 339  
ID AAR09245 standard; protein; 525 AA.  
DE t-PA deletion variant d297, d305.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 340  
ID AAR09238 standard; protein; 525 AA.  
DE t-PA deletion variant d300-301.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 341  
ID AAR09244 standard; protein; 525 AA.  
DE t-PA deletion variant d297, d300.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 342  
ID AAR09243 standard; protein; 525 AA.  
DE t-PA deletion variant d304-305.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 343  
ID AAR09222 standard; protein; 526 AA.  
DE t-PA deletion variant d298.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 344  
ID AAR09229 standard; protein; 526 AA.  
DE t-PA deletion variant d305.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 345  
ID AAR09224 standard; protein; 526 AA.  
DE t-PA deletion variant d300.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Indels: 0  
Query Match:  
RESULT 346  
ID AAR09221 standard; protein; 526 AA.  
DE t-PA deletion variant d297.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.



Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 347  
ID AAR09223 standard; protein; 526 AA.  
DE t-PA deletion variant d299.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 348  
ID AAR09225 standard; protein; 526 AA.  
DE t-PA deletion variant d301.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 349  
ID AAR09226 standard; protein; 526 AA.  
DE t-PA deletion variant d302.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 350  
ID AAR09227 standard; protein; 526 AA.  
DE t-PA deletion variant d303.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 351  
ID AAR09228 standard; protein; 526 AA.  
DE t-PA deletion variant d304.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 352  
ID AAR09229 standard; protein; 527 AA.  
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted  
DE or replaced and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GEMY ) GENETICS INST INC.  
PA (LARS ) LARSEN G R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 353  
ID AAP1747 standard; protein; 527 AA.  
DE Gln(117)-substituted tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 354  
ID AAP1748 standard; protein; 527 AA.  
DE Tissue plasminogen activator substituted at positions 117 and 119.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 355  
ID AAP1749 standard; protein; 527 AA.  
DE Tissue plasminogen activator substituted at positions 117 and 118.  
PN EP238304-A.  
PD 23-SEP-1987.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 356  
ID AAP1750 standard; protein; 527 AA.  
DE Tissue plasminogen activator substituted at positions 117 and 275.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 357  
ID AAP70168 standard; protein; 527 AA.  
DE Sequence of wild-type human tissue plasminogen activator (t-PA) from Hela  
DE cells.  
PN EP225286-A.  
PD 10-JUN-1987.  
PA (CIBA ) CIBA GEIGY AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 358  
ID AAP91683 standard; protein; 527 AA.  
DE Sequence of tissue plasminogen activator (tPA).  
PN WO8911531-A.  
PD 30-NOV-1989.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 359  
ID AAR04186 standard; protein; 527 AA.  
DE Plasminogen activator.  
PN EP365468-A.  
PD 25-APR-1990.  
PA (CIBA ) CIBA GEIGY AG.  
PA (UCPG-) UCP GEN-PHARMA AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 360  
ID AAR05806 standard; protein; 527 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 361  
ID AAR06236 standard; protein; 527 AA.  
DE Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 362  
ID AAR05489 standard; protein; 527 AA.  
DE tPA024 precursor protein.  
PN EP373896-A.  
PD 20-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
PA (YAMA ) NIPPON STEEL CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 363  
ID AAR05488 standard; protein; 527 AA.  
DE tPA024 precursor protein.  
PN EP373896-A.  
PD 20-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
PA (YAMA ) NIPPON STEEL CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 364

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ID AAR09266 standard; protein; 527 AA.
DE t-PA variant R267A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 365
ID AAR09268 standard; protein; 527 AA.
DE t-PA variant K296A, H297A, R298A, R299A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 366
ID AAR09269 standard; protein; 527 AA.
DE t-PA variant E303A, R304A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 367
ID AAR09277 standard; protein; 527 AA.
DE t-PA variant E426A, R427A, K429A, E430A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 368
ID AAR09255 standard; protein; 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 369
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 370
ID AAR09276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 371
ID AAR09256 standard; protein; 527 AA.
DE t-PA variant I210R, G211A, K212R, V213R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 372
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 373
ID AAR09271 standard; protein; 527 AA.
DE t-PA variant R339A, R342A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 374
ID AAR09275 standard; protein; 527 AA.
DE t-PA variant E410A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 375
ID AAR09274 standard; protein; 527 AA.
DE t-PA variant E408A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 376
ID AAR09272 standard; protein; 527 AA.
DE t-PA variant E347A, E348A, E349A, K351A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 377
ID AAR09281 standard; protein; 527 AA.
DE t-PA variant R449A, D453A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 378
ID AAR09215 standard; protein; 527 AA.
DE t-PA variant F305 H, T, N, K, R, Q.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 379
ID AAR09273 standard; protein; 527 AA.
DE t-PA variant D364A, D365A, D366A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 380
ID AAR09262 standard; protein; 527 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 381
ID AAR09280 standard; protein; 527 AA.
DE t-PA variant H445A, R449A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 382
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
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PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 383  
ID AAR09279 standard; protein; 527 AA.  
DE t-PA variant R462A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 384  
ID AAR09282 standard; protein; 527 AA.  
DE t-PA variant D460A, R462A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 385  
ID AAR11343 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #2.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 386  
ID AAR11342 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #1.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 387  
ID AAR11346 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #4.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 388  
ID AAR11347 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #5.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 389  
ID AAR11801 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #1.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 390  
ID AAR11345 standard; protein; 527 AA.  
DE Tissue plasminogen activator derivative #3.  
PN EP420502-A.  
PD 03-APR-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
PA (YAHA/) YAHARA H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 391  
ID AAR13911 standard; protein; 527 AA.  
DE T-PA deriv. (II).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 392  
ID AAR13914 standard; protein; 527 AA.  
DE T-PA deriv. (V).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 393  
ID AAR13912 standard; protein; 527 AA.  
DE T-PA deriv. (III).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 394  
ID AAR13910 standard; protein; 527 AA.  
DE T-PA deriv. (I).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 395  
ID AAR13913 standard; protein; 527 AA.  
DE T-PA deriv. (IV).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 396  
ID AAR21594 standard; protein; 527 AA.  
DE tPA variant - D95A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 397  
ID AAR21599 standard; protein; 527 AA.  
DE tPA variant - N117Q, D236A, D238A, K240A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 398  
ID AAR21600 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, T103N.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 399  
ID AAR21598 standard; protein; 527 AA.  
DE tPA variant - T103N, D236A, D238A, K240A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 3.64% Indels: 0
RESULT 400
ID AAR21593 standard; protein; 527 AA.
DE tPA variant - E94A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 401
ID AAR21596 standard; protein; 527 AA.
DE tPA variant - E94A, D95A, N117Q.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 402
ID AAR21595 standard; protein; 527 AA.
DE tPA variant - D95G.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 403
ID AAR21597 standard; protein; 527 AA.
DE tPA variant - E94A, D95A, D236A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 404
ID AAR21592 standard; protein; 527 AA.
DE tPA variant - generic form.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 405
ID AAR22620 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 406
ID AAR22619 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 407
ID AAR22617 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 408
ID AAR22621 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 409
ID AAR22618 standard; protein; 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 410
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 411
ID AAR20215 standard; protein; 527 AA.
DE R462E t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 412
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 413
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 414
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 415
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 416
ID AAR20223 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 417
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 418
ID AAR20216 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
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ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 419
ID AAR44808 standard; protein; 527 AA.
DE Human tPA variant N50.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 420
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 421
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 422
ID AAR44810 standard; protein; 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 423
ID AAR44816 standard; protein; 527 AA.
DE Human tPA variant (N67, N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 424
ID AAR44813 standard; protein; 527 AA.
DE Human tPA variant (N105, S107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 425
ID AAR44815 standard; protein; 527 AA.
DE Human tPA variant (N67, A197, A198, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 426
ID AAR44812 standard; protein; 527 AA.
DE Human tPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 427
ID AAR44817 standard; protein; 527 AA.
DE Human tPA variant (N67, A197, A198, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 428
ID AAR44814 standard; protein; 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 429
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60, N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 430
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60, N67, N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 431
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103, A460, A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 432
ID AAR70863 standard; protein; 527 AA.
DE Human t-PA variant (N67, A364, A365, A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 433
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67, A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 434
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103, A432, A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 435
ID AAR70864 standard; protein; 527 AA.
DE Human t-PA variant (N67, A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 436
ID AAR70871 standard; protein; 527 AA.
DE Human t-PA variant (N67, A449, A453).
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PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 437
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 438
ID AAR70866 standard; protein; 527 AA.
DE Human t-PA variant (N67,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 439
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 440
ID AAR70896 standard; protein; 527 AA.
DE Human t-PA variant (N103,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 441
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 442
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 443
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 444
ID AAR70858 standard; protein; 527 AA.
DE Human t-PA variant (N67,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 445
ID AAR70861 standard; protein; 527 AA.
DE Human t-PA variant (N67,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 446
ID AAR70897 standard; protein; 527 AA.
DE Human t-PA variant (N103,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 447
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 448
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 449
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 450
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 451
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 452
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 453
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 454
ID AAR70899 standard; protein; 527 AA.
DE Human t-PA variant (N103,A408).
PN US5385732-A.
PD 31-JAN-1995.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 455
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 456
ID AAR70862 standard; protein; 527 AA.
DE Human t-PA variant (N67,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 457
ID AAR70870 standard; protein; 527 AA.
DE Human t-PA variant (N67,A445,A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 458
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 459
ID AAR70856 standard; protein; 527 AA.
DE Human t-PA variant (N67,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 460
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 461
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 462
ID AAR70905 standard; protein; 527 AA.
DE Human t-PA variant (N103,A445,A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 463
ID AAR70902 standard; protein; 527 AA.
DE Human t-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 464
ID AAR70867 standard; protein; 527 AA.
DE Human t-PA variant (N67,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 465
ID AAR70869 standard; protein; 527 AA.
DE Human t-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 466
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 467
ID AAR99130 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 468
ID AAR99125 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 469
ID AAR99126 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 470
ID AAR99128 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 471
ID AAR99129 standard; protein; 527 AA.
DE Mutant human tissue plasminogen activator for fibrin clot lysis.
PN US5501853-A.
PD 26-MAR-1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 472
ID AAR99124 standard; protein; 527 AA.
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DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGERWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 473  
ID AAR99127 standard; protein; 527 AA.  
DE Mutant human tissue plasminogen activator for fibrin clot lysis.  
PN US5501853-A.  
PD 26-MAR-1996.  
PA (BEHW ) BEHRINGERWERKE AG.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 474  
ID AAW57779 standard; protein; 527 AA.  
DE R275E,H417E human tissue-type plasminogen activator protein mutant.  
PN WO9821320-A2.  
PD 22-MAY-1998.  
PA (SCRI ) SCRIPPS RES INST.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 475  
ID AAW57778 standard; protein; 527 AA.  
DE R275E,H417D human tissue-type plasminogen activator protein mutant.  
PN WO9821320-A2.  
PD 22-MAY-1998.  
PA (SCRI ) SCRIPPS RES INST.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 476  
ID AAW57780 standard; protein; 527 AA.  
DE R275E,K429Y human tissue-type plasminogen activator protein mutant.  
PN WO9821320-A2.  
PD 22-MAY-1998.  
PA (SCRI ) SCRIPPS RES INST.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 477  
ID AAW45907 standard; peptide; 527 AA.  
DE Single chain form of the intact t-PA molecule.  
PN WO9802454-A2.  
PD 22-JAN-1998.  
PA (ADPR-) ADPROTECH PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 478  
ID AAE24190 standard; protein; 527 AA.  
DE Human tissue plasminogen activator (tPA) protein.  
PN WO200240696-A2.  
PD 23-MAY-2002.  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 479  
ID AAG79362 standard; protein; 527 AA.  
DE Human tissue plasminogen activator.  
PN WO200243747-A2.  
PD 06-JUN-2002.  
PA (ISIS-) ISIS INNOVATION LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 480  
ID AAE25044 standard; protein; 527 AA.  
DE Human tissue plasminogen activator (tPA) protein.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 481

ID ADL92126 standard; protein; 527 AA.  
DE Alteplase protein sequence.  
PN WO200309862-A1.  
PD 04-DEC-2003.  
PA (NANO-) APPLIED NANOSYSTEMS BV.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 482  
ID AAP71451 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 483  
ID AAP71449 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 484  
ID AAP71450 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 485  
ID AAP90171 standard; peptide; 528 AA.  
DE Tissue plasminogen activator mutant 2K1 1K2.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 486  
ID AAR07033 standard; protein; 528 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 487  
ID AAR09218 standard; protein; 528 AA.  
DE t-PA insertion variant i305 H, T, N, K, R, Q.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 488  
ID AAR09216 standard; protein; 528 AA.  
DE t-PA insertion variant i304 H, T, N, K, R, Q.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 489  
ID AAR25435 standard; protein; 528 AA.  
DE T-PA variant R299D.  
PN WO9211377-A1.  
PD 09-JUL-1992.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 490



ID AAR68853 standard; protein; 528 AA.  
DE Bifibronection domain-delta 52-94-tissue plasminogen activator.  
PN US5376547-A.  
PD 27-DEC-1994.  
PA (AMHP ) AMERICAN HOME PROD CORP. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 491  
ID AAR092117 standard; protein; 529 AA.  
DE t-PA insertion variant 1304 HH.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 492  
ID AAR09220 standard; protein; 529 AA.  
DE t-PA insertion variant 1304H, 1305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 493  
ID AAR09219 standard; protein; 529 AA.  
DE t-PA insertion variant 1305 HH.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 494  
ID AAP61007 standard; protein; 530 AA.  
DE Sequence of tissue plasminogen activator (TPA) encoded by PUCH.  
PN DE3537176-A.  
PD 10-JUL-1986.  
PA (ZYMO ) ZYMOGENETICS INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 495  
ID AAP70882 standard; protein; 530 AA.  
DE Thrombolytic protein 1-19-1-21 having t-PA activity, deleted or replaced  
DE R275 is and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 496  
ID AAP71659 standard; protein; 530 AA.  
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced  
DE and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 497  
ID AAP70879 standard; protein; 530 AA.  
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted  
DE or replaced.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 498  
ID AAP70881 standard; protein; 530 AA.  
DE Thrombolytic protein 1-12-1-18 having t-PA activity, deleted or replaced  
DE R275 is and containing a modified N-linked glycosylation site.

PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 499  
ID AAP70449 standard; protein; 530 AA.  
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen  
DE activator (tPA).  
PN WO8705934-A.  
PD 08-OCT-1987.  
PA (CREA ) CREA R. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 500  
ID AAP92277 standard; protein; 530 AA.  
DE Sequence of modified tPA-type thrombolytic proteins.  
PN WO8810119-A.  
PD 29-DEC-1988.  
PA (GENY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 501  
ID AAP60700 standard; protein; 531 AA.  
DE Sequence of tissue plasminogen activator (t-PA) encoded by plasmid  
DE PTPA25.  
PN WO8601538-A.  
PD 13-MAR-1986.  
PA (BIOJ ) BIOGEN NV. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 502  
ID AAR07034 standard; protein; 531 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 503  
ID AAP90180 standard; peptide; 534 AA.  
DE Tissue plasminogen activator mutant Ult.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE ) INTEG GENETICS INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 504  
ID AAR11661 standard; protein; 537 AA.  
DE Tissue plasminogen activator deriv.  
PN JP03065184-A.  
PD 20-MAR-1991.  
PA (KANF ) KANEGAFUCHI CHEM KK. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 505  
ID AAR12846 standard; protein; 539 AA.  
DE t-PA growth domain deletion mutant.  
PN JP03130077-A.  
PD 03-JUN-1991.  
PA (KANF ) KANEGAFUCHI CHEM KK. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%  
RESULT 506  
ID AAP71745 standard; protein; 549 AA.  
DE des(Cys51-Asp87)t-PA with extra finger domain.  
PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC ) BEECHAM GROUP PLC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.64%

Result	ID	Standard	Protein	AA	Best Local Similarity	Query Match	Mismatches	Indels
RESULT 507	ID	AA111662 standard	protein	552 AA				
DE	DE	Tissue plasminogen activator deriv.						
PN	PN	JP03065184-A						
PD	PD	20-MAR-1991						
PA	PA	(KANF) KANEGAFUCHI CHEM KK.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 508	ID	AA06238 standard	protein	555 AA				
DE	DE	Novel mutant tissue plasminogen activator (tPA) encoded by plasmid						
PN	PN	EP379890-A						
PD	PD	01-AUG-1990						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 509	ID	AA23805 standard	protein	555 AA				
DE	DE	t-PA (Del 296-302) mutant						
PN	PN	WO9206203-A						
PD	PD	16-APR-1992						
PA	PA	(TEXA) UNIV TEXAS SYSTEM.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 510	ID	AA13148 standard	protein	556 AA				
DE	DE	T-PA variant contg. fibronectin for thrombosis lysis (2).						
PN	PN	JP03061482-A						
PD	PD	18-MAR-1991						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 511	ID	AA13020 standard	protein	557 AA				
DE	DE	T-PA variant contg. fibronectin for thrombosis lysis (4).						
PN	PN	JP03061482-A						
PD	PD	18-MAR-1991						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 512	ID	AA13149 standard	protein	557 AA				
DE	DE	T-PA variant contg. fibronectin for thrombosis lysis (4).						
PN	PN	JP03061482-A						
PD	PD	18-MAR-1991						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 513	ID	AA13153 standard	protein	558 AA				
DE	DE	T-PA with -ve charged finger and/or kringle domain (8).						
PN	PN	JP03061483-A						
PD	PD	18-MAR-1991						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 514	ID	AA13150 standard	protein	558 AA				
DE	DE	T-PA with -ve charged finger and/or kringle domain (3).						
PN	PN	JP03061483-A						
PD	PD	18-MAR-1991						
PA	PA	(FUJI) FUJISAWA PHARM CO LTD.						
Best Local Similarity		100.00%						
Query Match		3.64%						
RESULT 515	ID	AA13161 standard	protein	559 AA				
DE	DE	Tissue plasminogen activator analogue.						
PN	PN	EP293934-A						
PD	PD	07-DEC-1988</						

ID AAR96222 standard; protein; 559 AA.  
 DE Novel plasminogen activator.  
 PN US5504001-A.  
 PD 02-APR-1996.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 525

ID AAR96223 standard; protein; 559 AA.  
 DE Novel plasminogen activator.  
 PN US5504001-A.  
 PD 02-APR-1996.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 526

ID AAW23368 standard; protein; 559 AA.  
 DE Human tissue plasminogen activator deletion mutant.  
 PN US5656269-A.  
 PD 12-AUG-1997.  
 PA (CHIR) CHIRON CORP.  
 PA (BEHW) BEHRINGERWERKE AG.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 527

ID ABB57034 standard; protein; 559 AA.  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:41.  
 PN WO20018188-A2.  
 PD 22-NOV-2001.  
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 528

ID AAR12341 standard; protein; 560 AA.  
 DE T-PA variant contg. fibronectin for thrombosis lysis (3).  
 PN JP03061482-A.  
 PD 18-MAR-1991.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 529

ID AAP50219 standard; protein; 561 AA.  
 DE Tissue plasminogen activator encoded by cDNA clone.  
 PN EP143081-A.  
 PD 29-MAY-1985.  
 PA (CIBA) CIBA GEIGY AG.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 530

ID AAP70020 standard; protein; 561 AA.  
 DE Sequence of tissue plasminogen activator (tPA).  
 PN EP242836-A.  
 PD 28-OCT-1987.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 531

ID AAR12342 standard; protein; 561 AA.  
 DE T-PA with -ve charged finger and/or kringle domain (1).  
 PN JP03061483-A.  
 PD 18-MAR-1991.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 532

ID AAR12367 standard; protein; 561 AA.  
 DE T-PA with -ve charged finger and/or kringle domain (7).  
 PN JP03061483-A.  
 PD 18-MAR-1991.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 533

ID AAP30001 standard; protein; 562 AA.  
 DE Sequence of full length tissue plasminogen activator (t-Pa).  
 PN EP93619-A.  
 PD 09-NOV-1983.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 534

ID AAP50342 standard; protein; 562 AA.  
 DE Human tPA.  
 PN DK8406107-A.  
 PD 16-AUG-1985.  
 PA (GEMY) GENETICS INST INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 535

ID AAP60790 standard; protein; 562 AA.  
 DE Sequence of human pre-tissue plasminogen activator (pre-t-Pa).  
 PN GB2173804-A.  
 PD 22-OCT-1986.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 536

ID AAP60810 standard; protein; 562 AA.  
 DE Sequence of modified human tissue plasminogen activator (t-Pa).  
 PN FR2581652-A.  
 PD 14-NOV-1986.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 537

ID AAP60214 standard; protein; 562 AA.  
 DE Sequence of active human uterine tissue plasminogen activator (UTPA).  
 PN EP178105-A.  
 PD 16-APR-1986.  
 PA (INTE-) INTEG GENETICS INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 538

ID AAP70285 standard; protein; 562 AA.  
 DE Sequence encoded by human tissue plasminogen activator (t-Pa) cDNA clone.  
 PN EP236209-A.  
 PD 09-SEP-1987.  
 PA (GENE-) GENETICA.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 539

ID AAP81913 standard; protein; 562 AA.  
 DE Tissue plasminogen activator encoded by pEMpl-tPA.  
 PN WO8800242-A.  
 PD 14-JAN-1988.  
 PA (DAMO-) DAMON BIOTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 540

ID AAP80655 standard; protein; 562 AA.  
 DE Tissue plasminogen activator analogue.  
 PN EP293934-A.  
 PD 07-DEC-1988.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PA (NOVO) NOVO IND AS.  
 PA (EISA) EISA CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 541

ID AAP80656 standard; protein; 562 AA.  
 DE Tissue plasminogen activator analogue.  
 PN EP293934-A.  
 PD 07-DEC-1988.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PA (NOVO) NOVO IND AS.  
 PA (EISA) EISA CO LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 RESULT 542

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 542  
ID AAP94380 standard; protein; 562 AA.  
DE Amino acid sequence of tissue plasminogen activator (t-PA) protein.  
PN AU8817430-A.  
PD 08-DEC-1988.  
PA (NOVO ) NOVO IND AS.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (EISA ) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 543  
ID AAP82582 standard; protein; 562 AA.  
DE Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd  
DE for NGT.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (EISA ) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 544  
ID AAP82580 standard; protein; 562 AA.  
DE Tissue plasminogen activator with G-183 and S-186 substd for S and T.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (EISA ) EISAI CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 545  
ID AAP94406 standard; protein; 562 AA.  
DE Sequence encoded by native tPA of plasmid pST112.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 546  
ID AAP93716 standard; protein; 562 AA.  
DE Human melanoma t-PA encoded by plasmid pKG12.  
PN EP237066-A.  
PD 28-DEC-1988.  
PA (KABI ) KABIGEN AB.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 547  
ID AAP90916 standard; protein; 562 AA.  
DE Human tissue plasminogen activator.  
PN JP01174388-A.  
PD 10-JUL-1989.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 548  
ID AAP94238 standard; protein; 562 AA.  
DE Human tissue plasminogen activator (t-PA) gene.  
PN WO8900197-A.  
PD 12-JAN-1989.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 549  
ID AAR07079 standard; protein; 562 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 550  
ID AAR09287 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).

PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 551  
ID AAR09288 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 552  
ID AAR09286 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 553  
ID AAR09289 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT12 (Asp 67, Thr 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 554  
ID AAR09290 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue GP6 (Leu 66, Asp 67, Thr 68, Gln 117).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 555  
ID AAR05388 standard; protein; 562 AA.  
DE Thrombolytic protein.  
PN JP02119776-A.  
PD 07-MAY-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 556  
ID AAR09284 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (tPA) mutant Thr 478.  
PN WO8912680-A.  
PD 28-DEC-1989.  
PA (UNIW ) UNIV WASHINGTON.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 557  
ID AAR06237 standard; protein; 562 AA.  
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 558  
ID AAR04700 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S  
DE with altered residues 419 and 420.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0  
RESULT 559  
ID AAR04701 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with  
DE altered residue 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 560  
ID AAR04702 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S; K419S  
DE with altered residues 87 and 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 561  
ID AAR04699 standard; protein; 562 AA.  
DE Native tissue plasminogen activator (t-PA).  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 562  
ID AAR13727 standard; protein; 562 AA.  
DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.  
PN US041376-A.  
PD 20-AUG-1991.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 563  
ID AAR13441 standard; protein; 562 AA.  
DE MB1023 t-PA variant.  
PN US037752-A.  
PD 06-AUG-1991.  
PA (MONS ) MONSANTO CO.  
PA (MONS ) MONSANTO CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 564  
ID AAR13442 standard; protein; 562 AA.  
DE MB1083 t-PA variant with longer half-life.  
PN US037752-A.  
PD 06-AUG-1991.  
PA (MONS ) MONSANTO CO.  
PA (MONS ) MONSANTO CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 565  
ID AAR12343 standard; protein; 562 AA.  
DE T-PA with -ve charged finger and/or kringle domain (2).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 566  
ID AAR12366 standard; protein; 562 AA.  
DE T-PA with -ve charged finger and/or kringle domain (5).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 567  
ID AAR12425 standard; protein; 562 AA.

DE T-PA variant having Lys416 substitution (5).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 568  
ID AAR12423 standard; protein; 562 AA.  
DE T-PA variant having Lys416 substitution (1).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 569  
ID AAR12847 standard; protein; 562 AA.  
DE T-PA Kringle 1 domain substitution mutant.  
PN JP03127987-A.  
PD 31-MAY-1991.  
PA (KANP ) KANEGAFUCHI CHEM KK.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 570  
ID AAR23802 standard; protein; 562 AA.  
DE Zymogen-like t-PA (Ser 292, His 305).  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 571  
ID AAR23809 standard; protein; 562 AA.  
DE t-PA (Glu 299) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 572  
ID AAR23803 standard; protein; 562 AA.  
DE t-PA (Ser 304) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 573  
ID AAR23808 standard; protein; 562 AA.  
DE t-PA (Glu 298) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 574  
ID AAR23801 standard; protein; 562 AA.  
DE Zymogen-like t-PA (His 305).  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 575  
ID AAR23811 standard; protein; 562 AA.  
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 576  
ID AAR23807 standard; protein; 562 AA.  
DE t-PA (Tyr 297) mutant.

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PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 577
ID AAR23806 standard; protein; 562 AA.
DE t-PA (Glu 296) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 578
ID AAR23810 standard; protein; 562 AA.
DE t-PA (Gly 301) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 579
ID AAR23804 standard; protein; 562 AA.
DE t-PA (Glu 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA ) UNIV TEXAS SYSTEM.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 580
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).
PN US5200340-A.
PD 06-APR-1993.
PA (ZYMO ) ZYMOGENETICS INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 581
ID AAR44834 standard; protein; 562 AA.
DE Human tPA (R129W).
PN JP05304992-A.
PD 19-NOV-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 582
ID AAR35399 standard; protein; 562 AA.
DE tPA7.
PN JP05076361-A.
PD 30-MAR-1993.
PA (TAKE ) TAKEDA CHEM IND LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 583
ID AAR38674 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA).
PN WO9312225-A1.
PD 24-JUN-1993.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 584
ID AAR41545 standard; protein; 562 AA.
DE Modified tPA WB1012 with two K2 kringle domains.
PN US5244676-A.
PD 14-SEP-1993.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 585
ID AAR36220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.

PD 02-APR-1996.
PA (ZYMO ) ZYMOGENETICS INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 586
ID AAW47536 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275E.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 587
ID AAW47537 standard; protein; 562 AA.
DE Tissue plasminogen activator variant I276P.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 588
ID AAW47535 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275G.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 589
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 590
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.
PA (CANG-) CANGENE CORP.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 591
ID AAM48426 standard; protein; 562 AA.
DE Tissue type plasminogen activator, tPA.
PN KR141262-B1.
PD 15-JUN-1998.
PA (GLDS ) LG CHEM LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 592
ID AAY99590 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator t-PA.
PN WO200032759-A1.
PD 08-JUN-2000.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 593
ID AAU97700 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-PA) protein sequence.
PN WO200232446-A2.
PD 25-APR-2002.
PA (PFIZ ) PFIZER LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
Mismatches: 0
Indels: 0
RESULT 594
ID AAE37130 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (tPA) protein.
PN WO2003033009-A2.
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PD 24-APR-2003.  
PA (OMNI-) OMNIO AB.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 595  
ID ABR55851 standard; protein; 562 AA.  
DE Human tissue-type plasminogen activator (TPA).  
PN WO2003031464-A2.  
PD 17-APR-2003.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 596  
ID ABUS7646 standard; protein; 562 AA.  
DE Differentially expressed breast cancer associated protein #33.  
PN US2002156263-A1.  
PD 24-OCT-2002.  
PA (CHEN/) CHEN H.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 597  
ID ADN95624 standard; protein; 562 AA.  
DE Human BEC/LEC-related protein sequence SeqID547.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 598  
ID ADN49698 standard; protein; 562 AA.  
DE Human tissue type plasminogen activator TPA protein SeqID 26.  
PN WO2004033651-A2.  
PD 22-APR-2004.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 599  
ID ADO28679 standard; protein; 562 AA.  
DE Human tPA protein SEQ ID NO:108.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 600  
ID ABM80983 standard; protein; 562 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 601  
ID ADQ39248 standard; protein; 562 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 602  
ID AAP70475 standard; protein; 564 AA.  
DE Sequence of tissue plasminogen (TPA) analogue.  
PN WO8703906-A.  
PD 02-JUL-1987.  
PA (UPJO) UPJOHN CO.  
PA (MARO/) MAROTTI K R.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 603  
ID AAR22664 standard; protein; 564 AA.  
DE tPA analogue KK2A.

PN US106741-A.  
PD 21-APR-1992.  
PA (UPJO) UPJOHN CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 604  
ID ADI21256 standard; protein; 568 AA.  
DE Novel human protein #231.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 605  
ID AAR07477 standard; protein; 570 AA.  
DE t-PA variant MB1023.  
PN US4963357-A.  
PD 16-OCT-1990.  
PA (MONS) MONSANTO CO.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 606  
ID AAP90169 standard; peptide; 571 AA.  
DE Tissue plasminogen activator mutant 2G.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 607  
ID AAP90168 standard; peptide; 580 AA.  
DE Tissue plasminogen activator mutant 2F.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 608  
ID AAP71741 standard; protein; 586 AA.  
DE t-PA with extra finger domain.  
PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 609  
ID AAP71744 standard; protein; 586 AA.  
DE des(Cys61-Asp87)t-PA with extra finger- and growth factor-domains.  
PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 610  
ID AAP90172 standard; peptide; 592 AA.  
DE Tissue plasminogen activator mutant 1K1 2K2.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 611  
ID AAP70059 standard; protein; 593 AA.  
DE Hybrid plasminogen activator (PA) contg. urokinase kringle (UKK) 1-131 and tissue plasminogen activator (tPA) 92-527.  
PN EP213794-A.  
PD 11-MAR-1987.  
PA (AMHP) AMERICAN HOME PROD CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 612  
ID AAP71743 standard; protein; 594 AA.  
DE Ile(277)t-PA with extra finger-domain.

PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 613  
ID AAR06239 standard; protein; 605 AA.  
DE Novel mutant tissue plasminogen activator (tPA) encoded by plasmid plgn  
DE delta GTPA.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 614  
ID AAM40056 standard; protein; 615 AA.  
DE Human polypeptide SEQ ID NO 3201.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 615  
ID ADA50545 standard; protein; 615 AA.  
DE Human factor XII.  
PN US2003073652-A1.  
PD 17-APR-2003.  
PA (POLL/) POLLARD H.  
PA (POLL/) POLLARD B.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 616  
ID ADN04180 standard; protein; 615 AA.  
DE Antipsoxic protein sequence #285.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 617  
ID ADM98382 standard; protein; 615 AA.  
DE Human factor XII protein.  
PN US200407538-A1.  
PD 22-APR-2004.  
PA (POLL/) POLLARD H.  
PA (POLL/) POLLARD B.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 618  
ID ABM80709 standard; protein; 615 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO36372, SEQ:1829.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 619  
ID AAU11271 standard; protein; 621 AA.  
DE Human coagulation factor XII (F12) variant polypeptide.  
PN WO200179228-A2.  
PD 25-OCT-2001.  
PA (GENA-) GENAISANCE PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 620  
ID AAU11270 standard; protein; 621 AA.  
DE Human coagulation factor XII (F12) polypeptide.  
PN WO200179228-A2.  
PD 25-OCT-2001.  
PA (GENA-) GENAISANCE PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 621

ID AAP71742 standard; protein; 623 AA.  
DE Ile(277)t-PA with extra finger- and extra growth factor-domains.  
PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 622  
ID AAP71740 standard; protein; 623 AA.  
DE t-PA with extra finger domain and extra growth factor domain.  
PN EP241210-A.  
PD 14-OCT-1987.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 623  
ID AAP70060 standard; protein; 650 AA.  
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator  
DE (tPA) 1-91, urokinase kringle (UKK) 50-131 and tPA 92-527.  
PN EP213794-A.  
PD 11-MAR-1987.  
PA (AMHP ) AMERICAN HOME PROD CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 624  
ID AAP70084 standard; protein; 650 AA.  
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator  
DE (tPA) 1-261, urokinase kringle (UKK) 50-131 and tPA 262-527.  
PN EP213794-A.  
PD 11-MAR-1987.  
PA (AMHP ) AMERICAN HOME PROD CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 625  
ID ADE85979 standard; protein; 650 AA.  
DE Human tissue urokinase plasminogen activator.  
PN WO2003087393-A2.  
PD 23-OCT-2003.  
PA (GLOB-) GLOBAL BIOTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 626  
ID AAE06934 standard; protein; 658 AA.  
DE Human membrane-type serine protease (MTSP) 4-S splice variant.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 627  
ID ADI10379 standard; protein; 658 AA.  
DE Human cell surface protease #5.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 628  
ID ADJ46903 standard; protein; 658 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #5.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 629  
ID AAP90173 standard; peptide; 680 AA.  
DE Tissue plasminogen activator mutant 2K1 2K2.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0



RESULT 630  
ID AAP90176 standard; peptide; 704 AA.  
DE Tissue plasminogen activator mutant S-N.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 631  
ID AAP90177 standard; peptide; 718 AA.  
DE Tissue plasminogen activator mutant OMS.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 632  
ID AAP90178 standard; peptide; 779 AA.  
DE Tissue plasminogen activator mutant 2 Prot 1 CV.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 633  
ID AAR06824 standard; protein; 780 AA.  
DE Thrombomodulin analogue / t-PA fusion protein.  
PN WO9010081-A.  
PD 07-SEP-1990.  
PA (CODO-) CODON.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 634  
ID AAP90179 standard; peptide; 794 AA.  
DE Tissue plasminogen activator mutant 2 Prot 2 CV.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 635  
ID ABP43952 standard; protein; 795 AA.  
DE Human PRO618.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 636  
ID ADI16874 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SeqID 410.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 637  
ID ADI16880 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SeqID 416.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 638  
ID AAY41710 standard; protein; 802 AA.  
DE Human PRO618 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 639  
ID AAB44266 standard; protein; 802 AA.  
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 640  
ID AAB24052 standard; protein; 802 AA.  
DE Human PRO618 protein sequence SEQ ID NO:24.  
PN WO200053754-A1.  
PD 14-SEP-2000.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 641  
ID AAE06933 standard; protein; 802 AA.  
DE Human membrane-type serine protease (MTSP) 4-L splice variant.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 642  
ID AAU82755 standard; protein; 802 AA.  
DE Amino acid sequence of novel human protease #54.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 643  
ID ABO25212 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US200305039-A1.  
PD 13-MAR-2003.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 644  
ID ABU72218 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 645  
ID ABU84898 standard; protein; 802 AA.  
DE Human secreted and transmembrane polypeptide PRO618.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 646  
ID ABU61096 standard; protein; 802 AA.  
DE Human PRO618 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 647  
ID ABU80365 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein PRO618.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 648  
ID ADA24708 standard; protein; 802 AA.

DE Novel human secreted and transmembrane protein PRO618.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 649  
ID ABO19667 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 650  
ID ADA12369 standard; protein; 802 AA.  
DE Human secreted/transmembrane polypeptide PRO618.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 651  
ID ABO19558 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane polypeptide #26.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 652  
ID ADB73675 standard; protein; 802 AA.  
DE Human PRO polypeptide #26.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 653  
ID ADB76391 standard; protein; 802 AA.  
DE Human PRO polypeptide #26.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 654  
ID ADC3817 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 655  
ID ADC61577 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 656  
ID ADC63541 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 657  
ID ADC66641 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003060406-A1.

PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 658  
ID ADC68765 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 659  
ID ADC62825 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 660  
ID ADC67890 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 661  
ID ADC41210 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 662  
ID ADC67265 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 663  
ID ADC62201 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 664  
ID ADC41834 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 665  
ID ADE49203 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 666  
ID ADE35257 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203434-A1.  
PD 30-OCT-2003.

PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match:	3.64%	Indels: 0	Query Match:	3.64%
RESULT 667			RESULT 676	
ID ADE16371 standard; protein; 802 AA.			ID ADE48503 standard; protein; 802 AA.	
DE Human secreted/transmembrane protein, PRO618.			DE Human secreted/transmembrane protein, PRO618.	
PN US2003203435-A1.			PN US2003104536-A1.	
PD 30-OCT-2003.			PD 05-JUN-2003.	
PA (GETH ) GENENTECH INC.			PA (GETH ) GENENTECH INC.	
Best Local Similarity: 100.00%	Mismatches: 0		Best Local Similarity: 100.00%	Mismatches: 0
Query Match:	3.64%	Indels: 0	Query Match:	3.64%
RESULT 668			RESULT 677	
ID ADD72986 standard; protein; 802 AA.			ID ADE89604 standard; protein; 802 AA.	
DE Human secreted/transmembrane protein, PRO618.			DE Human secreted/transmembrane protein, PRO618.	
PN US2003203436-A1.			PN US2003130181-A1.	
PD 30-OCT-2003.			PD 10-JUL-2003.	
PA (GETH ) GENENTECH INC.			PA (ASHK/) ASHKENAZI A J.	
Best Local Similarity: 100.00%	Mismatches: 0		PA (BAKE/) BAKER K P.	
Query Match:	3.64%	Indels: 0	PA (BOTS/) BOTSTEIN D.	
RESULT 669			PA (DESN/) DESNOYERS L.	
ID ADD72344 standard; protein; 802 AA.			PA (EATO/) EATON D L.	
DE Human secreted/transmembrane protein, PRO618.			PA (FERR/) FERRARA N.	
PN US2003194781-A1.			PA (FILV/) FILVAROFF E.	
PD 16-OCT-2003.			PA (FONG/) FONG S.	
PA (GETH ) GENENTECH INC.			PA (GAOW/) GAO W.	
Best Local Similarity: 100.00%	Mismatches: 0		PA (GERB/) GERBER H.	
Query Match:	3.64%	Indels: 0	PA (GERR/) GERRITSEN M E.	
RESULT 670			PA (GODD/) GODDARD A.	
ID ADE16995 standard; protein; 802 AA.			PA (GODO/) GODOWSKI P J.	
DE Human secreted/transmembrane protein, PRO618.			PA (GIRM/) GIRMALDI J C.	
PN US2003203433-A1.			PA (GURN/) GURNEY A L.	
PD 30-OCT-2003.			PA (HILL/) HILLAN K J.	
PA (GETH ) GENENTECH INC.			PA (KLJA/) KLJAVIN I J.	
Best Local Similarity: 100.00%	Mismatches: 0		PA (KUOS/) KUO S S.	
Query Match:	3.64%	Indels: 0	PA (NAPI/) NAPIER M A.	
RESULT 671			PA (PANJ/) PAN J.	
ID ADF47009 standard; protein; 802 AA.			PA (PAON/) PAONI N F.	
DE Human secreted/transmembrane protein, PRO618.			PA (ROIM/) ROY M A.	
PN US2003195333-A1.			PA (SHEL/) SHELTON D L.	
PD 16-OCT-2003.			PA (STEW/) STEWART T A.	
PA (GETH ) GENENTECH INC.			PA (TUMA/) TUMAS D.	
Best Local Similarity: 100.00%	Mismatches: 0		PA (WILL/) WILLIAMS P M.	
Query Match:	3.64%	Indels: 0	PA (WOOD/) WOOD W I.	
RESULT 672			Best Local Similarity: 100.00%	Mismatches: 0
ID ADG52766 standard; protein; 802 AA.			Query Match:	3.64%
DE Human secreted/transmembrane protein, PRO618.			RESULT 678	
PN US2003216561-A1.			ID ADF61244 standard; protein; 802 AA.	
PD 20-NOV-2003.			DE Human secreted/transmembrane protein, PRO618.	
PA (GETH ) GENENTECH INC.			PN US2003195345-A1.	
Best Local Similarity: 100.00%	Mismatches: 0		PD 16-OCT-2003.	
Query Match:	3.64%	Indels: 0	PA (GETH ) GENENTECH INC.	
RESULT 673			Best Local Similarity: 100.00%	Mismatches: 0
ID ADG60086 standard; protein; 802 AA.			Query Match:	3.64%
DE Human secreted/transmembrane protein, PRO618.			RESULT 679	
PN US2003206915-A1.			ID ADF39936 standard; protein; 802 AA.	
PD 06-NOV-2003.			DE Human secreted/transmembrane protein, PRO618.	
PA (GETH ) GENENTECH INC.			PN US2003198994-A1.	
Best Local Similarity: 100.00%	Mismatches: 0		PD 23-OCT-2003.	
Query Match:	3.64%	Indels: 0	PA (GETH ) GENENTECH INC.	
RESULT 674			Best Local Similarity: 100.00%	Mismatches: 0
ID ADI60846 standard; protein; 802 AA.			Query Match:	3.64%
DE Human secreted/transmembrane protein, PRO618.			RESULT 680	
PN US2003077700-A1.			ID ADF45732 standard; protein; 802 AA.	
PD 24-APR-2003.			DE Human secreted/transmembrane protein, PRO618.	
PA (GETH ) GENENTECH INC.			PN US2003195148-A1.	
Best Local Similarity: 100.00%	Mismatches: 0		PD 16-OCT-2003.	
Query Match:	3.64%	Indels: 0	PA (GETH ) GENENTECH INC.	
RESULT 675			Best Local Similarity: 100.00%	Mismatches: 0
ID ADI10377 standard; protein; 802 AA.			Query Match:	3.64%
DE Human cell surface protease #4.			RESULT 681	
PN WO200295007-A2.			ID ADF24128 standard; protein; 802 AA.	
PD 28-NOV-2002.			DE Human secreted/transmembrane protein, PRO618.	
PA (CORV-) CORVAS INT INC.			PN US2003204055-A1.	
			PD 30-OCT-2003.	

PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 682	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 682
ID ADF40560 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003199021-A1. PD 23-OCT-2003.	ID ADF34119 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003194410-A1. PD 16-OCT-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 683	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 683
ID ADF23504 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003203402-A1. PD 30-OCT-2003.	ID ADF46356 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003195344-A1. PD 16-OCT-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 684	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 684
ID ADF33487 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003194780-A1. PD 16-OCT-2003.	ID ADG50342 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003207803-A1. PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 685	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 685
ID ADF26954 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003199436-A1. PD 23-OCT-2003.	ID ADG49718 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003215905-A1. PD 20-NOV-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 686	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 686
ID ADF27590 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003199437-A1. PD 23-OCT-2003.	ID ADG51590 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003215908-A1. PD 20-NOV-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 687	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 687
ID ADF41184 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003199435-A1. PD 23-OCT-2003.	ID ADG49094 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003216305-A1. PD 20-NOV-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 688	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 688
ID ADF32863 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003211091-A1. PD 13-NOV-2003.	ID ADG48470 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003216560-A1. PD 20-NOV-2003.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 689	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 689
ID ADF25229 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003211092-A1. PD 13-NOV-2003.	ID ADG50966 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2004005312-A1. PD 08-JAN-2004.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 690	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 690
ID ADF26330 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2003199674-A1. PD 23-OCT-2003.	ID ADG58910 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO618. PD US2004005657-A1. PD 08-JAN-2004.
PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 691	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64% Indels: 0 Mismatches: 0 RESULT 691

Query Match: 3.64% Indels: 0

RESULT 700  
ID ADG2366 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 701  
ID ADH25391 standard; protein; 802 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 702  
ID ADJ46901 standard; protein; 802 AA.  
DE Human transmembrane serine protease (WTSP) polypeptide #4.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 703  
ID ADM17168 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 704  
ID ADL07002 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 705  
ID ADT91615 standard; protein; 802 AA.  
DE Human PRO618 protein sequence.  
PN AU2002317529-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 706  
ID AAR20013 standard; protein; 807 AA.  
DE PA mutant plg 1-541 [Arg298-299->Gln298-299] t-PA 262-527.  
PN WO9118989-A.  
PD 12-DEC-1991.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 707  
ID ABB98140 standard; protein; 863 AA.  
DE Human PMM incyte ID 7484157CD1.  
PN WO200246383-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 708  
ID ABG24246 standard; protein; 913 AA.  
DE Novel human diagnostic protein #24237.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 709  
ID ABUI2066 standard; protein; 922 AA.  
DE Human NOVI2b CG92293-02 protein SEQ ID 52.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 710  
ID ADR43718 standard; protein; 932 AA.  
DE Human protease PRTS-6, SEQ ID 6.  
PN WO200220736-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 711  
ID AAU82743 standard; protein; 970 AA.  
DE Amino acid sequence of novel human protease #42.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 712  
ID ABUI2065 standard; protein; 986 AA.  
DE Human NOVI2a CG92293-01 protein SEQ ID 50.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 713  
ID ABP60993 standard; protein; 1031 AA.  
DE Novel human protein. SEQ ID 80.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (GLAX ) GLAXO GROUP LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 714  
ID AAP80692 standard; protein; 1039 AA.  
DE Hybrid plasminogen/t-PA compound 2.  
PN EP292326-A.  
PD 23-NOV-1988.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 715  
ID AAP80691 standard; protein; 1087 AA.  
DE Hybrid plasminogen/t-PA compound 1.  
PN EP292326-A.  
PD 23-NOV-1988.  
PA (BEEC ) BEECHAM GROUP PLC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 716  
ID ABG14588 standard; protein; 1576 AA.  
DE Novel human diagnostic protein #14579.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

RESULT 717  
ID ABG07870 standard; protein; 1576 AA.  
DE Novel human diagnostic protein #7861.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0

Query Match: 3.64% Indels: 0  
RESULT 718  
ID ABG1987 standard; protein; 1576 AA.  
DE Novel human diagnostic protein #1987.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 719  
ID ABG10218 standard; protein; 1576 AA.  
DE Novel human diagnostic protein #10209.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
RESULT 720  
ID AAV72112 standard; peptide; 12 AA.  
DE Peptide fragment #12 related to human serine protease.  
PN WO20008247-A2.  
PD 16-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 721  
ID ABG31651 standard; peptide; 12 AA.  
DE Human serine protease serine active site domain.  
PN US2002119925-A1.  
PD 29-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 722  
ID AAE17932 standard; peptide; 12 AA.  
DE Human gene 4 encoded serine protease fragment #1.  
PN WO200198476-A1.  
PD 27-DEC-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 723  
ID ABB52232 standard; peptide; 18 AA.  
DE Human API-180 tryptic digest peptide #4.  
PN WO200175454-A2.  
PD 11-OCT-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
PA (PFIZ) PFIZER INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 724  
ID ABB52105 standard; peptide; 18 AA.  
DE Human API-26 tryptic digest peptide #3.  
PN WO200175454-A2.  
PD 11-OCT-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
PA (PFIZ) PFIZER INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 725  
ID ABR58948 standard; peptide; 18 AA.  
DE Alzheimer's Disease-associated protein isoform, API-26, SEQ ID 68.  
PN WO2003028543-A2.  
PD 10-APR-2003.  
PA (PFIZ) PFIZER PROD INC.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 726  
ID ADN31742 standard; peptide; 18 AA.  
DE Human Alzheimer's disease-API tryptic digest peptide - SEQ ID 68.  
PN EPI408333-A2.  
PD 14-APR-2004.

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PA (PFIZ) PFIZER PROD INC.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 727  
ID ADR72151 standard; peptide; 40 AA.  
DE Human kallikrein 15 splice form 3 peptide.  
PN US2004180380-A1.  
PD 16-SEP-2004.  
PA (ENGE-) ENGNEOS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 728  
ID ABB63477 standard; protein; 141 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17223.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 729  
ID AAU79393 standard; protein; 171 AA.  
DE Novel human kallikrein KLK15, splice variant #3.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 730  
ID ADN10933 standard; protein; 171 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 731  
ID AAU82735 standard; protein; 222 AA.  
DE Amino acid sequence of novel human protease #34.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 732  
ID AAB03862 standard; protein; 223 AA.  
DE Human neurosin amino acid sequence.  
PN WO20031284-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 733  
ID AAR89430 standard; protein; 232 AA.  
DE Trypsin-like enzyme.  
PN AU9527248-A.  
PD 08-FEB-1996.  
PA (TEIJ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 734  
ID AAY28591 standard; protein; 233 AA.  
DE Pig Factor D.  
PN WO9942133-A1.  
PD 26-AUG-1999.  
PA (TANO-) TANOX INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 735  
ID AAB01942 standard; protein; 233 AA.  
DE Human endotheliasin 1 protease domain.  
PN WO200136604-A2.  
PD 25-MAY-2001.

PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 736  
ID ADI10391 standard; protein; 233 AA.  
DE Human cell surface protease #11.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 737  
ID ADJ46915 standard; protein; 233 AA.  
DE Human transmembrane serine protease (MTSP)-related polypeptide #1.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 738  
ID AAB21310 standard; protein; 239 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 739  
ID ADA50482 standard; protein; 241 AA.  
DE Human protease SEQ ID NO:80.  
PN WO2003040393-A2.  
PD 15-MAY-2003.  
PA (DECO-) DECODE GENETICS EHF. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 740  
ID AAR44532 standard; protein; 244 AA.  
DE Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL ) LILLY & CO ELI. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 741  
ID AAW22985 standard; protein; 244 AA.  
DE Human serine protease 59 (SP59).  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR ) SUNTORY LTD. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 742  
ID AAW51006 standard; protein; 244 AA.  
DE Protease M, a novel serine protease.  
PN WO9811238-A2.  
PD 19-MAR-1998.  
PA (DAND ) DANA FARBBER CANCER INST INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 743  
ID AAB21323 standard; protein; 244 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 744  
ID ABG96357 standard; protein; 244 AA.  
DE Human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 745  
ID AAE37572 standard; protein; 244 AA.  
DE Human 2047 protein.  
PN WO2003037258-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 746  
ID ADB0567 standard; protein; 244 AA.  
DE Ovarian cancer-associated protein #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 747  
ID ADN39212 standard; protein; 244 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 748  
ID ADI39734 standard; protein; 244 AA.  
DE Human protease M (prom) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 749  
ID ADI37158 standard; protein; 244 AA.  
DE Human protease m (protm).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 750  
ID ADN04074 standard; protein; 244 AA.  
DE Antipsoxiatic protein sequence #232.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 751  
ID ADN29289 standard; protein; 244 AA.  
DE Human kallikrein 6 associated protein.  
PN US2004097452-A1.  
PD 20-MAY-2004.  
PA (ISIS-) ISIS PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 752  
ID ADQ89076 standard; protein; 244 AA.  
DE Human urological disorder related protein 2047 SEQ:28.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 753  
ID ADR72624 standard; protein; 244 AA.  
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL. Mismatches: 0  
Best Local Similarity: 100.00%

Query Match: 3.36% Indels: 0  
RESULT 754  
ID ADR72876 standard; protein; 244 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 755  
ID AAP90531 standard; protein; 256 AA.  
DE Hypodermin B of ATCC # 67613.  
PN EP326419-A.  
PD 02-AUG-1989.  
PA (USDA) US SEC OF AGRIC.  
PA (CODO-) CODON.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 756  
ID ABB67188 standard; protein; 256 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28356.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 757  
ID ABB71152 standard; protein; 256 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40248.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 758  
ID ABB69404 standard; protein; 258 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35004.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 759  
ID ABB61002 standard; protein; 260 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9798.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 760  
ID AAO23287 standard; protein; 261 AA.  
DE Culex pipiens pallens trypsin protein.  
PN CN1354253-A.  
PD 19-JUN-2002.  
PA (UYNA-) UNIV NANJING MEDICAL.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 761  
ID ABB64194 standard; protein; 262 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 19374.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 762  
ID ABB63475 standard; protein; 272 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17217.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0  
RESULT 763  
ID ADJ83072 standard; protein; 345 AA.  
DE Human protein which is similar to DEBC protein - SEQ ID 63.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO) ALSOBROOK J P.  
PA (TCHE) TCHERNEV V T.  
PA (LIUX) LIU X.  
PA (SPYT) SPYTEK K A.  
PA (ZERH) ZERHUSEN B D.  
PA (PATT) PATTURAJAN M.  
PA (LEPL) LEFLEY D M.  
PA (BURG) BURGESS C E.  
PA (SHIM) SHIMKETS R A.  
PA (GROS) GROSSE W M.  
PA (SZEK) SEKERES E S.  
PA (VERN) VERNET C A M.  
PA (LILL) LI L.  
PA (CASM) CASMAN S J.  
PA (BOLD) BOLDOG F L.  
PA (GORM) GORMAN L.  
PA (GANG) GANGOLLI E A.  
PA (FERN) FERNANDES E R.  
PA (RIEG) RIEGER D K.  
PA (EDIN) EDINGER S R.  
PA (GUNT) GUNTHER E.  
PA (MILL) MILLET I.  
PA (SCIO) SCIORE P.  
PA (ELLE) ELLERMAN K.  
PA (MACD) MACDOUGALL J R.  
PA (SMIT) SMITHSON G.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 764  
ID AAO21900 standard; protein; 407 AA.  
DE Homologous human protease protein.  
PN WO200226947-A2.  
PD 04-APR-2002.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 765  
ID ADG31219 standard; protein; 416 AA.  
DE Novel mouse protein #20.  
PN WO2003089644-A1.  
PD 30-OCT-2003.  
PA (RIKE) RIKEN KK.  
PA (DNAP-) DNAFORM KK.  
PA (MITU) MITSUBISHI CHEM CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 766  
ID ABB77356 standard; protein; 417 AA.  
DE Mouse AST SEQ ID NO 2.  
PN JP2002065266-A.  
PD 05-MAR-2002.  
PA (TEIJ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 767  
ID ABB06970 standard; protein; 417 AA.  
DE Bovine AST protein sequence SEQ ID NO:33.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 768  
ID ABB06965 standard; protein; 417 AA.  
DE Mouse airway specific trypsin-like protease protein SEQ ID NO:2.  
PN WO200218562-A1.  
PD 07-MAR-2002.



PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 769  
ID ABB06973 standard; protein; 417 AA.  
DE Hamster AST protein sequence SEQ ID NO:39.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 770  
ID AAR9435 standard; protein; 418 AA.  
DE Trypsin-like enzyme.  
PN AU9527248-A.  
PD 08-FEB-1996.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 771  
ID AAY29502 standard; protein; 418 AA.  
DE Human lung tumour protein L86S-46 predicted extended protein sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 772  
ID AAY29498 standard; protein; 418 AA.  
DE Human lung tumour protein L86S-46 predicted amino acid sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 773  
ID AAY29501 standard; protein; 418 AA.  
DE Human lung tumour protein L86S-36 predicted extended protein sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 774  
ID AAB44428 standard; protein; 418 AA.  
DE Human lung tumour-specific antigen encoded by cDNA #38.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 775  
ID AAB44438 standard; protein; 418 AA.  
DE Human lung tumour-specific antigen encoded by cDNA #49.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 776  
ID AAB44437 standard; protein; 418 AA.  
DE Human lung tumour-specific antigen encoded by cDNA #48.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 777  
ID AAE06941 standard; protein; 418 AA.  
DE Human airway trypsin-like protease (HAT) protein.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 778  
ID AAE13769 standard; protein; 418 AA.  
DE Human lung tumour-specific protein L86S-46.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 779  
ID AAE13778 standard; protein; 418 AA.  
DE Human lung tumour-specific protein L86S-36.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 780  
ID AAE13779 standard; protein; 418 AA.  
DE Human lung tumour-specific protein L86S-46.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 781  
ID ABB77355 standard; protein; 418 AA.  
DE Human AST SEQ ID NO 1.  
PN JP2002065266-A.  
PD 05-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 782  
ID AAU76372 standard; protein; 418 AA.  
DE Human airway trypsin protease protein sequence.  
PN WO200206455-A2.  
PD 24-JAN-2002.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 783  
ID ABB06964 standard; protein; 418 AA.  
DE Human airway specific trypsin-like protease protein SEQ ID NO:1.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 784  
ID ABB06968 standard; protein; 418 AA.  
DE Macaca fascicularis AST protein sequence SEQ ID NO:29.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 785  
ID ABB06971 standard; protein; 418 AA.  
DE Rabbit AST protein sequence SEQ ID NO:35.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 786  
ID ABB06972 standard; protein; 418 AA.  
DE Guinea pig AST protein sequence SEQ ID NO:37.  
PN WO200218562-A1.  
PD 07-MAR-2002.  
PA (TEIJ ) TEIJIN LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

Query Match:	3.36%	Indels:	0
RESULT 787			
ID AD66390 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 82.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 788			
ID AD66391 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 83.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 789			
ID AD66370 standard; protein; 418 AA.			
DE Human lung tumour-specific related protein, SEQ ID No 62.			
PN WO200292001-A2.			
PD 21-NOV-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 790			
ID ADE87644 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #31.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 791			
ID ADE87645 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #32.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 792			
ID ADE87624 standard; protein; 418 AA.			
DE Human lung tumour antigen polypeptide #22.			
PN US2003118599-A1.			
PD 26-JUN-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 793			
ID ADI10402 standard; protein; 418 AA.			
DE Human cell surface protease #17.			
PN WO200295007-A2.			
PD 28-NOV-2002.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 794			
ID ADJ83071 standard; protein; 418 AA.			
DE Human airway trypsin-like protease protein - SEQ ID 62.			
PN US2003170630-A1.			
PD 11-SEP-2003.			
PA (ALSO/) ALSOBROOK J P.			
PA (TCHE/) TCHERNEV V T.			
PA (LIUX/) LIU X.			
PA (SPYT/) SPYTEK K A.			
PA (ZERH/) ZERHUSEN B D.			
PA (PATT/) PATTURAJAN M.			
PA (LEPL/) LEPLEY D M.			
PA (BURG/) BURGESS C E.			
PA (SHIM/) SHIMKETS R A.			
PA (GROS/) GROSSE W M.			
PA (SZEK/) SZEKERES E S.			

PA (VERN/) VERNET C A M.			
PA (LILL/) LI L.			
PA (CASW/) CASMAN S J.			
PA (BOLD/) BOLDOG F L.			
PA (GORM/) GORMAN L.			
PA (GANG/) GANGOLLI E A.			
PA (PERN/) FERNANDES E R.			
PA (RIEG/) RIEGER D K.			
PA (EDIN/) EDINGER S R.			
PA (GUNT/) GUNTHER E.			
PA (MILL/) MILLET I.			
PA (SCIO/) SCIORE P.			
PA (ELLE/) ELLERMAN K.			
PA (MACD/) MACDOUGALL J R.			
PA (SMIT/) SMITHSON G.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 795			
ID ADJ46926 standard; protein; 418 AA.			
DE Human transmembrane serine protease (MTSP)-related polypeptide #7.			
PN US2004001801-A1.			
PD 01-JAN-2004.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 796			
ID ADN04299 standard; protein; 418 AA.			
DE Antiprosoriatic protein sequence #344.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 797			
ID ADQ30692 standard; protein; 418 AA.			
DE Human airway trypsin-like protease HAT.			
PN WO2004053496-A1.			
PD 24-JUN-2004.			
PA (HINZ/) HINZMANN B.			
PA (HEID/) HEIDEN E.			
PA (HERM/) HERMANN K.			
PA (ROSE/) ROSENTHAL A.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 798			
ID AAY94709 standard; protein; 422 AA.			
DE Human DESCI protein variant #2.			
PN WO200050061-A1.			
PD 31-AUG-2000.			
PA (OHIS) UNIV OHIO STATE RES FOUND.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 799			
ID AAY94708 standard; protein; 422 AA.			
DE Human DESCI protein variant #1.			
PN WO200050061-A1.			
PD 31-AUG-2000.			
PA (OHIS) UNIV OHIO STATE RES FOUND.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 800			
ID AAB01946 standard; protein; 422 AA.			
DE Human endotheliasin 1 protein.			
PN WO200136604-A2.			
PD 25-MAY-2001.			
PA (CORV-) CORVAS INT INC.			
Best Local Similarity: 100.00%	Mismatches:	0	
Query Match:	3.36%	Indels:	0
RESULT 801			
ID AAE18723 standard; protein; 422 AA.			
DE Human DESCI-like serine protease homologue.			
PN WO200206453-A2.			
PD 24-JAN-2002.			

PA (FARB ) BAYER AG. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 802  
ID ABUS6527 standard; protein; 422 AA.  
DE Lung cancer-associated polypeptide #120.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 803  
ID ADI10410 standard; protein; 422 AA.  
DE Human cell surface protease #21.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 804  
ID ADI10981 standard; protein; 422 AA.  
DE Human cell surface protease #14.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 805  
ID ADJ83073 standard; protein; 422 AA.  
DE Human DESCI protein - SEQ ID 64.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 806  
ID ADJ47505 standard; protein; 422 AA.  
DE Human transmembrane serine protease (MTSP)-related polypeptide #4.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 807  
ID ADJ46934 standard; protein; 422 AA.  
DE Human transmembrane serine protease (MTSP)-related polypeptide #11.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 808  
ID AAY99414 standard; protein; 423 AA.  
DE Human PRO1461 (UNQ742) amino acid sequence SEQ ID NO:269.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 809  
ID AAB66163 standard; protein; 423 AA.  
DE Protein of the invention #75.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 810  
ID AAU01344 standard; protein; 423 AA.  
DE Human TANGO 361 amino acid sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 811  
ID AAU01400 standard; protein; 423 AA.  
DE Human TANGO 361, variant #2 amino acid sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 812  
ID AAU01401 standard; protein; 423 AA.  
DE Human TANGO 361, variant #3 amino acid sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 813  
ID AAU01399 standard; protein; 423 AA.  
DE Human TANGO 361, variant #1 amino acid sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 814  
ID AAU01402 standard; protein; 423 AA.  
DE Human TANGO 361, variant #4 amino acid sequence.  
PN WO200121631-A2.  
PD 29-MAR-2001.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 815  
ID AAU29183 standard; protein; 423 AA.  
DE Human PRO polypeptide sequence #160.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.36%  
RESULT 816  
ID AAB87578 standard; protein; 423 AA.  
DE Human PRO1461.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.



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ID ABU91818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003027277-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 838
ID ABU9511 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036141-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 839
ID ABU86352 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036146-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 840
ID ABU67565 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 841
ID ABU80593 standard; protein; 423 AA.
DE Human PRO protein #160.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 842
ID ABU90928 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 843
ID ABO33987 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 844
ID ABR99511 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040063-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 845
ID ABR98901 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040064-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 846
ID ABO16424 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003027267-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 847
ID ABR32324 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036160-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 848
ID ABO18965 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044925-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 849
ID ABR78386 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 850
ID ABU72004 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 851
ID ABU85122 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032114-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 852
ID ABO00261 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032101-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 853
ID ABO11593 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036124-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 854
ID ABO02238 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040054-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 855
ID ABU88812 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036133-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 856
ID ABU83507 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036134-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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RESULT 857
ID ABO06308 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 858
ID ABR59344 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461, SEQ ID NO:320.
PN US2003027275-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 859
ID ABO09406 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003027324-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 860
ID ABO19270 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 861
ID ABO11288 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036123-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 862
ID ABR66906 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036148-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 863
ID ABO16119 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040060-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 864
ID ABO13825 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044916-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 865
ID ABU71558 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 866
ID ABU65728 standard; protein; 423 AA.
DE Human secreted/transmembrane protein, SEQ ID 320.
PN US2003036156-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 867
ID ABR70122 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 868
ID ABO03763 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036128-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 869
ID ABR67211 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027266-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 870
ID ABO15814 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 871
ID ABU56095 standard; protein; 423 AA.
DE Human secreted/transmembrane protein, PRO1461.
PN US2003022298-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 872
ID ABU72339 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 873
ID ABU65423 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032102-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 874
ID ABU95368 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036117-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 875
ID ABU71271 standard; protein; 423 AA.
DE Human PRO1461 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 876
ID ABO07881 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032130-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 877
ID ABR70122 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003022138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 878  
ID ABR69455 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 879  
ID ABO01596 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 880  
ID ABU91398 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 881  
ID ABR60195 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 882  
ID ABU91012 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 883  
ID ABR67930 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 884  
ID ABR65318 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 885  
ID ABR68540 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 886  
ID ABR71952 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 887  
ID ABO06661 standard; protein; 423 AA.

ID ABU95432 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 888  
ID ABU99122 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 889  
ID ABU83202 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 890  
ID ABU95058 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 891  
ID ABU90606 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 892  
ID ABU84117 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 893  
ID ABU93768 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 894  
ID ABR65013 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 895  
ID ABO27333 standard; protein; 423 AA.  
DE Human secreted/transmembrane polypeptide PRO1461.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 896  
ID ABR68845 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 897  
ID ABO06661 standard; protein; 423 AA.

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DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036125-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 908
ID ABU81198 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 909
ID ABR59890 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 910
ID ABU94078 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 911
ID ABU99931 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 912
ID ABR66601 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 913
ID ABR91019 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040058-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 914
ID AB053312 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 915
ID ABU94446 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 916
ID ABU79328 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 917
ID ABU86657 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032129-A1.

DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036125-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 898
ID ABR99206 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040068-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 899
ID ABU57090 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003027280-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 900
ID ABU86042 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003022300-A1.
PD 30-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 901
ID ABU82329 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036136-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 902
ID ABU87340 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036138-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 903
ID ABU83812 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032109-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 904
ID ABO08186 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003040066-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 905
ID ABU92528 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003045694-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 906
ID ABU81897 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 907
ID ABU66061 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036157-A1.
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PD 13-FEB-2003. Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 918  
ID ABU86962 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 919  
ID ABU94751 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 920  
ID ABO04678 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 921  
ID ABR70427 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 922  
ID ABU98592 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US20030322301-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 923  
ID ABR65991 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003031655-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 924  
ID ABR64708 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 925  
ID ABU79633 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 926  
ID ABU93024 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003031642-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 927  
ID ABU95983 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003031645-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0  
RESULT 928  
ID ABU91203 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US20030316154-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 929  
ID ABU90296 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US20030316153-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 930  
ID ABO09711 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 931  
ID ABO10983 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US20030316150-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 932  
ID ABR71037 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 933  
ID ABU98315 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 934  
ID ABU87645 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 935  
ID ABU91513 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 936  
ID ABU89320 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US20030316634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 937  
ID ABU84727 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

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RESULT 938
ID ABR69817 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032122-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 939
ID ABU00194 standard; protein; 423 AA.
DE Human PRO protein #160.
PN US20030306139-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 940
ID ABU00194 standard; protein; 423 AA.
DE Human PRO protein #160.
PN US20030306139-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 941
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 942
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PN US2003017541-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 943
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein (PRO) #160.
PN US2003017543-A1.
PD 23-JAN-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 944
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein (PRO) #160.
PN US20030306152-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 945
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein #160.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 946
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein #160.
PN US20030306152-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 947
ID ABU00194 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003032115-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 948
ID ABU00194 standard; protein; 423 AA.
DE Human secreted and transmembrane protein PRO1461.
PN US2003032140-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 949
ID ABR70732 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 950
ID ABO05083 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 951
ID ABO08491 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044922-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 952
ID ABO05698 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032118-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 953
ID ABR74087 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US20030306135-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 954
ID ABR95679 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 955
ID ABR80976 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 956
ID ABR81281 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 957
ID ABM00977 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049769-A1.
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PA 13-MAR-2003
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 958
ID ABR88579 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 959
ID ABM77400 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 960
ID ABO28884 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 961
ID ABO31629 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 962
ID ABM08046 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 963
ID ABO40526 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 964
ID ABO35951 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 965
ID ABO44090 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 966
ID ADA78072 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 967
ID ABR97876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 968
ID ABO03153 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 969
ID ABR90409 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 970
ID ABM17323 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 971
ID ABR95069 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 972
ID ABR95374 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 973
ID ADB17163 standard; protein; 423 AA.
DE Human transmembrane PRO polypeptide (SeqID 106).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 974
ID ABO21612 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 975
ID ABR97876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 976
ID ABR87664 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068705-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 977  
ID ABM77705 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 978  
ID ABM27935 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 979  
ID ABM06216 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 980  
ID ABM03722 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 981  
ID ABM35173 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 982  
ID ABM26410 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 983  
ID ABO48192 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 984  
ID ABR92934 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064482-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 985  
ID ABO24695 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003065159-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 986  
ID ABM11706 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 987  
ID ABM02807 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 988  
ID ABM16103 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 989  
ID ABO27664 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 990  
ID ABM29155 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 991  
ID ABM07131 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068899-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 992  
ID ABM21225 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 993  
ID ABM09571 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 994  
ID ABO41441 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068895-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 995			
ID ABO36256 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003068703-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 996			
ID ABO43785 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003068732-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 997			
ID ABO44291 standard; protein; 423 AA.			
DE Human secreted/transmembrane polypeptide PRO 1461.			
PN US2003018172-A1.			
PD 23-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1000			
ID ABO02543 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003040061-A1.			
PD 27-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1001			
ID ABO03458 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003036127-A1.			
PD 20-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1002			
ID ABO02543 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003040061-A1.			
PD 27-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1003			
ID ABO44291 standard; protein; 423 AA.			
DE Human secreted/transmembrane polypeptide PRO 1461.			
PN US2003018172-A1.			
PD 23-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1004			
ID ABR30714 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003073130-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1005			
ID ABR73782 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003054468-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1006			
ID ABO17034 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003054470-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1007			
ID ABR94459 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003044917-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1008			
ID ABR75966 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003044929-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1009			
ID ABR71342 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003059880-A1.			
PD 27-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1010			
ID ABR93239 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064465-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1011			
ID ABR93544 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003054478-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1012			
ID ABR87969 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068718-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		
RESULT 1013			
ID ABO33656 standard; protein; 423 AA.			
DE Novel human secreted and transmembrane protein PRO1461.			
PN US2003073130-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%	Mismatches: 0		
Query Match: 3.36%	Indels: 0		

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Query Match: 3.36% Indels: 0
RESULT 1014
ID ABO27969 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1015
ID ABO30104 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1016
ID ABO33313 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1017
ID ABO5001 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1018
ID ABO8961 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1019
ID ABO36561 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1020
ID ABO35646 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1021
ID ABO39611 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1022
ID ABM10486 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1023
ID ABM12011 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1024
ID ABO52157 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1025
ID ABO52462 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1026
ID ADA1968 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1027
ID ABO23780 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1028
ID ADB17351 standard; protein; 423 AA.
DE Human transmembrane PRO polypeptide (SeqID 106).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1029
ID ABR97286 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1030
ID ABR87054 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1031
ID ABM11096 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1032
ID ABM28240 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1033  
ID ABO32239 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1034  
ID ABM15366 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1035  
ID ABM06521 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1036  
ID ABM04332 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1037  
ID ABM22445 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1038  
ID ABM07741 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1039  
ID ABO40831 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1040  
ID ABM35478 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1041  
ID ABM33241 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003087374-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1042  
ID ABO52767 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1043  
ID ABO50327 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1044  
ID ABU99321 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1045  
ID ABO04373 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1046  
ID ABO06003 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1047  
ID ABM18543 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1048  
ID ABR97571 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1049  
ID ABR80671 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1050  
ID ABM01282 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

RESULT 1051  
ID ABR88984 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1052  
ID ABM13536 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1053  
ID ABM20920 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1054  
ID ABO42051 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1055  
ID ABO42661 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1056  
ID ABM10181 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1057  
ID ABO38696 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1058  
ID ABM32936 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1059  
ID ABM22750 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003083733-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1060  
ID ABM74961 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003096353-A1.  
PD 22-MAY-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1061  
ID ADA79864 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1062  
ID ABR96351 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1063  
ID ABM02502 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1064  
ID ABR86444 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1065  
ID ABR86749 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1066  
ID ABM16713 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1067  
ID ABM29765 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1068  
ID ABO29189 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1069  
ID ABM23970 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0



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Query Match: 3.36% Indels: 0
RESULT 1070
ID ABM23360 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1071
ID ABM22140 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1072
ID ABM28545 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1073
ID ABM28850 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1074
ID ABM66494 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1075
ID ABM75876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1076
ID ABM34156 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1077
ID ABM34461 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1078
ID ABO37781 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1079
ID ABO34219 standard; protein; 423 AA.
DE Human secreted/transmembrane polypeptide PRO 1461.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1080
ID ABR96656 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1081
ID ABR99816 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1082
ID ABM00367 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1083
ID ABM00672 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1084
ID ABO21307 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1085
ID ABO22222 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1086
ID ADA20140 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1087
ID ABR85834 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1088
ID ABM00367 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1089
ID ABM00672 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1090
ID ABO20392 standard; protein; 423 AA.
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Query Match:	3.36%	Indels:	0
RESULT 1089			
ID ABO29799 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003068700-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1090			
ID ABM23665 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068736-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1091			
ID ABM29460 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003068679-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1092			
ID ABO38391 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003068767-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1093			
ID ABO45691 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003073182-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1094			
ID ABM20615 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003104557-A1.			
PD 05-JUN-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1095			
ID ADA81591 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003092121-A1.			
PD 15-MAY-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1096			
ID ABO16729 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003027276-A1.			
PD 06-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1097			
ID ABO18355 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003044920-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1098			
ID ABO22782 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064464-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1099			
ID ABO23087 standard; protein; 423 AA.			
DE Human PRO polypeptide #160.			
PN US2003054461-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1100			
ID ABR92629 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064446-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1101			
ID ABR81586 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003049744-A1.			
PD 13-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1102			
ID ABM78010 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003049783-A1.			
PD 13-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1103			
ID ABR9799 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003073171-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1104			
ID ABM26715 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003032121-A1.			
PD 13-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1105			
ID ABM13841 standard; protein; 423 AA.			
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.			
PN US2003064458-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1106			
ID ABO28579 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064460-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0
RESULT 1107			
ID ABO30409 standard; protein; 423 AA.			
DE Human secreted/transmembrane protein (PRO) #160.			
PN US2003064464-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	3.36%	Indels:	0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1108  
ID ABO07436 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1109  
ID ABO04027 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1110  
ID ABO37171 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1111  
ID ABO41746 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1112  
ID ABO35341 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1113  
ID ABO25190 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1114  
ID ABO47582 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1115  
ID ABO47887 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1116  
ID ABO48497 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

RESULT 1117  
ID ABO51547 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1118  
ID ABO51852 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1119  
ID ABO50632 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1120  
ID ABR79756 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1121  
ID ABM17018 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1122  
ID ABO18050 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1123  
ID ABO21002 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1124  
ID ABR96961 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1125  
ID ABM12316 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1126  
ID ABM16408 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064449-A1.

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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1127
ID ABM24275 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064441-A1.
PD 03-APR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1128
ID ABM14756 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1129
ID ABM04637 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1130
ID ABM06826 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1131
ID ABM09266 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073174-A1.
PD 17-APR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1132
ID ABO39306 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1133
ID ABM75571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1134
ID ABM25495 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1135
ID ABM20005 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1136
ID ABO46911 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1137
ID ABO47216 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1138
ID ADA8389 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1139
ID ABR71647 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032133-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1140
ID ABR72257 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003032136-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1141
ID ABR98596 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036129-A1.
PD 20-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1142
ID ABO06966 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040053-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1143
ID ABR84919 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040057-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1144
ID ABR73477 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1145
ID ABR76571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003044932-A1.
PD 06-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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Query Match: 3.36% Indels: 0  
RESULT 1146  
ID ABR73172 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1147  
ID ABM18238 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1148  
ID ABO20697 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1149  
ID ABO25440 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1150  
ID ABO25745 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1151  
ID ABR94154 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1152  
ID ABR80061 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1153  
ID ABM11401 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1154  
ID ABO33008 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1155  
ID ABO30714 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.

PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1156  
ID ABO31019 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1157  
ID ABM27325 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1158  
ID ABM30070 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1159  
ID ABM05606 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1160  
ID ABM15671 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1161  
ID ABM08656 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1162  
ID ABO42356 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1163  
ID ABO38086 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1164  
ID ABO45996 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003049754-A1.

PD 13-MAR-2003.	Best Local Similarity: 100.00%	Mismatches: 0
PA (GETH ) GENENTECH INC.	Query Match: 3.36%	Indels: 0
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
RESULT 1165		
ID ABM66799 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003068688-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1166		
ID ADB20432 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003082767-A1.		
PD 01-MAY-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1167		
ID ABM19700 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003104552-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1168		
ID ABO49412 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003049774-A1.		
PD 13-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1169		
ID ABO49717 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003049775-A1.		
PD 13-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1170		
ID ADA78684 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003073181-A1.		
PD 17-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1171		
ID ABR86274 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003068720-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1172		
ID ADA00437 standard; protein; 423 AA.		
DE Human secreted/transmembrane polypeptide PRO 1461.		
PN US2003027992-A1.		
PD 06-FEB-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1173		
ID ABM27020 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003068739-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1174		
ID ABO3417 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003068763-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1175		
ID ABO39916 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003068689-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1176		
ID ABO50022 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003049776-A1.		
PD 13-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1177		
ID ABO50937 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003049780-A1.		
PD 13-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1178		
ID ABO5393 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein (PRO) #160.		
PN US2003036126-A1.		
PD 20-FEB-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1179		
ID ABR74697 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US200304924-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1180		
ID ABO44509 standard; protein; 423 AA.		
DE Human secreted/transmembrane protein PRO1461.		
PN US2003044841-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1181		
ID ABR77176 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003044927-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1182		
ID ABM17933 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		
PN US2003040072-A1.		
PD 27-FEB-2003.		
PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 3.36%	Indels: 0	
RESULT 1183		
ID ABR95984 standard; protein; 423 AA.		
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.		

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PN US2003040073-A1.
PD 27-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1184
ID ABO21917 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1185
ID ABO20087 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1186
ID ABO24390 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1187
ID ABR86139 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1188
ID ABM10791 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1189
ID ABM76790 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1190
ID ABR89494 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1191
ID ABM12621 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1192
ID ABM05911 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1193
ID ABO35036 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1194
ID ABM03112 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1195
ID ABM19090 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1196
ID ABM19395 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1197
ID ABO46606 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1198
ID ABO49107 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1199
ID ABR69150 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1200
ID ABR89189 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1201
ID ABR72562 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1202
ID ABR74392 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
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PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1203
ID ABO18660 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1204
ID ABR80366 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1205
ID ABO1587 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1206
ID ABO2197 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1207
ID ABR87359 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068887-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1208
ID ABO12926 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1209
ID ABO30680 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1210
ID ABO24580 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1211
ID ABO29494 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1212
ID ABO31324 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1213
ID ABO14451 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1214
ID ABO09876 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1215
ID ABO39001 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1216
ID ABO34766 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1217
ID ABO51242 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1218
ID ABO04068 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1219
ID ABO10538 standard; protein; 423 AA.
DE Human PRO polypeptide #160.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1220
ID ABR77781 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1221
ID ABR78991 standard; protein; 423 AA.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1222  
ID ABO24085 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1223  
ID ABR93849 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1224  
ID ABO1892 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1225  
ID ABM78315 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1226  
ID ABO33533 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1227  
ID ABR90104 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1228  
ID ABM27630 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1229  
ID ABM13231 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1230  
ID ABO31934 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068731-A1.

PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1231  
ID ABM14146 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1232  
ID ABM08351 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1233  
ID ABO40221 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1234  
ID ABM74656 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1235  
ID ABM33851 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1236  
ID ABM20310 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1237  
ID ABO48802 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1238  
ID ABR72867 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1239  
ID ABO15509 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

RESULT 1240  
ID ABR5224 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1241  
ID ABO15204 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1242  
ID ABO17339 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1243  
ID ABO17628 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1244  
ID ABR5529 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1245  
ID ABO17095 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003054484-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1246  
ID ABO28274 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003064459-A1.  
PD 03-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1247  
ID ABO23055 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068757-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1248  
ID ABO30375 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068723-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1249  
ID ABO21835 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068741-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1250  
ID ABO21530 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068744-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1251  
ID ABO15061 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068766-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1252  
ID ABO41136 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068694-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1253  
ID ABO36866 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068715-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1254  
ID ABO37476 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003068726-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1255  
ID ABO75266 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1256  
ID ABO33546 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1257  
ID ABO46301 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1258  
ID ADA82755 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1259  
ID ADB85679 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1260  
ID ADB31900 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1261  
ID ADB31290 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1262  
ID ADB86063 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1263  
ID ADB32205 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1264  
ID ADB32510 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1265  
ID ADB68358 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1266  
ID ADB68165 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1267  
ID ADB31595 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

RESULT 1268  
ID ADB30985 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1269  
ID ADB90982 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1270  
ID ADC07062 standard; protein; 423 AA.  
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1271  
ID ADC18138 standard; protein; 423 AA.  
DE Human secreted polypeptide #75.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1272  
ID ADC17241 standard; protein; 423 AA.  
DE Mammalian PRO polypeptide (SeqID 106).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1273  
ID ADC14939 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1274  
ID ADC52434 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1275  
ID ADD05793 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1276  
ID ADD70784 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1277

ID ADD39861 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1278  
ID ADD70307 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1279  
ID ADD36110 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1280  
ID ADD38428 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1281  
ID ADD39384 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1282  
ID ADD38907 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1283  
ID ADD40338 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1284  
ID ADE50559 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003089179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1285  
ID ADE20171 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1286  
ID ADE50082 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1287  
ID ADE21640 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003083628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1288  
ID ADF30065 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1289  
ID ADF5958 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1290  
ID ADG01111 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1291  
ID ADG08664 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1292  
ID ADG02788 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1293  
ID ADG01495 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1294  
ID ADF95670 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1295  
ID ADF95285 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.

PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1296  
ID ADG12485 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1297  
ID ADH24138 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1298  
ID ADH34164 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1299  
ID ADH23997 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1300  
ID ADH23968 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1301  
ID ADH09145 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1302  
ID ADG53372 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1303  
ID ADH24648 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1304  
ID ADH37504 standard; protein; 423 AA.  
DE Human secreted and transmembrane protein PRO1461.  
PN US2003181646-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1305  
ID ADH02093 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1306  
ID ADH37674 standard; protein; 423 AA.  
DE Human secreted and transmembrane protein PRO1461.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1307  
ID ADG85712 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1308  
ID ADH24308 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1309  
ID ADH38602 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1310  
ID ADG83723 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1311  
ID ADH29531 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1312  
ID ADH27647 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1313  
ID ADH37844 standard; protein; 423 AA.  
DE Human secreted and transmembrane protein PRO1461.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1314
ID ADH38021 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1315
ID ADH57441 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1316
ID ADH53583 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1317
ID ADH3753 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1318
ID ADH52089 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1319
ID ADH49944 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1320
ID ADI25454 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1321
ID ADH90247 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1322
ID ADI25624 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1323
ID ADH97798 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1324
ID ADH99462 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1325
ID ADI03646 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1326
ID ADI12003 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1327
ID ADH90077 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1328
ID ADH98478 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1329
ID ADI11153 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1330
ID ADI11663 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1331
ID ADH98308 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
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RESULT 1332  
ID ADH98648 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1333  
ID ADH98138 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1334  
ID ADI05126 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1335  
ID ADI03476 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1336  
ID ADI04871 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1337  
ID ADH78325 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1338  
ID ADI19669 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1339  
ID ADH90417 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1340  
ID ADI03136 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1341  
ID ADH79542 standard; protein; 423 AA.

ID ADH77985 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1342  
ID ADH97968 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1343  
ID ADI01353 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003190689-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1344  
ID ADI02048 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1345  
ID ADI03306 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1346  
ID ADI11493 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1347  
ID ADI02395 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1348  
ID ADI11833 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1349  
ID ADI05470 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1350  
ID ADH79542 standard; protein; 423 AA.

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DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1351
ID AD119499 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1352
ID AD105300 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1353
ID ADH79712 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1354
ID AD101538 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1355
ID AD101708 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1356
ID AD101878 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1357
ID ADH79882 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1358
ID AD104700 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1359
ID AD102836 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003040013-A1.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1360
ID ADH78155 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1361
ID AD125794 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1362
ID AD125964 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1363
ID ADK65476 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1364
ID ADH98818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1365
ID ADH80059 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1366
ID ADL32926 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1367
ID ADM30460 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1368
ID ADL93789 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003040013-A1.
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PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1369  
ID ADC52244 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1370  
ID ADE74457 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1371  
ID ADE75069 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein (PRO) #160.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1372  
ID ADE96642 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1373  
ID ADF25953 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1374  
ID ADF24852 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1375  
ID ADF29588 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1376  
ID ADE97119 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1377  
ID ADF96282 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0

RESULT 1378  
ID ADG04553 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1379  
ID ADG00713 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1380  
ID ADH06676 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1381  
ID ADH06506 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1382  
ID ADG68927 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1383  
ID ADH27817 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1384  
ID ADH25158 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1385  
ID ADH33790 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1386  
ID ADG82969 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1387

ID ADH03157 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1388  
ID ADH02433 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1389  
ID ADH08040 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1390  
ID ADG69437 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1391  
ID ADH39257 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1392  
ID ADH04111 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1393  
ID ADH03634 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1394  
ID ADH26250 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003088770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1395  
ID ADG83998 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1396  
ID ADG85542 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1397  
ID ADH06336 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1398  
ID ADH30166 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1399  
ID ADH24478 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1400  
ID ADH33219 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1401  
ID ADG69607 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1402  
ID ADH07870 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1403  
ID ADG85882 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1404  
ID ADH39428 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1405  
ID ADH33620 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.

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PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1406
ID ADH33960 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1407
ID ADH01170 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1408
ID ADG69777 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1409
ID ADH02263 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1410
ID ADG69267 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1411
ID ADG86052 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1412
ID ADH24988 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1413
ID ADH39605 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1414
ID ADH02603 standard; protein; 423 AA.
DE Human PRO polypeptide #53.
PN US2003180840-A1.
PD 08-JAN-2004.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1415
ID ADG69097 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1416
ID ADH07700 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1417
ID ADG86222 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1418
ID ADH24818 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1419
ID ADH25866 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1420
ID ADH38432 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1421
ID ADH57271 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1422
ID ADH52258 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.36% Indels: 0
RESULT 1423
ID ADH04588 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PN US2004005626-A1.
PD 08-JAN-2004.
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PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1424  
ID ADH49624 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1425  
ID ADH90587 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1426  
ID ADI11323 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1427  
ID ADH98988 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1428  
ID ADI02218 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1429  
ID ADH61589 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1430  
ID ADH90757 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1431  
ID ADJ54958 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US200402321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1432  
ID ADJ98632 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1433  
ID ADJ98802 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1434  
ID ADH78961 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1435  
ID ADJ99195 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1436  
ID ADJ99365 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1437  
ID ADJ98983 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1438  
ID ADH79130 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1439  
ID ADK00991 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1440  
ID ADK14512 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1441  
ID ADJ64729 standard; protein; 423 AA.  
DE Human PRO polypeptide #160.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0  
RESULT 1442  
ID ADM31625 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1443  
ID ADM36672 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1444  
ID ADM40477 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1445  
ID ADM80961 standard; protein; 423 AA.  
DE Human PRO polypeptide #53.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1446  
ID ADL94788 standard; protein; 423 AA.  
DE Human secreted/transmembrane protein PRO1461.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1447  
ID ADN38085 standard; protein; 423 AA.  
DE Novel human secreted and transmembrane protein PRO1461.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1448  
ID ADO89174 standard; protein; 423 AA.  
DE Human urological disorder related protein 32409 SEQ:126.  
PN WO2004085576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1449  
ID AAR06459 standard; protein; 431 AA.  
DE v-PA beta.  
PN EP383417-A.  
PD 22-AUG-1990.  
PA (SCHD ) SCHERING AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.36% Indels: 0  
RESULT 1450  
ID AAR14930 standard; protein; 13 AA.  
DE OT-2 antibody binding peptide (3).  
PN WO9117258-A.  
PD 14-NOV-1991.  
PA (CETU ) CETUS CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0

RESULT 1451  
ID AAE17240 standard; peptide; 14 AA.  
DE Human transmembrane serine protease-related type I fibronectin domain #1.  
PN WO200196538-A2.  
PD 20-DEC-2001.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1452  
ID AAE18999 standard; peptide; 14 AA.  
DE Human matritase-like serine protease related fibronectin domain #1.  
PN WO200208392-A2.  
PD 31-JAN-2002.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1453  
ID AAR67942 standard; protein; 22 AA.  
DE (1-3)-beta-D-glucan sensitive factor peptide fragment 10.  
PN WO9501432-A1.  
PD 12-JAN-1995.  
PA (SEKK ) SEIKAGAKU KOGYO CO LTD.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1454  
ID AAE17246 standard; peptide; 24 AA.  
DE Serine protease peptide #2 of the trypsin family.  
PN WO200196538-A2.  
PD 20-DEC-2001.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1455  
ID AAE19007 standard; peptide; 24 AA.  
DE Human matritase-like serine protease related peptide #3.  
PN WO200208392-A2.  
PD 31-JAN-2002.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1456  
ID AAE17239 standard; peptide; 35 AA.  
DE Human transmembrane serine protease-related apple domain #1.  
PN WO200196538-A2.  
PD 20-DEC-2001.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1457  
ID AAE19008 standard; peptide; 35 AA.  
DE Human matritase-like serine protease related apple domain #2.  
PN WO200208392-A2.  
PD 31-JAN-2002.  
PA (FARB ) BAYER AG.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1458  
ID AAM50210 standard; protein; 97 AA.  
DE Human plasminogen-like AMF4 C-terminal polypeptide.  
PN WO200174897-A2.  
PD 11-OCT-2001.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1459  
ID ADA05696 standard; protein; 102 AA.  
DE Human NOVIIE protein SEQ ID NO:56.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1460

ID ADN62860 standard; protein; 102 AA.  
DE Human NOV11d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATI/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTI/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1461  
ID AAR33961 standard; protein; 105 AA.  
DE Hepatocyte growth factor converting protease fragment.  
PN EF596524-A2.  
PD 11-MAY-1994.  
PA (MITU/) MITSUBISHI KASEI CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1462  
ID AAB71662 standard; protein; 118 AA.  
DE Human colon associated protein #10.  
PN WO200112781-A1.  
PD 22-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1463  
ID ADA05694 standard; protein; 119 AA.  
DE Human NOV11d protein SEQ ID NO:54.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1464  
ID ADA05700 standard; protein; 119 AA.  
DE Human NOV11g protein SEQ ID NO:60.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1465

ID ADN62858 standard; protein; 119 AA.  
DE Human NOV11d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATI/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTI/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1466  
ID ADG75740 standard; protein; 141 AA.  
DE Human protein modification and maintenance molecule polypeptide SeqID64.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
RESULT 1467  
ID ADA05688 standard; protein; 142 AA.  
DE Human NOV11a protein SEQ ID NO:48.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.08% Indels: 0  
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ID ADN62852 standard; protein; 142 AA.  
DE Human NOV11a.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATI/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.



ID AAU75082 standard; protein; 178 AA.  
DE Human prostatic-like serine protease protein.  
PN WO200198467-A2.  
PD 27-DEC-2001.  
PA (FARB) BAYER AG. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
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ID AD116332 standard; protein; 181 AA.  
DE Human protein modification and maintenance molecule (PMM4) protein #17.  
PN WO2003100016-A2.  
PD 04-DEC-2003.  
PA (INCY-) INCYTE CORP. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1482  
ID ABG75787 standard; protein; 191 AA.  
DE Serine protease zymogen domain consensus sequence, PD000000046, #1.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAP-) KAPILLER-LIBERMANN R. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1483  
ID AAG73966 standard; protein; 193 AA.  
DE Human colon cancer antigen protein SEQ ID NO:4730.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
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RESULT 1484  
ID ADM79155 standard; protein; 194 AA.  
DE Human delta trypsin variant protein.  
PN WO2004033494-A1.  
PD 22-APR-2004.  
PA (UNIX) UNISEARCH LTD. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1485  
ID ADG42737 standard; protein; 199 AA.  
DE Human beta trypsin precursor protein #3.  
PN US2003202971-A1.  
PD 30-OCT-2003.  
PA (MAJU) MAJUMDER K. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
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RESULT 1486  
ID ADJ5806 standard; peptide; 199 AA.  
DE Peptide homologous to a fragment of a human NOV12 protein SeqID 98.  
PN US2003199455-A1.  
PD 23-OCT-2003.  
PA (MALY) MALYANKAR U M.  
PA (TCHE) TCHERNEV V T.  
PA (PADI) PADIGARU M.  
PA (TAUP) TAUPIER R J.  
PA (SPYT) SPYTEK K A.  
PA (GUOX) GUO X.  
PA (SPAD) SPADERNA S K.  
PA (BOLD) BOLDG F L.  
PA (GERL) GERLACH V.  
PA (ELLE) ELLERMAN K.  
PA (MACD) MACDOUGALL J R.  
PA (SMIT) SMITHSON G. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1487  
ID ADM76644 standard; protein; 199 AA.  
DE Human NOV12 protein-related protein fragment SeqID98.  
PN WO2004009634-A2.  
PD 29-JAN-2004.  
PA (CURA-) CURAGEN CORP. Mismatches: 0  
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RESULT 1488  
ID AAY28641 standard; protein; 207 AA.  
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PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
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ID ABR48479 standard; protein; 207 AA.  
DE Human Plasminogen.  
PN WO200294864-A2.  
PD 28-NOV-2002.  
PA (GEST) GENSET. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1490  
ID ADQ67690 standard; protein; 211 AA.  
DE Novel human protein sequence #2356.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1491  
ID AD117075 standard; protein; 225 AA.  
DE Murine NOVX protein homologue SeqID 611.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
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RESULT 1492  
ID ADM79152 standard; protein; 226 AA.  
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PD 22-APR-2004.  
PA (UNIX) UNISEARCH LTD. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
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RESULT 1493  
ID AAB21312 standard; protein; 228 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
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RESULT 1494  
ID AD110641 standard; protein; 228 AA.  
DE Cell surface protease.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1495  
ID ADG65348 standard; protein; 228 AA.  
DE Alternative PDI from Human MTSP12.  
PN WO2003104394-A2.  
PD 18-DEC-2003.  
PA (DEND-) DENDREON SAN DIEGO LLC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 3.08%  
RESULT 1496  
ID ADJ47165 standard; protein; 228 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #16.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC. Mismatches: 0  
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PD 17-FEB-1994.
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.08% Indels: 0
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Best Local Similarity: 100.00% Mismatches: 0
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OM nucleic - protein search, using frame\_plus\_n2p model

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Searched: 513545 seqs, 74649064 residues

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SUMMARIES

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89	11	3.1	22	3	US-09-330-945-31	Sequence 31, Appl	162	11	3.1	333	4	US-08-991-761A-8	Sequence 8, Appl
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128	11	3.1	267	2	US-09-016-366A-23	Sequence 23, Appl	201	11	3.1	791	1	US-08-991-761A-13	Sequence 13, Appl
129	11	3.1	267	2	US-08-978-404B-18	Sequence 18, Appl	202	11	3.1	791	1	US-08-643-219-1	Sequence 1, Appl
130	11	3.1	267	4	US-09-917-254-101	Sequence 101, App	203	11	3.1	791	2	US-09-131-995-1	Sequence 1, Appl
131	11	3.1	267	4	US-09-949-016-9575	Sequence 9575, Ap	204	11	3.1	791	2	US-08-832-087B-1	Sequence 1, Appl
132	11	3.1	270	2	US-08-978-404B-8	Sequence 8, Appl	205	11	3.1	791	3	US-08-851-350-1	Sequence 1, Appl
133	11	3.1	273	2	US-08-978-404B-19	Sequence 19, Appl	206	11	3.1	791	3	US-09-132-154-1	Sequence 1, Appl
134	11	3.1	273	2	US-08-978-404B-3	Sequence 3, Appl	207	11	3.1	791	4	US-08-991-761A-6	Sequence 6, Appl
135	11	3.1	273	2	US-08-978-404B-6	Sequence 6, Appl	208	11	3.1	791	4	US-08-924-287A-1	Sequence 1, Appl
136	11	3.1	273	2	US-08-978-404B-14	Sequence 14, Appl	209	11	3.1	809	4	US-08-991-761A-9	Sequence 9, Appl
137	11	3.1	274	2	US-09-016-366A-21	Sequence 21, Appl	210	11	3.1	810	1	US-07-854-603-2	Sequence 2, Appl
138	11	3.1	274	2	US-08-978-404B-5	Sequence 5, Appl	211	11	3.1	810	1	US-08-147-000B-29	Sequence 29, Appl
139	11	3.1	274	2	US-08-978-404B-16	Sequence 16, Appl	212	11	3.1	810	3	US-09-086-514-1	Sequence 1, Appl
140	11	3.1	276	2	US-09-016-366A-15	Sequence 15, Appl	213	11	3.1	810	4	US-09-192-012-5	Sequence 5, Appl
141	11	3.1	276	2	US-08-978-404B-21	Sequence 21, Appl	214	11	3.1	810	4	US-08-991-761A-11	Sequence 11, Appl
142	11	3.1	276	2	US-08-978-404B-15	Sequence 15, Appl	215	11	3.1	810	4	US-09-403-736-1	Sequence 1, Appl
143	11	3.1	278	1	US-09-880-503-5	Sequence 5, Appl	216	11	3.1	810	4	US-09-403-736-1	Sequence 1, Appl
144	11	3.1	278	3	US-08-382-828C-4	Sequence 4, Appl	217	11	3.1	810	6	5200340-8	Patent No. 5200340
145	11	3.1	282	3	US-09-330-945-4	Sequence 4, Appl	218	11	3.1	810	6	5200340-8	Patent No. 5200340
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147	11	3.1	284	4	US-09-387-375-7	Sequence 7, Appl	220	11	3.1	812	1	US-08-451-932-1	Sequence 1, Appl
148	11	3.1	284	4	US-10-041-400A-7	Sequence 7, Appl	221	11	3.1	812	1	US-08-452-260-1	Sequence 1, Appl
149	11	3.1	284	4	US-10-042-091A-7	Sequence 13, Appl	222	11	3.1	812	1	US-08-326-785-1	Sequence 1, Appl
150	11	3.1	288	4	US-09-386-642-13	Sequence 14, Appl	223	11	3.1	812	2	US-08-612-788-1	Sequence 1, Appl
151	11	3.1	289	4	US-09-386-642-14	Sequence 14, Appl	224	11	3.1	812	2	US-08-605-598B-1	Sequence 1, Appl
152	11	3.1	289	3	US-08-944-483-66	Sequence 66, Appl	225	11	3.1	812	2	US-08-429-743-1	Sequence 1, Appl
153	11	3.1	300	1	US-08-148-910-1	Sequence 1, Appl	226	11	3.1	812	2	US-08-866-735-1	Sequence 1, Appl
154	11	3.1	306	2	US-08-448-937A-1	Sequence 1, Appl	227	11	3.1	812	3	US-09-066-028-1	Sequence 3, Appl
155	11	3.1	316	4	US-08-560-098A-45	Sequence 45, Appl	228	11	3.1	812	4	US-09-192-012-3	Sequence 3, Appl
156	11	3.1	316	4	US-09-387-375-9	Sequence 9, Appl	229	11	3.1	812	4	US-09-192-012-9	Sequence 9, Appl
157	11	3.1	316	4	US-10-041-400A-9	Sequence 9, Appl	230	11	3.1	812	4	US-09-335-325-1	Sequence 1, Appl
158	11	3.1	319	4	US-10-042-091A-9	Sequence 9, Appl	231	11	3.1	812	4	US-08-991-761A-7	Sequence 7, Appl

232	11	3-1	812	4	US-08-991-761A-12	Sequence 12, Appl	305	10	2-8	267	4	US-09-004-729-67	Sequence 67, Appl
233	11	3-1	812	5	PCT-US95-05107-1	Sequence 1, Appl	306	10	2-8	306	1	US-08-330-978-1	Sequence 1, Appl
234	11	3-1	814	1	US-08-750-711-1	Sequence 1, Appl	307	10	2-8	306	1	US-08-474-042-1	Sequence 1, Appl
235	10	2-8	42	1	US-08-293-778-13	Sequence 13, Appl	308	10	2-8	306	1	US-08-484-558-1	Sequence 1, Appl
236	10	2-8	90	4	US-09-270-767-57991	Sequence 57991, A	309	10	2-8	306	1	US-08-774-592-1	Sequence 1, Appl
237	10	2-8	125	3	US-08-906-769-97	Sequence 97, Appl	310	10	2-8	319	4	US-09-270-767-42672	Sequence 42672, A
238	10	2-8	125	3	US-08-906-616-97	Sequence 97, Appl	311	10	2-8	326	3	US-09-411-977-3	Sequence 3, Appl
239	10	2-8	125	3	US-08-817-795-97	Sequence 97, Appl	312	10	2-8	326	4	US-10-057-951-3	Sequence 3, Appl
240	10	2-8	125	3	US-08-639-075A-97	Sequence 97, Appl	313	10	2-8	376	4	US-09-820-003-2	Sequence 2, Appl
241	10	2-8	125	3	US-09-012-431-97	Sequence 97, Appl	314	10	2-8	393	4	US-09-759-143-934	Sequence 934, App
242	10	2-8	125	3	US-09-012-692-97	Sequence 97, Appl	315	10	2-8	416	2	US-09-000-846-2	Sequence 2, Appl
243	10	2-8	125	3	US-08-906-613-97	Sequence 97, Appl	316	10	2-8	417	4	US-09-820-002-4	Sequence 4, Appl
244	10	2-8	125	5	PCT-US95-14442A-97	Sequence 97, Appl	317	10	2-8	437	1	US-08-487-037-2	Sequence 2, Appl
245	10	2-8	141	4	US-09-949-016-7265	Sequence 7265, Ap	318	10	2-8	448	1	US-08-295-411-3	Sequence 3, Appl
246	10	2-8	151	4	US-09-270-767-33178	Sequence 33178, A	319	10	2-8	448	2	US-08-955-471-3	Sequence 3, Appl
247	10	2-8	151	4	US-09-270-767-48395	Sequence 48395, A	320	10	2-8	448	5	PCT-US92-10068-1	Sequence 1, Appl
248	10	2-8	159	3	US-09-518-046-24	Sequence 24, Appl	321	10	2-8	448	5	PCT-US92-10242-3	Sequence 3, Appl
249	10	2-8	161	3	US-09-261-416-8	Sequence 8, Appl	322	10	2-8	452	4	US-09-949-016-7182	Sequence 7182, Ap
250	10	2-8	164	3	US-09-518-046-25	Sequence 25, Appl	323	10	2-8	487	1	US-08-469-486-53	Sequence 53, Appl
251	10	2-8	200	3	US-09-008-271A-5	Sequence 5, Appl	324	10	2-8	487	2	US-08-469-658-2	Sequence 2, Appl
252	10	2-8	204	4	US-09-252-991A-25056	Sequence 25056, A	325	10	2-8	488	1	US-08-487-037-1	Sequence 1, Appl
253	10	2-8	232	1	US-07-990-301A-4	Sequence 4, Appl	326	10	2-8	488	4	US-09-367-777-44	Sequence 44, Appl
254	10	2-8	232	3	US-08-944-483-45	Sequence 45, Appl	327	10	2-8	488	4	US-09-367-791A-27	Sequence 27, Appl
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257	10	2-8	241	1	US-08-484-558-4	Sequence 4, Appl	330	10	2-8	492	3	US-09-342-749-2	Sequence 2, Appl
258	10	2-8	241	1	US-08-774-592-4	Sequence 4, Appl	331	10	2-8	492	4	US-09-691-840-2	Sequence 2, Appl
259	10	2-8	242	3	US-08-944-483-29	Sequence 29, Appl	332	10	2-8	492	4	US-09-685-166A-895	Sequence 895, App
260	10	2-8	245	3	US-08-906-769-121	Sequence 121, App	333	10	2-8	492	4	US-09-879-792-14	Sequence 14, Appl
261	10	2-8	245	3	US-08-906-616-121	Sequence 121, App	334	10	2-8	492	4	US-09-679-426-895	Sequence 895, App
262	10	2-8	245	3	US-08-639-075A-121	Sequence 121, App	335	10	2-8	492	4	US-09-759-143-895	Sequence 895, App
263	10	2-8	245	3	US-09-012-431-121	Sequence 121, App	336	10	2-8	496	4	US-09-759-143-932	Sequence 932, App
264	10	2-8	245	3	US-09-012-692-121	Sequence 121, App	337	10	2-8	510	4	US-09-949-016-9524	Sequence 9524, A
265	10	2-8	245	3	US-08-906-613-121	Sequence 121, App	338	10	2-8	510	4	US-09-949-016-11074	Sequence 11074, A
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267	10	2-8	248	2	US-08-851-974-3	Sequence 3, Appl	340	9	2-5	9	3	US-09-518-046-58	Sequence 58, Appl
268	10	2-8	248	2	US-09-213-390-3	Sequence 3, Appl	341	9	2-5	9	4	US-09-618-259-27	Sequence 27, Appl
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274	10	2-8	255	3	US-08-906-769-83	Sequence 83, Appl	347	9	2-5	64	1	US-08-485-455B-75	Sequence 75, Appl
275	10	2-8	255	3	US-08-906-616-83	Sequence 83, Appl	348	9	2-5	64	2	US-08-482-130C-75	Sequence 75, Appl
276	10	2-8	255	3	US-08-817-795-83	Sequence 83, Appl	349	9	2-5	64	2	US-08-484-211C-75	Sequence 75, Appl
277	10	2-8	255	3	US-08-639-075A-83	Sequence 83, Appl	350	9	2-5	64	3	US-08-906-769-75	Sequence 75, Appl
278	10	2-8	255	3	US-09-012-431-83	Sequence 83, Appl	351	9	2-5	64	3	US-08-906-616-75	Sequence 75, Appl
279	10	2-8	255	3	US-09-012-692-83	Sequence 83, Appl	352	9	2-5	64	3	US-08-817-795-75	Sequence 75, Appl
280	10	2-8	255	3	US-08-906-613-83	Sequence 83, Appl	353	9	2-5	64	3	US-08-485-443B-75	Sequence 75, Appl
281	10	2-8	255	5	PCT-US95-14442A-83	Sequence 67, Appl	354	9	2-5	64	3	US-08-639-075A-75	Sequence 75, Appl
282	10	2-8	255	2	US-09-027-337-3	Sequence 3, Appl	355	9	2-5	64	3	US-09-012-431-75	Sequence 75, Appl
283	10	2-8	256	3	US-08-906-769-89	Sequence 89, Appl	356	9	2-5	64	3	US-09-012-692-75	Sequence 75, Appl
284	10	2-8	256	3	US-08-906-616-89	Sequence 89, Appl	357	9	2-5	64	3	US-08-906-613-75	Sequence 75, Appl
285	10	2-8	256	3	US-08-906-616-89	Sequence 89, Appl	358	9	2-5	64	5	PCT-US95-14442A-75	Sequence 75, Appl
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287	10	2-8	256	3	US-08-639-075A-89	Sequence 89, Appl	360	9	2-5	84	3	US-08-906-616-99	Sequence 99, Appl
288	10	2-8	256	3	US-09-012-431-89	Sequence 89, Appl	361	9	2-5	84	3	US-08-817-795-99	Sequence 99, Appl
289	10	2-8	256	3	US-09-032-215-27	Sequence 27, Appl	362	9	2-5	84	3	US-08-639-075A-99	Sequence 99, Appl
290	10	2-8	256	3	US-09-032-215-32	Sequence 32, Appl	363	9	2-5	84	3	US-09-012-431-99	Sequence 99, Appl
291	10	2-8	256	3	US-09-012-692-89	Sequence 89, Appl	364	9	2-5	84	3	US-09-012-692-99	Sequence 99, Appl
292	10	2-8	256	3	US-08-906-613-89	Sequence 89, Appl	365	9	2-5	84	3	US-08-906-613-99	Sequence 99, Appl
293	10	2-8	256	4	US-09-644-600-3	Sequence 3, Appl	366	9	2-5	84	5	PCT-US95-14442A-99	Sequence 99, Appl
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299	10	2-8	267	3	US-08-639-075A-145	Sequence 145, App	372	9	2-5	144	4	US-09-489-039A-11953	Sequence 11953, A
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302	10	2-8	267	3	US-08-749-699-67	Sequence 67, Appl	375	9	2-5	145	3	US-08-639-075A-123	Sequence 123, App
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304	10	2-8	267	3	US-08-906-613-145	Sequence 145, App	377	9	2-5	145	3	US-08-906-613-123	Sequence 123, App

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380	9	2.5	159	4	US-09-618-259-5	Sequence 5, Appli	453	9	2.5	237	3	US-09-100-264-12	Sequence 12, Appli
c 381	9	2.5	206	4	US-09-252-991A-17271	Sequence 17271, A	454	9	2.5	237	4	US-09-303-339-2	Sequence 2, Appli
c 382	9	2.5	206	4	US-09-248-796A-21349	Sequence 21349, A	455	9	2.5	237	4	US-08-843-076D-1	Sequence 1, Appli
c 383	9	2.5	213	3	US-08-906-769-149	Sequence 149, App	456	9	2.5	237	4	US-08-843-076D-7	Sequence 7, Appli
384	9	2.5	213	3	US-08-906-616-149	Sequence 149, App	457	9	2.5	237	4	US-08-843-076D-8	Sequence 8, Appli
385	9	2.5	213	3	US-08-639-075A-149	Sequence 149, App	458	9	2.5	237	4	US-09-303-208-1	Sequence 1, Appli
386	9	2.5	213	3	US-09-012-431-149	Sequence 149, App	459	9	2.5	237	5	US-08-462-515-3	Sequence 10, Appli
387	9	2.5	213	3	US-09-012-692-149	Sequence 149, App	460	9	2.5	237	5	PCT-US94-07329-10	Sequence 10, Appli
388	9	2.5	213	3	US-08-906-613-149	Sequence 149, App	461	9	2.5	237	5	PCT-US94-17329-11	Sequence 11, Appli
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391	9	2.5	223	2	US-08-484-211C-17	Sequence 17, Appli	464	9	2.5	237	5	PCT-US95-06157-8	Sequence 8, Appli
392	9	2.5	223	3	US-08-481-795-17	Sequence 17, Appli	465	9	2.5	238	3	US-08-767-820A-8	Sequence 8, Appli
393	9	2.5	223	3	US-08-485-443B-17	Sequence 17, Appli	466	9	2.5	238	3	US-08-767-820A-8	Sequence 8, Appli
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404	9	2.5	225	2	US-09-154-344-12	Sequence 12, Appli	477	9	2.5	240	3	US-09-074-659-11	Sequence 11, Appli
405	9	2.5	225	4	US-09-644-600-4	Sequence 4, Appli	478	9	2.5	241	4	US-09-106-468-11	Sequence 11, Appli
406	9	2.5	225	4	US-09-654-600A-41	Sequence 41, Appli	479	9	2.5	241	4	US-09-106-466A-11	Sequence 11, Appli
407	9	2.5	226	3	US-08-944-483-41	Sequence 41, Appli	480	9	2.5	242	3	US-09-657-986B-2	Sequence 2, Appli
408	9	2.5	227	3	US-08-944-483-40	Sequence 40, Appli	481	9	2.5	242	3	US-09-004-731-36	Sequence 36, Appli
409	9	2.5	228	1	US-08-278-091-10	Sequence 10, Appli	482	9	2.5	242	3	US-08-749-699-36	Sequence 36, Appli
410	9	2.5	228	1	US-08-483-859-10	Sequence 10, Appli	483	9	2.5	242	4	US-09-004-729-36	Sequence 36, Appli
411	9	2.5	228	1	US-08-472-173-10	Sequence 10, Appli	484	9	2.5	242	4	US-09-959-352-34	Sequence 34, Appli
412	9	2.5	228	2	US-08-487-167-10	Sequence 10, Appli	485	9	2.5	242	4	US-08-768-859A-10	Sequence 10, Appli
413	9	2.5	228	2	US-08-482-816-10	Sequence 10, Appli	486	9	2.5	244	3	US-08-767-820A-10	Sequence 10, Appli
414	9	2.5	228	2	US-08-296-149-10	Sequence 10, Appli	487	9	2.5	244	3	US-08-622-046B-5	Sequence 5, Appli
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416	9	2.5	228	2	US-08-615-271-10	Sequence 10, Appli	489	9	2.5	244	3	US-08-622-046B-16	Sequence 16, Appli
417	9	2.5	228	3	US-09-074-660-10	Sequence 10, Appli	490	9	2.5	244	3	US-08-944-483-74	Sequence 74, Appli
418	9	2.5	228	3	US-09-074-659-10	Sequence 10, Appli	491	9	2.5	244	3	US-08-100-264-5	Sequence 5, Appli
419	9	2.5	228	3	US-09-106-468-10	Sequence 10, Appli	492	9	2.5	244	3	US-08-843-076D-5	Sequence 5, Appli
420	9	2.5	228	3	US-09-106-466A-10	Sequence 10, Appli	493	9	2.5	244	5	US-08-843-076D-5	Sequence 5, Appli
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422	9	2.5	229	2	US-08-557-146-13	Sequence 13, Appli	495	9	2.5	245	3	US-08-944-483-69	Sequence 69, Appli
423	9	2.5	229	2	US-09-154-344-13	Sequence 13, Appli	496	9	2.5	247	2	US-08-851-974-1	Sequence 1, Appli
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431	9	2.5	233	2	US-08-738-413B-9	Sequence 9, Appli	504	9	2.5	250	4	US-09-270-767-33709	Sequence 33709, A
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437	9	2.5	237	2	US-08-844-024-2	Sequence 2, Appli	510	9	2.5	253	3	US-08-930-188-2	Sequence 2, Appli
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444	9	2.5	237	3	US-08-767-820A-21	Sequence 21, Appli	517	9	2.5	259	4	US-10-165-442-2	Sequence 2, Appli
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529	9	2.5	261	3	US-09-100-264-7	Sequence 7, Appli	602	9	2.5	855	4	US-09-644-600-2	Sequence 2, Appli
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534	9	2.5	261	4	US-09-618-259-10	Sequence 10, Appl	607	9	2.5	902	4	US-09-654-600A-10	Sequence 10, Appl
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538	9	2.5	265	4	US-09-949-016-7716	Sequence 7716, Ap	611	9	2.5	1400	3	US-09-879-957-37	Sequence 37, Appli
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552	9	2.5	349	4	US-09-949-016-9668	Sequence 9668, Ap	625	8	2.2	10	2	US-08-724-548-8	Sequence 8, Appli
553	9	2.5	352	4	US-09-902-540-9796	Sequence 9796, Ap	626	8	2.2	10	3	US-07-978-674B-6	Sequence 6, Appli
554	9	2.5	356	2	US-08-681-151-1	Sequence 1, Appli	627	8	2.2	10	3	US-07-978-674B-7	Sequence 7, Appli
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556	9	2.5	376	2	US-08-558-269-10	Sequence 10, Appl	629	8	2.2	16	3	US-08-602-999A-384	Sequence 384, App
557	9	2.5	376	2	US-09-410-882-10	Sequence 10, Appl	630	8	2.2	16	4	US-09-500-124-384	Sequence 384, App
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561	9	2.5	400	3	US-09-004-731-30	Sequence 30, Appl	634	8	2.2	17	4	US-09-500-124-374	Sequence 374, App
562	9	2.5	400	3	US-09-004-731-33	Sequence 33, Appl	635	8	2.2	17	4	US-09-879-792-17	Sequence 17, Appl
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590	9	2.5	615	1	US-08-462-261-3	Sequence 3, Appli	663	8	2.2	68	2	US-08-484-211C-77	Sequence 77, Appl
591	9	2.5	615	5	PCT-US92-11357-3	Sequence 3, Appli	664	8	2.2	68	3	US-08-906-769-77	Sequence 77, Appl
592	9	2.5	622	3	US-08-952-967-8	Sequence 8, Appli	665	8	2.2	68	3	US-08-906-616-77	Sequence 77, Appl
593	9	2.5	622	4	US-09-054-272-42	Sequence 42, Appl	666	8	2.2	68	3	US-08-817-795-77	Sequence 77, Appl
594	9	2.5	638	2	US-08-681-151-3	Sequence 3, Appli	667	8	2.2	68	3	US-08-485-443B-77	Sequence 77, Appl
595	9	2.5	645	4	US-09-270-767-42233	Sequence 42233, A	668	8	2.2	68	3	US-08-639-075A-77	Sequence 77, Appl
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671	8	2.2	68	3	US-08-906-613-77	Sequence 77, Appl	744	8	2.2	113	4	US-09-513-999C-4899	Sequence 4899, Ap
672	8	2.2	68	5	PCT-US95-14442A-77	Sequence 77, Appl	745	8	2.2	115	4	US-09-489-039A-8475	Sequence 8475, Ap
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683	8	2.2	72	3	US-08-906-769-87	Sequence 87, Appl	756	8	2.2	144	4	US-09-618-259-4	Sequence 4, Appli
684	8	2.2	72	3	US-08-906-616-87	Sequence 87, Appl	757	8	2.2	151	3	US-09-518-046-21	Sequence 21, Appl
685	8	2.2	72	3	US-08-917-795-87	Sequence 87, Appl	c 758	8	2.2	152	4	US-09-621-976-4307	Sequence 4307, Ap
686	8	2.2	72	3	US-08-639-075A-87	Sequence 87, Appl	759	8	2.2	154	3	US-09-261-416-5	Sequence 5, Appli
687	8	2.2	72	3	US-09-012-431-87	Sequence 87, Appl	c 760	8	2.2	155	3	US-08-209-747-15	Sequence 15, Appl
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690	8	2.2	72	5	PCT-US95-14442A-87	Sequence 87, Appl	763	8	2.2	158	4	US-09-248-796A-22805	Sequence 22805, A
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694	8	2.2	80	2	US-08-484-211C-59	Sequence 59, Appl	767	8	2.2	172	4	US-09-543-681A-8317	Sequence 8317, Ap
695	8	2.2	80	3	US-08-906-769-59	Sequence 59, Appl	768	8	2.2	178	3	US-08-705-875A-8	Sequence 8, Appli
696	8	2.2	80	3	US-08-906-616-59	Sequence 59, Appl	769	8	2.2	178	3	US-09-220-731-23	Sequence 23, Appl
697	8	2.2	80	3	US-08-917-795-59	Sequence 59, Appl	770	8	2.2	178	4	US-09-242-999-8	Sequence 8, Appli
698	8	2.2	80	3	US-08-485-443B-59	Sequence 59, Appl	771	8	2.2	180	6	5273901-7	Patent No. 5273901
699	8	2.2	80	3	US-08-639-075A-59	Sequence 59, Appl	772	8	2.2	180	6	5482709-6	Patent No. 5482709
700	8	2.2	80	3	US-09-012-431-59	Sequence 59, Appl	773	8	2.2	180	6	5273901-7	Patent No. 5273901
701	8	2.2	80	3	US-09-012-692-59	Sequence 59, Appl	774	8	2.2	180	6	5482709-6	Patent No. 5482709
702	8	2.2	80	5	PCT-US95-14442A-59	Sequence 59, Appl	c 775	8	2.2	181	2	US-08-726-306A-56	Sequence 56, Appl
703	8	2.2	86	1	US-08-485-455D-53	Sequence 53, Appl	776	8	2.2	182	4	US-09-489-039A-13484	Sequence 13484, A
704	8	2.2	86	2	US-08-482-130C-53	Sequence 53, Appl	777	8	2.2	182	4	US-09-328-925-12	Sequence 12, Appl
705	8	2.2	86	2	US-08-484-211C-53	Sequence 53, Appl	c 778	8	2.2	185	4	US-09-489-039A-8929	Sequence 8929, Ap
706	8	2.2	86	2	US-08-906-769-53	Sequence 53, Appl	779	8	2.2	190	2	US-08-845-998-4	Sequence 4, Appli
707	8	2.2	86	3	US-08-906-616-53	Sequence 53, Appl	780	8	2.2	190	2	US-09-206-537-4	Sequence 4, Appli
708	8	2.2	86	3	US-08-906-616-53	Sequence 53, Appl	781	8	2.2	190	3	US-09-206-537-6	Sequence 6, Appli
709	8	2.2	86	3	US-08-917-795-53	Sequence 53, Appl	782	8	2.2	190	3	US-09-430-854-4	Sequence 4, Appli
710	8	2.2	86	3	US-08-485-443B-53	Sequence 53, Appl	783	8	2.2	190	3	US-09-430-854-6	Sequence 6, Appli
711	8	2.2	86	3	US-08-639-075A-53	Sequence 53, Appl	784	8	2.2	197	4	US-09-385-219A-32	Sequence 32, Appl
712	8	2.2	86	3	US-09-012-431-53	Sequence 53, Appl	785	8	2.2	198	3	US-08-906-769-133	Sequence 133, App
713	8	2.2	86	3	US-09-012-692-53	Sequence 53, Appl	786	8	2.2	198	3	US-08-906-616-133	Sequence 133, App
714	8	2.2	86	3	US-08-906-613-53	Sequence 53, Appl	787	8	2.2	198	3	US-08-639-075A-133	Sequence 133, App
715	8	2.2	86	5	PCT-US95-14442A-53	Sequence 53, Appl	788	8	2.2	198	3	US-09-012-431-133	Sequence 133, App
716	8	2.2	94	4	US-09-270-767-60718	Sequence 60718, A	789	8	2.2	198	3	US-09-012-692-133	Sequence 133, App
717	8	2.2	97	1	US-08-485-455D-63	Sequence 63, Appl	790	8	2.2	198	3	US-08-906-613-133	Sequence 133, App
718	8	2.2	97	2	US-08-482-130C-63	Sequence 63, Appl	791	8	2.2	200	4	US-09-270-767-46385	Sequence 46385, A
719	8	2.2	97	2	US-08-484-211C-63	Sequence 63, Appl	c 792	8	2.2	201	4	US-09-248-796A-19314	Sequence 19314, A
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721	8	2.2	97	3	US-08-906-616-63	Sequence 63, Appl	c 794	8	2.2	202	4	US-09-902-540-11464	Sequence 11464, A
722	8	2.2	97	3	US-08-917-795-63	Sequence 63, Appl	c 795	8	2.2	210	4	US-09-252-991A-28014	Sequence 28014, A
723	8	2.2	97	3	US-08-485-443B-63	Sequence 63, Appl	797	8	2.2	211	3	US-09-220-731-25	Sequence 25, Appl
724	8	2.2	97	3	US-08-639-075A-63	Sequence 63, Appl	798	8	2.2	211	4	US-09-242-999-20	Sequence 20, Appl
725	8	2.2	97	3	US-09-012-431-63	Sequence 63, Appl	799	8	2.2	218	3	US-09-578-303-3	Sequence 3, Appli
726	8	2.2	97	3	US-09-012-692-63	Sequence 63, Appl	800	8	2.2	221	4	US-09-959-392-33	Sequence 33, Appl
727	8	2.2	97	3	US-08-906-613-63	Sequence 63, Appl	c 801	8	2.2	222	1	US-08-126-593A-2	Sequence 2, Appli
728	8	2.2	97	5	PCT-US95-14442A-63	Sequence 63, Appl	c 802	8	2.2	222	1	US-08-454-039A-2	Sequence 2, Appli
c 729	8	2.2	98	4	US-09-621-976-6623	Sequence 6623, Ap	c 803	8	2.2	222	1	US-08-278-091-9	Sequence 9, Appli
730	8	2.2	99	3	US-08-906-769-93	Sequence 93, Appl	804	8	2.2	223	1	US-08-278-091-13	Sequence 13, Appl
731	8	2.2	99	3	US-08-906-616-93	Sequence 93, Appl	805	8	2.2	223	1	US-08-483-859-9	Sequence 9, Appli
732	8	2.2	99	3	US-08-917-795-93	Sequence 93, Appl	806	8	2.2	223	1	US-08-483-859-13	Sequence 13, Appl
733	8	2.2	99	3	US-08-639-075A-93	Sequence 93, Appl	807	8	2.2	223	1	US-08-472-173-9	Sequence 9, Appli
734	8	2.2	99	3	US-09-012-431-93	Sequence 93, Appl	808	8	2.2	223	1	US-08-472-173-13	Sequence 13, Appl
735	8	2.2	99	3	US-09-012-692-93	Sequence 93, Appl	809	8	2.2	223	2	US-08-487-167-9	Sequence 9, Appli
736	8	2.2	99	3	US-08-906-613-93	Sequence 93, Appl	810	8	2.2	223	2	US-08-487-167-13	Sequence 13, Appl
737	8	2.2	99	5	PCT-US95-14442A-93	Sequence 93, Appl	811	8	2.2	223	2	US-08-482-816-9	Sequence 9, Appli
c 738	8	2.2	100	4	US-09-893-600-3	Sequence 3, Appli	812	8	2.2	223	2	US-08-482-816-13	Sequence 13, Appl
c 739	8	2.2	103	4	US-09-248-796A-27234	Sequence 27234, A	813	8	2.2	223	2	US-08-296-149-9	Sequence 9, Appli
740	8	2.2	103	4	US-09-640-211A-1145	Sequence 1145, Ap	814	8	2.2	223	2	US-08-296-149-13	Sequence 13, Appl
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742	8	2.2	111	4	US-09-270-767-51006	Sequence 51006, A							



816	8	2.2	223	2	US-08-801-499-13	Sequence 13, Appl	889	8	2.2	242	4	US-09-004-729-41	Sequence 41, Appl
817	8	2.2	223	2	US-08-615-271-9	Sequence 9, Appl	890	8	2.2	243	4	US-09-252-991A-17532	Sequence 17532, A
818	8	2.2	223	2	US-08-615-271-13	Sequence 13, Appl	891	8	2.2	246	2	US-08-978-404B-44	Sequence 44, Appl
819	8	2.2	223	3	US-09-074-660-9	Sequence 9, Appl	892	8	2.2	246	3	US-08-906-769-127	Sequence 127, Appl
820	8	2.2	223	3	US-09-074-660-13	Sequence 13, Appl	893	8	2.2	246	3	US-08-906-616-127	Sequence 127, Appl
821	8	2.2	223	3	US-09-074-659-9	Sequence 9, Appl	894	8	2.2	246	3	US-08-639-075A-127	Sequence 127, Appl
822	8	2.2	223	3	US-09-074-659-13	Sequence 13, Appl	895	8	2.2	246	3	US-09-012-431-127	Sequence 127, Appl
823	8	2.2	223	3	US-09-106-468-9	Sequence 9, Appl	896	8	2.2	246	3	US-09-012-692-127	Sequence 127, Appl
824	8	2.2	223	3	US-09-106-468-13	Sequence 13, Appl	897	8	2.2	246	3	US-08-906-613-127	Sequence 127, Appl
825	8	2.2	223	3	US-09-106-466A-9	Sequence 9, Appl	898	8	2.2	247	2	US-08-956-267A-2	Sequence 2, Appl
826	8	2.2	223	3	US-09-106-466A-13	Sequence 13, Appl	899	8	2.2	248	1	US-08-238-130-2	Sequence 2, Appl
827	8	2.2	223	3	US-09-106-467-9	Sequence 9, Appl	900	8	2.2	248	2	US-08-921-426-4	Sequence 4, Appl
828	8	2.2	223	3	US-09-106-467-13	Sequence 13, Appl	901	8	2.2	248	3	US-08-816-915-4	Sequence 4, Appl
829	8	2.2	223	4	US-09-601-318-2	Sequence 2, Appl	902	8	2.2	248	3	US-08-906-769-111	Sequence 111, Appl
c 830	8	2.2	223	4	US-09-270-767-46491	Sequence 46491, A	903	8	2.2	248	3	US-08-906-616-111	Sequence 111, Appl
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832	8	2.2	224	1	US-08-766-982-13	Sequence 13, Appl	905	8	2.2	248	3	US-08-639-075A-111	Sequence 111, Appl
833	8	2.2	224	3	US-08-944-483-34	Sequence 34, Appl	906	8	2.2	248	3	US-09-012-431-111	Sequence 111, Appl
834	8	2.2	224	3	US-08-944-483-36	Sequence 36, Appl	907	8	2.2	248	3	US-09-032-215-37	Sequence 37, Appl
835	8	2.2	224	3	US-09-296-219-13	Sequence 13, Appl	908	8	2.2	248	3	US-09-012-692-111	Sequence 111, Appl
836	8	2.2	225	2	US-09-027-337-5	Sequence 5, Appl	909	8	2.2	248	3	US-08-906-613-111	Sequence 111, Appl
837	8	2.2	225	3	US-09-004-731-13	Sequence 13, Appl	910	8	2.2	248	5	PCT-US95-07743-4	Sequence 4, Appl
838	8	2.2	225	3	US-08-749-699-13	Sequence 13, Appl	911	8	2.2	248	5	PCT-US95-14442A-111	Sequence 111, Appl
839	8	2.2	225	4	US-09-004-729-13	Sequence 13, Appl	912	8	2.2	249	4	US-09-949-016-8770	Sequence 8770, Ap
840	8	2.2	225	4	US-09-644-600-5	Sequence 5, Appl	913	8	2.2	250	3	US-08-944-483-51	Sequence 51, Appl
841	8	2.2	225	4	US-09-654-600A-5	Sequence 5, Appl	c 914	8	2.2	250	4	US-09-949-016-11092	Sequence 11092, A
842	8	2.2	228	3	US-09-004-731-10	Sequence 10, Appl	915	8	2.2	253	3	US-08-906-769-131	Sequence 131, Appl
843	8	2.2	228	3	US-08-749-699-10	Sequence 10, Appl	916	8	2.2	253	3	US-08-906-616-131	Sequence 131, Appl
844	8	2.2	228	4	US-09-004-729-10	Sequence 10, Appl	917	8	2.2	253	3	US-08-639-075A-131	Sequence 131, Appl
845	8	2.2	229	3	US-09-120-582-2	Sequence 2, Appl	918	8	2.2	253	3	US-09-012-431-131	Sequence 131, Appl
846	8	2.2	232	1	US-08-278-091-8	Sequence 8, Appl	919	8	2.2	253	3	US-09-012-692-131	Sequence 131, Appl
847	8	2.2	232	1	US-08-483-859-8	Sequence 8, Appl	920	8	2.2	253	3	US-08-906-613-131	Sequence 131, Appl
848	8	2.2	232	1	US-08-472-173-8	Sequence 8, Appl	921	8	2.2	254	4	US-09-252-991A-18443	Sequence 18443, A
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850	8	2.2	232	2	US-08-487-167-8	Sequence 8, Appl	923	8	2.2	255	3	US-08-906-616-91	Sequence 91, Appl
851	8	2.2	232	2	US-08-482-816-8	Sequence 8, Appl	924	8	2.2	255	3	US-08-817-795-91	Sequence 91, Appl
852	8	2.2	232	2	US-08-296-149-8	Sequence 8, Appl	925	8	2.2	255	3	US-08-639-075A-91	Sequence 91, Appl
853	8	2.2	232	2	US-08-801-499-8	Sequence 8, Appl	926	8	2.2	255	3	US-09-012-431-91	Sequence 91, Appl
854	8	2.2	232	2	US-08-978-404B-45	Sequence 45, Appl	927	8	2.2	255	3	US-09-012-692-91	Sequence 91, Appl
855	8	2.2	232	2	US-08-615-271-8	Sequence 8, Appl	928	8	2.2	255	3	US-08-906-613-91	Sequence 91, Appl
856	8	2.2	232	3	US-09-074-660-8	Sequence 8, Appl	c 929	8	2.2	255	4	US-09-252-991A-22405	Sequence 22405, A
857	8	2.2	232	3	US-09-074-659-8	Sequence 8, Appl	930	8	2.2	255	5	PCT-US95-14442A-91	Sequence 91, Appl
858	8	2.2	232	3	US-08-906-769-81	Sequence 81, Appl	931	8	2.2	258	1	US-08-744-026-3	Sequence 3, Appl
859	8	2.2	232	3	US-09-106-468-8	Sequence 8, Appl	932	8	2.2	258	2	US-09-102-732-3	Sequence 3, Appl
860	8	2.2	232	3	US-08-306-616-81	Sequence 81, Appl	933	8	2.2	258	3	US-09-004-731-16	Sequence 16, Appl
861	8	2.2	232	3	US-08-817-795-81	Sequence 81, Appl	934	8	2.2	258	3	US-09-004-731-19	Sequence 19, Appl
862	8	2.2	232	3	US-09-106-466A-8	Sequence 8, Appl	935	8	2.2	258	3	US-09-261-767-3	Sequence 3, Appl
863	8	2.2	232	3	US-08-639-075A-81	Sequence 81, Appl	936	8	2.2	258	3	US-08-749-699-16	Sequence 16, Appl
864	8	2.2	232	3	US-09-106-467-8	Sequence 8, Appl	937	8	2.2	258	3	US-08-749-699-19	Sequence 19, Appl
865	8	2.2	232	3	US-09-012-431-81	Sequence 81, Appl	938	8	2.2	258	4	US-09-004-729-16	Sequence 16, Appl
866	8	2.2	232	3	US-08-906-613-81	Sequence 81, Appl	939	8	2.2	258	4	US-09-004-729-19	Sequence 19, Appl
867	8	2.2	232	3	PCT-US95-14442A-81	Sequence 81, Appl	940	8	2.2	260	3	US-08-906-769-139	Sequence 139, Appl
868	8	2.2	233	4	US-09-636-382A-24	Sequence 24, Appl	941	8	2.2	260	3	US-08-906-616-139	Sequence 139, Appl
869	8	2.2	234	4	US-08-944-483-46	Sequence 46, Appl	942	8	2.2	260	3	US-08-639-075A-139	Sequence 139, Appl
870	8	2.2	234	4	US-09-513-999C-7815	Sequence 7815, Ap	943	8	2.2	260	3	US-09-012-431-139	Sequence 139, Appl
871	8	2.2	234	4	US-08-640-211A-835	Sequence 835, Ap	944	8	2.2	260	3	US-09-012-692-139	Sequence 139, Appl
872	8	2.2	235	3	US-08-944-483-48	Sequence 48, Appl	945	8	2.2	260	3	US-08-906-613-139	Sequence 139, Appl
873	8	2.2	235	3	US-08-684-862-5	Sequence 5, Appl	946	8	2.2	261	3	US-08-163-919A-2	Sequence 2, Appl
874	8	2.2	236	2	US-08-738-413B-10	Sequence 10, Appl	947	8	2.2	261	4	US-08-462-515-2	Sequence 2, Appl
875	8	2.2	237	3	US-09-004-731-22	Sequence 22, Appl	948	8	2.2	261	5	PCT-US94-14073-2	Sequence 2, Appl
876	8	2.2	237	3	US-08-749-699-22	Sequence 22, Appl	949	8	2.2	261	6	5270178-5	Patent No. 5270178
877	8	2.2	237	3	US-09-004-729-22	Sequence 22, Appl	950	8	2.2	261	6	5270178-19	Patent No. 5270178
878	8	2.2	237	4	US-09-004-729-22	Sequence 22, Appl	951	8	2.2	261	6	5270178-20	Patent No. 5270178
879	8	2.2	238	4	US-08-944-483-39	Sequence 39, Appl	952	8	2.2	261	6	5270178-21	Patent No. 5270178
880	8	2.2	238	4	US-09-664-595A-15	Sequence 15, Appl	953	8	2.2	261	6	5270178-5	Patent No. 5270178
881	8	2.2	239	3	US-09-004-731-44	Sequence 44, Appl	954	8	2.2	261	6	5270178-19	Patent No. 5270178
882	8	2.2	239	3	US-08-749-699-44	Sequence 44, Appl	955	8	2.2	261	6	5270178-20	Patent No. 5270178
883	8	2.2	239	4	US-09-004-729-44	Sequence 44, Appl	956	8	2.2	261	6	5270178-21	Patent No. 5270178
884	8	2.2	241	3	US-08-944-483-59	Sequence 59, Appl	957	8	2.2	262	1	US-07-720-189-1	Sequence 1, Appl
885	8	2.2	241	3	US-08-944-483-60	Sequence 60, Appl	958	8	2.2	262	1	US-08-744-026-4	Sequence 4, Appl
886	8	2.2	242	3	US-09-004-731-41	Sequence 41, Appl	959	8	2.2	262	2	US-08-790-137-1	Sequence 1, Appl
887	8	2.2	242	3	US-09-032-215-47	Sequence 47, Appl	960	8	2.2	262	2	US-08-790-137-3	Sequence 3, Appl
888	8	2.2	242	3	US-08-749-699-41	Sequence 41, Appl	961	8	2.2	262	2	US-08-681-151-4	Sequence 4, Appl

962	8	2.2	262	2	US-09-102-732-4	Sequence 4, Appli	1035	8	2.2	300	4	US-09-242-999-4	Sequence 4, Appli
963	8	2.2	262	2	US-08-824-874-4	Sequence 4, Appli	1036	8	2.2	300	4	US-09-242-999-6	Sequence 6, Appli
964	8	2.2	262	2	US-08-807-151-4	Sequence 4, Appli	1037	8	2.2	302	3	US-08-765-856-4	Sequence 4, Appli
965	8	2.2	262	3	US-09-261-767-4	Sequence 4, Appli	1038	8	2.2	302	3	US-08-935-009A-4	Sequence 4, Appli
966	8	2.2	262	3	US-09-210-084-4	Sequence 4, Appli	1039	8	2.2	302	3	US-08-220-731-26	Sequence 26, Appli
967	8	2.2	262	3	US-09-478-957-4	Sequence 4, Appli	1040	8	2.2	302	3	US-09-242-999-22	Sequence 22, Appli
968	8	2.2	262	4	US-09-764-762-4	Sequence 4, Appli	1041	8	2.2	304	3	US-09-088-651-2	Sequence 2, Appli
969	8	2.2	262	4	US-09-618-259-9	Sequence 9, Appli	1042	8	2.2	308	3	US-08-705-875A-10	Sequence 10, Appli
970	8	2.2	263	2	US-08-790-137-4	Sequence 4, Appli	1043	8	2.2	310	4	US-09-252-991A-19986	Sequence 10, Appli
971	8	2.2	263	2	US-08-824-874-5	Sequence 5, Appli	1044	8	2.2	310	4	US-09-242-999-10	Sequence 10, Appli
972	8	2.2	263	2	US-08-807-151-5	Sequence 5, Appli	1045	8	2.2	311	3	US-09-179-558-66	Sequence 66, Appli
973	8	2.2	263	3	US-09-210-084-5	Sequence 5, Appli	1046	8	2.2	311	4	US-09-722-825-66	Sequence 66, Appli
974	8	2.2	263	3	US-09-478-957-5	Sequence 5, Appli	1047	8	2.2	311	4	US-09-722-825-66	Sequence 66, Appli
975	8	2.2	263	4	US-09-764-762-5	Sequence 5, Appli	1048	8	2.2	311	4	US-09-722-708-66	Sequence 66, Appli
976	8	2.2	265	4	US-08-968-686-10	Sequence 10, Appli	1049	8	2.2	312	4	US-09-636-382A-15	Sequence 15, Appli
977	8	2.2	267	4	US-09-248-796A-15322	Sequence 15322, A	1050	8	2.2	317	4	US-09-949-016-6011	Sequence 6011, Ap
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981	8	2.2	268	3	US-09-032-215-42	Sequence 42, Appli	1054	8	2.2	334	4	US-09-949-016-8549	Sequence 8549, Ap
982	8	2.2	268	4	US-09-764-762-1	Sequence 1, Appli	1055	8	2.2	334	4	US-09-949-016-8571	Sequence 8571, Ap
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1263	8	2.2	1239	3	US-09-285-503-2	Sequence 2, Appli	1336	7	1.9	10	2	US-08-724-548-45	Sequence 45, Appli
1264	8	2.2	1239	3	US-09-709-126-2	Sequence 2, Appli	1337	7	1.9	10	2	US-08-724-548-45	Sequence 45, Appli
1265	8	2.2	1239	3	US-09-871-385A-2	Sequence 2, Appli	1338	7	1.9	10	2	US-08-724-548-48	Sequence 48, Appli
1266	8	2.2	1248	2	US-09-080-897-2	Sequence 2, Appli	1339	7	1.9	10	2	US-08-724-548-48	Sequence 48, Appli
1267	8	2.2	1248	3	US-09-323-735-2	Sequence 4, Appli	1340	7	1.9	10	2	US-08-716-317-31	Sequence 31, Appli
1268	8	2.2	1255	3	US-09-080-897-4	Sequence 4, Appli	1341	7	1.9	10	2	US-08-716-317-31	Sequence 31, Appli
1269	8	2.2	1255	3	US-08-899-595-1	Sequence 1, Appli	1342	7	1.9	10	3	US-07-978-674B-5	Sequence 5, Appli
1270	8	2.2	1255	3	US-09-323-735-4	Sequence 4, Appli	1343	7	1.9	10	3	US-07-978-674B-9	Sequence 9, Appli
1271	8	2.2	1297	3	US-09-540-248A-17	Sequence 17, Appli	1344	7	1.9	10	3	US-07-978-674B-45	Sequence 45, Appli
1272	8	2.2	1315	3	US-08-899-595-3	Sequence 3, Appli	1345	7	1.9	10	3	US-07-978-674B-46	Sequence 46, Appli
1273	8	2.2	1327	3	US-09-196-387-2	Sequence 2, Appli	1346	7	1.9	10	3	US-07-978-674B-47	Sequence 47, Appli
1274	8	2.2	1327	4	US-09-841-835-2	Sequence 2, Appli	1347	7	1.9	10	3	US-07-978-674B-48	Sequence 48, Appli
1275	8	2.2	1327	4	US-09-972-115A-8	Sequence 8, Appli	1348	7	1.9	10	3	US-07-978-674B-49	Sequence 49, Appli
1276	8	2.2	1400	3	US-08-630-915A-37	Sequence 37, Appli	1349	7	1.9	10	3	US-09-101-649-7	Sequence 7, Appli
1277	8	2.2	1400	4	US-09-879-957-37	Sequence 37, Appli	1350	7	1.9	10	3	US-09-101-649-18	Sequence 18, Appli
1278	8	2.2	1497	4	US-09-060-854B-2	Sequence 2, Appli	1351	7	1.9	10	3	US-09-101-649-25	Sequence 25, Appli
1279	8	2.2	1497	4	US-09-060-854B-2	Sequence 2, Appli	1352	7	1.9	10	3	US-09-101-649-32	Sequence 32, Appli
1280	8	2.2	1497	4	US-09-529-904-3	Sequence 3, Appli	1353	7	1.9	10	3	US-09-101-649-39	Sequence 39, Appli
1281	8	2.2	1497	4	US-09-529-904-3	Sequence 3, Appli	1354	7	1.9	10	3	US-09-101-649-53	Sequence 53, Appli
1282	8	2.2	1527	4	US-09-695-795A-4	Sequence 4, Appli	1355	7	2.0	10	6	5252466-18	Patent No. 5252466
1283	8	2.2	1614	4	US-09-060-299-42	Sequence 42, Appli	1356	7	2.0	10	6	5252466-18	Patent No. 5252466
1284	8	2.2	1614	4	US-09-402-923A-42	Sequence 42, Appli	1357	7	2.0	10	6	5252466-18	Patent No. 5252466
1285	8	2.2	1874	4	US-09-602-787A-46	Sequence 46, Appli	1358	7	2.0	13	3	US-09-058-562-32	Sequence 32, Appli
1286	8	2.2	1958	1	US-07-945-283-2	Sequence 2, Appli	1359	7	2.0	14	3	US-08-595-945-13	Sequence 13, Appli
1287	8	2.2	2508	4	US-09-627-650B-7	Sequence 7, Appli	1360	7	2.0	15	1	US-07-720-189-6	Sequence 6, Appli
1288	8	2.2	2508	4	US-09-436-063C-7	Sequence 7, Appli	1361	7	2.0	15	3	US-08-602-999A-310	Sequence 310, App
1289	8	2.2	2544	4	US-09-627-650B-3	Sequence 3, Appli	1362	7	2.0	15	3	US-08-602-999A-346	Sequence 346, App
1290	8	2.2	2544	4	US-09-436-063C-3	Sequence 3, Appli	1363	7	2.0	15	3	US-08-602-999A-352	Sequence 352, App
1291	8	2.2	2601	4	US-09-627-650B-9	Sequence 9, Appli	1364	7	2.0	15	3	US-08-602-999A-354	Sequence 354, App
1292	8	2.2	2601	4	US-09-436-063C-9	Sequence 9, Appli	1365	7	2.0	15	3	US-08-602-999A-381	Sequence 381, App
1293	8	2.2	3118	2	US-08-457-273B-8	Sequence 8, Appli	1366	7	2.0	15	3	US-08-602-999A-382	Sequence 382, App
1294	8	2.2	3119	1	US-08-246-982A-16	Sequence 16, Appli	1367	7	2.0	15	3	US-08-602-999A-415	Sequence 415, App
1295	8	2.2	3119	1	US-08-453-265-16	Sequence 16, Appli	1368	7	2.0	15	3	US-08-602-999A-423	Sequence 423, App
1296	8	2.2	3472	4	US-09-408-020-4	Sequence 4, Appli	1369	7	2.0	15	3	US-08-602-999A-453	Sequence 453, App
1297	8	2.2	3730	4	US-09-949-016-9908	Sequence 9908, Ap	1370	7	2.0	15	4	US-09-500-124-310	Sequence 310, App
1298	7	1.9	8	1	US-07-969-307A-18	Sequence 18, Appli	1371	7	2.0	15	4	US-09-500-124-346	Sequence 346, App
1299	7	2.0	9	1	US-07-819-361-5	Sequence 5, Appli	1372	7	2.0	15	4	US-09-500-124-348	Sequence 348, App
1300	7	1.9	9	1	US-07-969-307A-19	Sequence 19, Appli	1373	7	2.0	15	4	US-09-500-124-352	Sequence 352, App
1301	7	2.0	9	1	US-08-179-574-5	Sequence 5, Appli	1374	7	2.0	15	4	US-09-500-124-354	Sequence 354, App
1302	7	2.0	9	1	US-08-485-455D-10	Sequence 10, Appli	1375	7	2.0	15	4	US-09-500-124-381	Sequence 381, App
1303	7	1.9	9	1	US-08-425-069-12	Sequence 12, Appli	1376	7	2.0	15	4	US-09-500-124-382	Sequence 382, App
1304	7	2.0	9	2	US-08-482-130C-10	Sequence 10, Appli	1377	7	2.0	15	4	US-09-500-124-415	Sequence 415, App
1305	7	2.0	9	2	US-08-484-211C-10	Sequence 10, Appli	1378	7	2.0	15	4	US-09-500-124-423	Sequence 423, App
1306	7	1.9	9	2	US-08-317-844B-12	Sequence 12, Appli	1379	7	2.0	15	4	US-09-500-124-453	Sequence 453, App
1307	7	1.9	9	3	US-08-159-339A-157	Sequence 157, App	1380	7	1.9	16	2	US-08-308-494A-2	Sequence 2, Appli
1308	7	2.0	9	3	US-08-506-769-10	Sequence 10, Appli	1381	7	2.0	16	3	US-08-602-999A-344	Sequence 344, App
1309	7	2.0	9	3	US-08-906-616-10	Sequence 10, Appli	1382	7	2.0	16	3	US-08-602-999A-422	Sequence 422, App
1310	7	2.0	9	3	US-08-817-795-10	Sequence 10, Appli	1383	7	2.0	16	4	US-09-500-124-344	Sequence 344, App
1311	7	2.0	9	3	US-08-485-443B-10	Sequence 10, Appli	1384	7	2.0	16	4	US-09-500-124-422	Sequence 422, App
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1313	7	2.0	9	3	US-09-012-431-10	Sequence 10, Appli	1386	7	1.9	16	4	US-09-314-540A-3	Sequence 3, Appli
1314	7	2.0	9	3	US-09-012-692-10	Sequence 10, Appli	1387	7	1.9	17	3	US-08-890-157A-1	Sequence 1, Appli
1315	7	2.0	9	3	US-08-906-613-10	Sequence 10, Appli	1388	7	1.9	17	3	US-08-836-922-18	Sequence 18, Appli
1316	7	2.0	9	3	US-09-510-738A-87	Sequence 87, Appli	1389	7	2.0	17	3	US-08-602-999A-380	Sequence 380, App
1317	7	2.0	9	3	US-09-502-600-49	Sequence 49, Appli	1390	7	2.0	17	3	US-08-602-999A-413	Sequence 413, App
1318	7	2.0	9	3	US-09-502-600-84	Sequence 84, Appli	1391	7	2.0	17	3	US-08-602-999A-416	Sequence 416, App
1319	7	2.0	9	3	US-09-502-600-119	Sequence 119, App	1392	7	2.0	17	4	US-09-500-124-380	Sequence 380, App
1320	7	2.0	9	3	US-09-502-600-124	Sequence 124, App	1393	7	2.0	17	4	US-09-500-124-413	Sequence 413, App
1321	7	2.0	9	3	US-09-502-600-135	Sequence 135, App	1394	7	2.0	17	4	US-09-500-124-416	Sequence 416, App
1322	7	2.0	9	3	US-09-343-011B-6	Sequence 6, Appli	1395	7	1.9	18	1	US-09-639-881-18	Sequence 18, Appli
1323	7	2.0	9	4	US-09-861-966-87	Sequence 87, Appli	1396	7	1.9	18	1	US-08-240-712-33	Sequence 33, Appli
1324	7	2.0	9	4	US-09-295-924B-9	Sequence 9, Appli	1397	7	1.9	18	1	US-08-443-890-33	Sequence 33, Appli
1325	7	2.0	9	4	US-09-918-243-49	Sequence 49, Appli	1398	7	2.0	18	3	US-08-602-999A-303	Sequence 303, App
1326	7	2.0	9	4	US-09-918-243-84	Sequence 84, Appli	1399	7	2.0	18	3	US-08-602-999A-371	Sequence 371, App



Db 21 LysIlePheAsnGlyThrGluCysGlyArgAsnSerGlnProTrrpGlnValGlyLeuPhe 40  
Qy 241 GAGGACACAGCTGGCTGGGGGTGCTCTATTGACACAGTGGTCTCTACAGC 300  
Db 41 GluGlyThrSerLeuArgCysGlyGlyValLeuIleAspHisArgTrrpValLeuThrAla 60  
Qy 301 GCTCACTGAGCGGACAGAGTACTGGGTGGCCCTGGGGGAACACAGCTCAGCCAGCTC 360  
Db 61 AlaHisCysSerGlySerArgTrrpValArgLeuGlyGluHisSerLeuSerGlnLeu 80  
Qy 361 GACTGACGACAGACATCGGCACAGCGCTTCTCTGTGACCCATCCCGCTACCTGGGA 420  
Db 81 AspTrrpThrGluGlnIleArgHisSerGlyPheSerValThrHisProGlyTrrLeuGly 100  
Qy 421 GCCTGACGAGCAGACAGACACTCCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 480  
Db 101 AlaSerThrSerHisGluHisAspLeuArgLeuLeuArgLeuProValArgVal 120  
Qy 481 ACCAGCAGCTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCCGAGTGC 540  
Db 121 ThrSerSerValGlnProLeuProLeuProAsnAspCysAlaThrAlaGlyThrGluCys 140  
Qy 541 CACGTCTCAGCTGGGACATCCACACACACACAGAACCCATTCCTGGATCTGCTCCAG 600  
Db 141 HisValSerGlyTrrpGlyIleThrAsnHisProArgAsnProPheProAspLeuGln 160  
Qy 601 TGCCTCACTCTCCATCTCCATGCTCCATGCTCCATGCTCCATGCTCCATGCTCCATG 660  
Db 161 CysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyValTrrpGlyArgIle 180  
Qy 661 ACAGCAACATGCTGTGTGTCAGCGCGCTGCCCGGGGAGAGTCCCTGCCAGGGTGAATCT 720  
Db 181 ThrSerAsnMetValCysAlaGlyValProGlyGlnAspAlaCysGlnGlyAspSer 200  
Qy 721 GGGGCGCCCTGGTGTGGGAGTCTTCAAGTCTGGTCTGGTCTGGGCTGGTCTGGGCTGG 780  
Db 201 GlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSerTrrpGlySerValGly 220  
Qy 781 CCCTGTGGACAGATGGATCCCTGGAGTCTACACCTATATTTGC 825  
Db 221 ProCysGlyGlnAspGlyIleProGlyValTrrpGlyThrTrrpGlyCys 235

## RESULT 2

US-09-949-016-8151  
; Sequence 8151, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8151  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8151

Alignment Scores:  
Pred. No.: 1,14e-195 Length: 249  
Score: 222.00 Matches: 249  
Percent Similarity: 98.81% Conservative: 0  
Best Local Similarity: 98.81% Mismatches: 0  
Query Match: 62.18% Indels: 3

DB: 4 Gaps: 0  
US-10-015-385A-193 (1-1091) x US-09-949-016-8151 (1-249)  
Qy 115 CCCACCATGGGCTCAGCATCTTTTGTCTCTGTGTCTCTGGCTCAGCCAGCAGCC 174  
Db 1 ProThrMetGlyLeuSerIlePheLeuLeuLeuCysValLeuGlyLeuSerGlnAlaAla 20  
Qy 175 ACACCGAAGATTTCAATGGCAGTGGCGCTAACTCAGCCCTGGCAGGTGGGG 234  
Db 21 ThrProLysIlePheAsnGlyThrGluCysGlyArgAsnSerGlnProTrrpGlnValGly 40  
Qy 235 CTGTTTGAAGGACACAGCTCGCTGGCGGGGTGCTTATTGACACAGTGGGTCTCT 294  
Db 41 LeuPheGluGlyThrSerLeuArgCysGlyGlyValLeuIleAspHisArgTrrpValLeu 60  
Qy 295 ACAGCGGCTCACTGACGGGACAGAGTACTGGGTGGCTGGGGGAACACAGCCTCAGC 354  
Db 61 ThrAlaAlaHisCysSerGly---ArgTrrpValArgLeuGlyGluHisSerLeuSer 79  
Qy 355 CAGCTCGACTGACCGACAGATCCGACAGCGGCTTCTCTGTGACCCATCCCGCTAC 414  
Db 80 GlnLeuAspTrrpThrGluGlnIleArgHisSerGlyPheSerValThrHisProGlyTrr 99  
Qy 415 CTGGAGGCTCGACAGACAGACAGACAGACCTCCGGCTGTGGCTGGCTGGCTGGCTGC 474  
Db 100 LeuGlyAlaSerThrSerHisGluHisAspLeuArgLeuLeuArgLeuProVal 119  
Qy 475 CGCTTAACACAGCGGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGCAC 534  
Db 120 ArgValThrSerSerValGlnProLeuProLeuProAsnAspCysAlaThrAlaGlyThr 139  
Qy 535 GAGTCCCACTGCTCAGGCTGGGGCATCACCAACACACCGAACCCCATTCCTCCGGATCTG 594  
Db 140 GluCysHisValSerGlyTrrpGlyIleThrAsnHisProArgAsnProPheProAspLeu 159  
Qy 595 CTCAGTGCCTCAACCTTCCATCTCTCCATGCTCCCATGCTCCATGCTGGTGTGTATCCGG 654  
Db 160 LeuGlnCysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyValTrrpGly 179  
Qy 655 AGAATCAGACGACACATGCTGTGTGTCAGCGCGCTCCCGGGCAGAGTCCCTGCCAGGT 714  
Db 180 ArgIleThrSerAsnMetValCysAlaGlyValProGlyGlnAspAlaCysGlnGly 199  
Qy 715 GATTCCTGGGGCCCTCTGTGTGTGGGGAGTCTTCAAGTCTGTCTTGGGGTCT 774  
Db 200 AspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSerTrrpGlySer 219  
Qy 775 GTGGGGCTGTGGACAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTG 834  
Db 220 ValGlyProCysGlyGlnAspGlyIleProGlyValTrrpGlyThrTrrpGlyCysLysTrrVal 239  
Qy 835 GACTCGATCCGATGATCATGAGGAACAAC 864  
Db 240 AspTrrpIleArgMetIleMetArgAsn 249

## RESULT 3

US-09-244-111-6  
; Sequence 6, Application US/09244111  
; Patent No. 6566498  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides  
; FILE REFERENCE: PF391  
; CURRENT APPLICATION NUMBER: US/09/244,111  
; CURRENT FILING DATE: 1999-02-04  
; EARLIER APPLICATION NUMBER: 60/073,961  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 162  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-244-111-6

Alignment Scores:  
Pred. No.: 5,36e-77 Length: 162  
Score: 93.00 Matches: 93  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.05% Indels: 0  
DB: 4 Gaps: 0

US-10-015-385A-193 (1-1091) x US-09-244-111-6 (1-162)

QY 586 CCGATCTGCTCCAGTCCCTCAACCTCTCCATGCTCCCATGCCACCTGCCATGTGTG 645  
Db 70 ProAspLeuLeuGlnCysLeuAsnLeuSerIleValSerHisAlaThrCysHisGlyVal 89  
QY 646 TATCCCGGAGNATCAGACACATGCTGTGTGCGAGCGCGCTCCCGGGCAGGATGCC 705  
Db 90 TyrProGlyArgIleThrSerAsnMetValCysAlaGlyGlyValProGlyGlnAspAla 109  
QY 706 TGCAGGGTGATCTGGGGGCCCTGGTGTGTGGGGAGTCTTCAAGTCTGTGGTCC 765  
Db 110 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSer 129  
QY 766 TGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATTTCG 825  
Db 130 TrpGlySerValGlyProCysGlyGlnAspGlyIleProGlyValTyrThrTyrIleCys 149  
QY 826 AGTATGTGAGTGGATCCGGATGATCATGATCATGAGGAACAAC 864  
Db 150 LysTyrValAspTrpIleArgMetIleMetArgAsnAsn 162

RESULT 4  
5200340-4  
; Patent No. 5200340  
; APPLICANT: POSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,  
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI  
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN  
; ACTIVATORS  
; NUMBER OF SEQUENCES: 34  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/53,412  
; FILING DATE: 22-MAY-1987  
; SEQ ID NO:4:  
; LENGTH: 138  
5200340-4

Alignment Scores:  
Pred. No.: 0.00209 Length: 138  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5200340-4 (1-138)

QY 700 GATGCTCCAGGTGATTCGGGGCCCTGGTGTGTGGGGAGTCTT 738  
Db 83 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 95

RESULT 5  
5200340-4  
; Patent No. 5200340  
; APPLICANT: POSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,  
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI  
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN  
; ACTIVATORS  
; NUMBER OF SEQUENCES: 34  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/53,412  
; FILING DATE: 22-MAY-1987

; SEQ ID NO:4:  
; LENGTH: 138  
5200340-4

Alignment Scores:  
Pred. No.: 0.00209 Length: 138  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5200340-4 (1-138)

QY 700 GATGCTCCAGGTGATTCGGGGCCCTGGTGTGTGGGGAGTCTT 738  
Db 83 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 95

RESULT 6  
5223425-6  
; Patent No. 5223425  
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,  
; BARRY M.; WHITE, TYLER R.  
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT  
; D ACTIVITY  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/277,963  
; FILING DATE: 30-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 34,203  
; FILING DATE: 02-APR-1987  
; SEQ ID NO:6:  
; LENGTH: 222  
5223425-6

Alignment Scores:  
Pred. No.: 0.00197 Length: 222  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-6 (1-222)

QY 712 GGTGATTCGGGGCCCTGGTGTGTGGGGAGTCTT 750  
Db 176 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 188

RESULT 7  
5223425-6  
; Patent No. 5223425  
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,  
; BARRY M.; WHITE, TYLER R.  
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT  
; D ACTIVITY  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/277,963  
; FILING DATE: 30-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 34,203  
; FILING DATE: 02-APR-1987  
; SEQ ID NO:6:  
; LENGTH: 222  
5223425-6

Alignment Scores:  
Pred. No.: 0.00197 Length: 222  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0





APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6232456e  
US-08-944-483-70

Alignment Scores:  
Pred. No.: 0.00195 Length: 243  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x US-08-944-483-70 (1-243)

QY 700 GATGCTGCAGGTGATCTGGGGCCCCCTGGTGT 738  
Db 185 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 197

RESULT 12  
5223425-4  
Patent No. 5223425  
APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,  
BARRY M.; WHITE, TYLER R.  
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT  
D ACTIVITY  
NUMBER OF SEQUENCES: 19  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/277,963  
FILING DATE: 30-NOV-1988  
PRIOR APPLICATION DATA:

APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park

APPLICATION NUMBER: 34,203  
FILING DATE: 02-APR-1987  
SEQ ID NO: 4:  
LENGTH: 250  
5223425-4

Alignment Scores:  
Pred. No.: 0.00195 Length: 250  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-4 (1-250)

QY 712 GGTGATTCTGGGGCCCCCTGGTGTGGGGAGTCCTT 750  
Db 203 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 215

RESULT 13  
5223425-4  
Patent No. 5223425  
APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,  
BARRY M.; WHITE, TYLER R.  
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT  
D ACTIVITY  
NUMBER OF SEQUENCES: 19  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/277,963  
FILING DATE: 30-NOV-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 34,203  
FILING DATE: 02-APR-1987  
SEQ ID NO: 4:  
LENGTH: 250  
5223425-4

Alignment Scores:  
Pred. No.: 0.00195 Length: 250  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 6 Gaps: 0

US-10-015-385A-193 (1-1091) x 5223425-4 (1-250)

QY 712 GGTGATTCTGGGGCCCCCTGGTGTGGGGAGTCCTT 750  
Db 203 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 215

RESULT 14  
US-08-944-483-72  
Sequence 72, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park

/ STATE: IL  
/ COUNTRY: USA  
/ ZIP: 60064-3500  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSeq for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/944,483  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Becker, Cheryl L.  
/ REGISTRATION NUMBER: 35,441  
/ REFERENCE/DOCKET NUMBER: 6183.US.01  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 847/935-1729  
/ TELEFAX: 847/938-2623  
/ TELEX:  
/ INFORMATION FOR SEQ ID NO: 72:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 252 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: NO. 6232456e  
/ US-08-944-483-72

Alignment Scores:  
Pred. No.: 0.00195 Length: 252  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 3 Gaps: 0

US-10-015-385A-193 (1-1091) x US-08-944-483-72 (1-252)

QY 700 GATGCTGCCAGGTGATTCTGGGGCCCCCTGGTGTGT 738  
Db 197 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 209

## RESULT 15

US-09-027-337-8  
/ Sequence 8, Application US/09027337B  
/ Patent No. 5972616  
/ GENERAL INFORMATION:  
/ APPLICANT: O'Brien, Timothy J.  
/ APPLICANT: Tanimoto, Hirotsoshi  
/ TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in  
/ TITLE OF INVENTION: Breast and Ovarian Carcinomas  
/ FILE REFERENCE: D6064  
/ CURRENT APPLICATION NUMBER: US/09/027,337B  
/ CURRENT FILING DATE: 1998-02-20  
/ NUMBER OF SEQ ID NOS: 13  
/ SEQ ID NO 8  
/ LENGTH: 253  
/ TYPE: PRT  
/ ORGANISM: Unknown  
/ FEATURE:  
/ OTHER INFORMATION: Serine protease catalytic domain of tissue plasminogen  
/ OTHER INFORMATION: activator (Tpa) homologous to similar domain in TADG-15  
US-09-027-337-8

Alignment Scores:  
Pred. No.: 0.00194 Length: 253  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0  
US-10-015-385A-193 (1-1091) x US-09-027-337-8 (1-253)  
QY 700 GATGCTGCCAGGTGATTCTGGGGCCCCCTGGTGTGT 738  
Db 198 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 210

Search completed: March 5, 2005, 23:47:13  
Job time : 50.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 5, 2005, 23:34:20 ; Search time 49 Seconds  
(without alignments)  
4284.591 Million cell updates/sec

Title: US-10-015-385A-193

Perfect score: 357

Sequence: 1 caagcaggtcatccctctgg.....aggggcaaaaaaaaaa 1091

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p-model -DRV=xlp  
-Q/cgn2\_1/USPTO\_spool\_p/US1015385/runat\_05032005\_173710\_18168/app\_query.fasta\_1.1287  
-DB=PIR79 -QFMT=fastan -SUFFIX=olin2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptp  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10015385 @CGN 1.1 63 @runat\_05032005\_173710\_18168 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	3.6	246	1 DBHU	complement factor
2	13	3.6	394	2 JS0600	t-plasminogen acti
3	13	3.6	431	2 JS0599	t-plasminogen acti
4	13	3.6	477	1 A34369	t-plasminogen acti
5	13	3.6	477	2 JS0597	t-plasminogen acti
6	13	3.6	477	2 JS0598	t-plasminogen acti
7	13	3.6	559	1 A29941	t-plasminogen acti
8	13	3.6	559	1 A35029	t-plasminogen acti
9	13	3.6	562	1 UKHUT	t-plasminogen acti
10	13	3.6	593	2 S45281	coagulation factor
11	13	3.6	603	2 S28941	coagulation factor
12	13	3.6	615	1 KFHU12	coagulation factor
13	13	3.6	1524	2 T30337	polyprotein - Afri
14	12	3.4	191	2 S54115	complement factor

15	12	3.4	254	2 S65465	trypsin-like prote
16	12	3.4	256	1 TRFP	trypsin-like prote
17	12	3.4	264	2 S32794	trypsin-like prote
18	12	3.4	267	2 S40006	trypsin (EC 3.4.21
19	12	3.4	271	2 S41308	serine proteinase
20	12	3.4	274	2 S35339	trypsin (EC 3.4.21
21	12	3.4	275	2 S40007	trypsin (EC 3.4.21
22	12	3.4	275	2 S40005	trypsin (EC 3.4.21
23	12	3.4	277	2 S35340	trypsin (EC 3.4.21
24	12	3.4	285	2 T35195	probable serine pr
25	11	3.1	126	2 A23473	chymotrypsin-like
26	11	3.1	225	2 S45356	probable serine pr
27	11	3.1	237	2 S55378	serine proteinase
28	11	3.1	237	2 S68702	trypsin (EC 3.4.2
29	11	3.1	260	2 I56559	neuropsin - mouse
30	11	3.1	264	2 J38136	chymotrypsin-like
31	11	3.1	266	2 J38136	chymotrypsin-like
32	11	3.1	270	2 S56160	mast cell tryptase
33	11	3.1	273	2 A47246	tryptase (EC 3.4.2
34	11	3.1	274	2 JC4171	tryptase (EC 3.4.2
35	11	3.1	275	2 C35863	tryptase (EC 3.4.2
36	11	3.1	275	2 B35863	tryptase (EC 3.4.2
37	11	3.1	275	2 A35863	tryptase (EC 3.4.2
38	11	3.1	275	2 A32410	tryptase (EC 3.4.2
39	11	3.1	276	2 A38654	mast cell proteina
40	11	3.1	309	2 B49878	coagulation factor
41	11	3.1	343	1 A57014	proctasin (EC 3.4.
42	11	3.1	400	1 A48050	coagulation factor
43	11	3.1	431	1 UKHU	u-plasminogen acti
44	11	3.1	433	1 JN0560	u-plasminogen acti
45	11	3.1	442	1 UKPG	u-plasminogen acti
46	11	3.1	442	1 UKPG	u-plasminogen acti
47	11	3.1	455	2 A61545	plasmin (EC 3.4.21
48	11	3.1	460	2 B61545	plasmin (EC 3.4.21
49	11	3.1	555	1 A45688	hepatocyte growth
50	11	3.1	790	1 PLFG	plasmin (EC 3.4.21
51	11	3.1	810	1 PLHU	plasmin (EC 3.4.21
52	11	3.1	810	2 I46260	plasmin (EC 3.4.21
53	11	3.1	810	2 B30848	plasmin (EC 3.4.21
54	11	3.1	812	1 PLBO	plasmin (EC 3.4.21
55	11	3.1	812	1 PLMS	plasmin (EC 3.4.21
56	11	3.1	1004	2 T30338	oviductin (EC 3.4.
57	11	3.1	2616	2 A57096	nudel protein prec
58	11	3.1	4548	1 S00657	apoprotein(a) (EC
59	10	2.8	30	2 C32946	serine proteinase
60	10	2.8	43	2 A61168	cocoanase (EC 3.4.
61	10	2.8	61	2 P80049	serine proteinase
62	10	2.8	161	2 I42744	coagulation factor
63	10	2.8	161	2 I48158	coagulation factor
64	10	2.8	238	1 TRWV5Y	trypsin-like prote
65	10	2.8	244	2 A46721	chymase (EC 3.4.21
66	10	2.8	244	2 A34910	mast cell proteina
67	10	2.8	248	2 A35520	natural killer cel
68	10	2.8	248	2 S33755	granzyme-like prot
69	10	2.8	249	2 A55634	granzyme M (EC 3.4
70	10	2.8	254	1 TRWV3Y	trypsin-like prote
71	10	2.8	254	2 S35585	chymotrypsin-like
72	10	2.8	258	2 A45161	serine proteinase
73	10	2.8	263	1 I55608	complement factor
74	10	2.8	303	2 T13598	trypsin homolog -
75	10	2.8	375	1 A23689	limulus clotting e
76	10	2.8	417	1 S00845	hepsin (EC 3.4.21
77	10	2.8	475	1 EXCH	coagulation factor
78	10	2.8	482	1 EXRT	coagulation factor
79	10	2.8	488	1 EXHU	coagulation factor
80	10	2.8	492	1 EXBO	coagulation factor
81	10	2.8	705	1 C1HURB	complement subcomp
82	9	2.5	73	2 S44462	elastase (EC 3.4.2
83	9	2.5	195	2 T03245	G-box binding fact
84	9	2.5	213	2 S17537	fibrinolytic prote
85	9	2.5	214	2 S17680	fibrinolytic prote
86	9	2.5	226	2 S69370	duodenase - bovine
87	9	2.5	226	2 JE0151	myonase (EC 3.4.-

88	9	2.5	232	2	S32398	serine proteinase	161	9	2.5	638	1	KORTPL	plasma kallikrein
89	9	2.5	234	2	F42696	thrombin (EC 3.4.21)	162	9	2.5	761	2	JC5759	brain-specific ser
90	9	2.5	235	2	E42696	thrombin (EC 3.4.21)	163	9	2.5	786	1	A47547	serine proteinase
91	9	2.5	236	2	A28566	T-cell suppressor	164	9	2.5	855	2	JC7731	membrane-bound arg
92	9	2.5	236	2	C42696	thrombin (EC 3.4.21)	165	9	2.5	907	2	E96636	hypothetical prote
93	9	2.5	236	2	T45835	hypothetical prote	166	9	2.5	1019	1	A56318	enteropeptidase (E
94	9	2.5	237	1	TRCY1	trypsin (EC 3.4.21)	167	9	2.5	1034	1	A53663	enteropeptidase (E
95	9	2.5	243	2	A56338	venom proteinase (	168	9	2.5	1035	1	A43090	enteropeptidase (E
96	9	2.5	244	2	S72219	chymotrypsin B - A	169	9	2.5	1113	2	JEO315	low-density lipopr
97	9	2.5	244	2	S72219	chymase (EC 3.4.21)	170	9	2.5	3848	2	T17414	TipC protein - sli
98	9	2.5	245	1	KYBOA	chymotrypsin (EC 3	171	8	2.2	30	2	A32946	trypsin-like serin
99	9	2.5	245	1	KYBOB	chymotrypsin (EC 3	172	8	2.2	72	2	A42856	EPF autoantibody-r
100	9	2.5	245	1	A48598	kallikrein-like se	173	8	2.2	75	2	A37002	catoxinin I (EC 3
101	9	2.5	246	2	A32692	cytotoxic T-lympho	174	8	2.2	81	2	A18966	tissue kallikrein
102	9	2.5	246	2	S64707	chymase (EC 3.4.21)	175	8	2.2	82	1	FDFLAW	antifreeze protein
103	9	2.5	247	1	PRMSCL	granzyme B (EC 3.4	176	8	2.2	82	2	S02326	antifreeze protein
104	9	2.5	247	1	S64708	chymase (EC 3.4.21)	177	8	2.2	82	2	I51125	antifreeze protein
105	9	2.5	248	1	S01007	granzyme F (EC 3.4	178	8	2.2	82	2	A05161	antifreeze protein
106	9	2.5	248	2	S55067	trypsin (EC 3.4.21)	179	8	2.2	90	2	JEO210	proteinase (EC 3.4
107	9	2.5	248	2	S01006	cytotoxic T-lympho	180	8	2.2	94	2	PC2013	tissue kallikrein
108	9	2.5	248	2	S43259	granzyme-like prot	181	8	2.2	100	2	T17126	hypothetical prote
109	9	2.5	251	2	T10262	mast cell serine p	182	8	2.2	101	2	H69091	ribosomal protein
110	9	2.5	251	2	JC2125	chymase (EC 3.4.21)	183	8	2.2	102	2	A72518	hypothetical prote
111	9	2.5	252	2	A36172	procytotoxic T-lym	184	8	2.2	103	2	T47718	hypothetical prote
112	9	2.5	253	2	A53968	serine proteinase	185	8	2.2	109	2	S58673	RNA-binding protei
113	9	2.5	256	2	T10109	trypsin (EC 3.4.21)	186	8	2.2	110	2	AC2391	RNA-binding protei
114	9	2.5	258	1	S44184	chymotrypsin (EC 3	187	8	2.2	126	2	T16727	hypothetical prote
115	9	2.5	258	2	T13591	tail fiber adhesin	188	8	2.2	129	2	T19263	hypothetical prote
116	9	2.5	258	4	S70439	pancreatic elastas	189	8	2.2	129	2	A70967	hypothetical prote
117	9	2.5	259	1	S49129	chymotrypsin (EC 3	190	8	2.2	133	2	H84217	hypothetical prote
118	9	2.5	260	2	S00276	tail fiber protein	191	8	2.2	135	2	A70659	hypothetical prote
119	9	2.5	261	1	A32297	seminogelase (EC 3	192	8	2.2	135	2	E96750	hypothetical prote
120	9	2.5	261	1	S35711	seminogelase (EC 3	193	8	2.2	135	2	S34952	histone H1 - Euplo
121	9	2.5	261	2	A25986	tissue kallikrein	194	8	2.2	136	2	T29282	hypothetical prote
122	9	2.5	261	2	S40162	cathpsin G (EC 3	195	8	2.2	142	2	S12311	glycine-rich RNA-b
123	9	2.5	263	1	KYRTB	chymotrypsin (EC 3	196	8	2.2	146	2	T06796	glycine-rich RNA-b
124	9	2.5	263	2	A31299	chymotrypsin (EC 3	197	8	2.2	149	2	S35208	serine proteinase
125	9	2.5	263	2	A21195	chymotrypsin (EC 3	198	8	2.2	152	2	G96010	hypothetical expor
126	9	2.5	263	2	S47537	chymotrypsin (EC 3	199	8	2.2	154	2	T19332	hypothetical prote
127	9	2.5	265	2	I48679	neutrophil elastas	200	8	2.2	154	2	E96603	unknown protein F1
128	9	2.5	266	1	ELPG	pancreatic elastas	201	8	2.2	154	2	E96728	hypothetical prote
129	9	2.5	266	1	ELRT1	pancreatic elastas	202	8	2.2	155	2	D84187	hypothetical prote
130	9	2.5	266	2	S54146	trypsin (EC 3.4.21)	203	8	2.2	157	2	S04536	embryonic abundan
131	9	2.5	267	4	A56615	probable pancreati	204	8	2.2	161	2	H85120	probable proline-r
132	9	2.5	269	2	A49334	Ras homolog Rad -	205	8	2.2	166	1	KNRZG1	glycine-rich cell
133	9	2.5	274	2	A45754	trypsin (EC 3.4.21)	206	8	2.2	166	2	T18691	hypothetical prote
134	9	2.5	281	1	A61021	acrosin (EC 3.4.21)	207	8	2.2	168	1	S12312	glycine-rich RNA-b
135	9	2.5	366	2	JEO105	testicular serine	208	8	2.2	169	1	S38331	glycine-rich RNA-b
136	9	2.5	367	2	D82763	UDP-N-acetylglucos	209	8	2.2	169	2	A49247	merozoite surface
137	9	2.5	367	2	S04336	regulatory protein	210	8	2.2	171	2	H84709	merozoite surface
138	9	2.5	378	1	S36202	acrosin (EC 3.4.21)	211	8	2.2	176	2	D49247	hypothetical prote
139	9	2.5	415	1	A34170	hepsin (EC 3.4.21)	212	8	2.2	182	2	T30760	glycine-rich cell
140	9	2.5	416	1	S33777	acrosin (EC 3.4.21)	213	8	2.2	183	1	KNRZG2	nodulin-20 precurs
141	9	2.5	420	2	A37344	acrosin (EC 3.4.21)	214	8	2.2	185	2	B26669	GCR 1 protein - fr
142	9	2.5	420	2	A55283	acrosin (EC 3.4.21)	215	8	2.2	188	2	S49192	myosin alkali ligh
143	9	2.5	421	1	S11674	acrosin (EC 3.4.21)	216	8	2.2	192	1	MOCHLA	myosin alkali ligh
144	9	2.5	421	1	S29599	acrosin (EC 3.4.21)	217	8	2.2	192	1	MORBLA	myosin regulatory
145	9	2.5	421	2	S29599	acrosin (EC 3.4.21)	218	8	2.2	195	2	S28845	nodulin-20a - soyb
146	9	2.5	431	2	A47538	hypothetical prote	219	8	2.2	195	2	T07735	hypothetical prote
147	9	2.5	432	2	T08944	hypothetical prote	220	8	2.2	196	2	T08808	hypothetical prote
148	9	2.5	436	2	JX0172	acrosin (EC 3.4.21)	221	8	2.2	201	2	T49792	alternative splici
149	9	2.5	437	2	S18407	acrosin (EC 3.4.21)	222	8	2.2	201	2	C40040	alternative splici
150	9	2.5	528	2	D46449	hypothetical prote	223	8	2.2	201	2	S26404	glycine-rich prote
151	9	2.5	558	2	JC5878	plasma hyaluronan-	224	8	2.2	203	1	JQ1061	eggshell protein 2
152	9	2.5	560	1	JC4795	plasma hyaluronan-	225	8	2.2	207	2	B44994	eggshell protein 2
153	9	2.5	583	2	A29154	complement factor	226	8	2.2	207	2	I53154	hypothetical prote
154	9	2.5	613	2	S15468	complement C3b/C4b	227	8	2.2	207	2	B95348	hypothetical prote
155	9	2.5	617	2	S10511	thrombin (EC 3.4.2	228	8	2.2	211	2	S28304	hypothetical prote
156	9	2.5	618	2	A35827	thrombin (EC 3.4.2	229	8	2.2	212	2	A44994	eggshell protein 1
157	9	2.5	622	1	TBBU	thrombin (EC 3.4.2	230	8	2.2	212	2	T49559	related to proline
158	9	2.5	625	1	TBBU	thrombin (EC 3.4.2	231	8	2.2	214	1	KNNI2S	glycine-rich prote
159	9	2.5	638	1	KQHUP	plasma kallikrein	232	8	2.2	214	2	C96798	hypothetical prote
160	9	2.5	638	1	KQMSPL	plasma kallikrein	233	8	2.2	216	1	KYVH20	chymotrypsin (EC 3

234	8	2.2	218	1	KYVH2C	chymotrypsin (EC 3	307	8	2.2	261	2	G87535	regulatory protein
235	8	2.2	219	2	AEO283	proline-rich prote	308	8	2.2	262	1	A31372	granzyme A (EC 3.4
236	8	2.2	220	2	AE0284	probable membrane	309	8	2.2	262	1	JC4803	venombin A (EC 3.4
237	8	2.2	221	2	T04592	nodulin-30 - kidne	310	8	2.2	262	1	KOHU	tissue kallikrein
238	8	2.2	222	2	T04592	glycine-rich cell	311	8	2.2	263	2	S15686	tissue kallikrein
239	8	2.2	224	2	TS1742	RNA helicase RH11	312	8	2.2	264	2	S65663	granzyme 3 (EC 3.4
240	8	2.2	227	2	G70555	hypothetical prote	313	8	2.2	265	2	A38894	serine proteinase
241	8	2.2	229	1	TRBOTR	trypsin (EC 3.4.21	314	8	2.2	265	2	JU0260	trypsin (EC 3.4.21
242	8	2.2	229	1	TRDFS	trypsin (EC 3.4.21	315	8	2.2	265	2	T15451	hypothetical prote
243	8	2.2	230	2	I48685	mast cell proteina	316	8	2.2	265	2	T10495	chymotrypsin (EC 3
244	8	2.2	231	1	TRPQTR	trypsin (EC 3.4.21	317	8	2.2	269	2	B26823	pancreatic elastas
245	8	2.2	231	1	S31778	trypsin (EC 3.4.21	318	8	2.2	269	2	C26823	pancreatic elastas
246	8	2.2	232	1	KQFG	tissue kallikrein	319	8	2.2	269	2	B32410	pancreatic elastas
247	8	2.2	232	1	A54361	venombin A (EC 3.4	320	8	2.2	269	2	A26823	pancreatic elastas
248	8	2.2	235	1	S65621	venombin AB (EC 3	321	8	2.2	270	2	A60830	keratin, 70k type
249	8	2.2	236	1	A31211	snake venom factor	322	8	2.2	270	2	F95962	probable taurin up
250	8	2.2	236	1	A41456	venombin A (EC 3.4	323	8	2.2	271	1	ELRT2	pancreatic elastas
251	8	2.2	236	1	B32121	snake venom factor	324	8	2.2	271	2	S29239	chymotrypsin (EC 3
252	8	2.2	236	2	I42696	thrombin (EC 3.4.2	325	8	2.2	271	2	A25528	pancreatic elastas
253	8	2.2	238	2	S31779	trypsin (EC 3.4.21	326	8	2.2	272	2	JC4170	trypsin-like prote
254	8	2.2	239	2	A27207	tissue kallikrein	327	8	2.2	274	2	I47078	coagulation factor
255	8	2.2	239	2	S49193	GCR 101 protein -	328	8	2.2	275	2	T02559	probable spliceoso
256	8	2.2	240	2	S39047	trypsin (EC 3.4.21	329	8	2.2	276	2	T33925	hypothetical prote
257	8	2.2	240	2	A46179	U2 snRNP auxiliary	330	8	2.2	280	2	G84839	late embryogenesis
258	8	2.2	241	2	S39048	trypsin (EC 3.4.21	331	8	2.2	281	2	T13596	trypsin homolog -
259	8	2.2	242	2	S31776	trypsin (EC 3.4.21	332	8	2.2	281	2	I38707	probable Ar-hook D
260	8	2.2	242	2	S31775	trypsin (EC 3.4.21	333	8	2.2	282	2	T21222	hypothetical prote
261	8	2.2	242	2	S49489	trypsin (EC 3.4.21	334	8	2.2	282	2	T26635	hypothetical prote
262	8	2.2	243	2	A35871	trypsin (EC 3.4.21	335	8	2.2	284	2	S74256	homeotic protein s
263	8	2.2	244	2	D96707	probable zinc fing	336	8	2.2	285	2	I48144	coagulation factor
264	8	2.2	246	1	TRDGC	trypsin (EC 3.4.21	337	8	2.2	285	2	E84766	probable Ar-hook D
265	8	2.2	246	1	TRRT1	trypsin (EC 3.4.21	338	8	2.2	288	2	S68798	RNA-binding protei
266	8	2.2	246	1	B25528	trypsin (EC 3.4.21	339	8	2.2	291	1	S31415	glycine-rich prote
267	8	2.2	246	2	TRRT2	trypsin (EC 3.4.21	340	8	2.2	291	1	B40040	alternative splici
268	8	2.2	247	1	A25852	trypsin (EC 3.4.21	341	8	2.2	292	2	C84470	hypothetical prote
269	8	2.2	247	1	B25852	trypsin (EC 3.4.21	342	8	2.2	302	2	T06435	ribonuclease S5 ho
270	8	2.2	247	1	TRDG	trypsin (EC 3.4.21	343	8	2.2	308	2	D70875	probable PE protei
271	8	2.2	247	2	S13813	trypsin (EC 3.4.21	344	8	2.2	309	2	T19389	hypothetical prote
272	8	2.2	247	2	A27547	trypsin (EC 3.4.21	345	8	2.2	310	2	T33611	hypothetical prote
273	8	2.2	248	1	PRMSC2	granzyme C (EC 3.4	346	8	2.2	311	2	T02783	probable homeotic
274	8	2.2	248	2	S55066	trypsin (EC 3.4.21	347	8	2.2	312	1	J01559	polyhedron envelop
275	8	2.2	248	2	C91080	hypothetical prote	348	8	2.2	312	2	T21351	hypothetical prote
276	8	2.2	248	2	D85925	hypothetical prote	349	8	2.2	313	2	T30486	polynedral calyx p
277	8	2.2	248	2	A40040	alternative splici	350	8	2.2	314	2	D71410	hypothetical prote
278	8	2.2	250	2	S55493	serine proteinase	351	8	2.2	314	2	T48514	hypothetical prote
279	8	2.2	250	2	S15685	kallikrein, glandu	352	8	2.2	315	2	T41868	hypothetical prote
280	8	2.2	251	2	PC1235	29K serine protei	353	8	2.2	315	2	T29525	hypothetical prote
281	8	2.2	252	2	T45737	hypothetical prote	354	8	2.2	316	2	I50151	acidic ribosomal p
282	8	2.2	255	1	A28169	venombin A (EC 3.4	355	8	2.2	317	1	RSHP0	acidic ribosomal p
283	8	2.2	255	1	B84777	hypothetical prote	356	8	2.2	317	1	RSMS10	acidic ribosomal p
284	8	2.2	256	1	NGMSA	7S nerve growth fa	357	8	2.2	317	2	T29960	hypothetical prote
285	8	2.2	257	1	JC2479	venombin B (EC 3.4	358	8	2.2	318	2	H86342	hypothetical prote
286	8	2.2	257	2	S33772	tissue kallikrein	359	8	2.2	321	2	A38712	fibillarlin [valid
287	8	2.2	257	2	B45061	granzyme A (EC 3.4	360	8	2.2	323	2	S20099	transforming prote
288	8	2.2	258	2	I56220	tryptase 2 - rat	361	8	2.2	327	2	D87645	sensor histidine k
289	8	2.2	258	2	A29259	Ubx protein - fruit	362	8	2.2	329	2	S28442	exB protein - Pse
290	8	2.2	259	1	TRSMG	trypsin (EC 3.4.21	363	8	2.2	330	2	S74255	homeotic protein s
291	8	2.2	259	1	S68424	allergen Der f III	364	8	2.2	332	2	S03871	spherulin 4 precu
292	8	2.2	259	2	A29746	tissue kallikrein	365	8	2.2	333	2	A39065	homeotic protein E
293	8	2.2	260	2	A37938	tissue kallikrein	366	8	2.2	338	1	TVNSPB	transforming prote
294	8	2.2	260	2	A45061	granzyme A (EC 3.4	367	8	2.2	338	2	IS3043	transforming prote
295	8	2.2	260	2	B38594	troponin I - fruit	368	8	2.2	341	2	C83578	hypothetical prote
296	8	2.2	261	1	EGMSB	tissue kallikrein	369	8	2.2	345	1	B41732	heterogeneous nucl
297	8	2.2	261	1	KOWS1	tissue kallikrein	370	8	2.2	345	2	C86272	F7A19.1 protein -
298	8	2.2	261	1	NGMSG	7S nerve growth fa	371	8	2.2	356	1	WJHU2H	homeotic protein H
299	8	2.2	261	1	TRMSG5	tissue kallikrein	372	8	2.2	356	2	G82523	endo-1,4-beta-gluc
300	8	2.2	261	2	A28062	gamma-amin (EC 3	373	8	2.2	367	1	S02193	cellular tumor ant
301	8	2.2	261	2	A25606	tissue kallikrein	374	8	2.2	371	2	C70626	hypothetical prote
302	8	2.2	261	2	S01971	tissue kallikrein	375	8	2.2	378	2	JC47434	cysteine proteinas
303	8	2.2	261	2	JE0236	tissue kallikrein	376	8	2.2	378	2	JC4648	nitrite reductase
304	8	2.2	261	2	A41020	tissue kallikrein	377	8	2.2	381	2	B86175	protein F19p19.21
305	8	2.2	261	2	A24378	tissue kallikrein	378	8	2.2	382	2	AC3073	transcription regu
306	8	2.2	261	2	A29745	tissue kallikrein	379	8	2.2	384	2	H88924	protein F33E11.2 [



526	8	2.2	1675	2	T31473	hypothetical prote	c 599	7	1.9	107	2	T29406	hypothetical prote
527	8	2.2	1714	1	S18644	multifunctional am	600	7	2.0	108	2	T26880	hypothetical prote
528	8	2.2	1726	2	A39401	merozoite surface	601	7	2.0	109	1	R6UTP1	acidic ribosomal p
529	8	2.2	1733	1	B45344	probable nuclear a	602	7	2.0	109	2	T02039	acidic ribosomal p
530	8	2.2	1795	2	F97713	190K antigen precu	603	7	2.0	109	2	T02716	acidic ribosomal p
531	8	2.2	1841	2	T38091	cell division cont	604	7	2.0	109	2	F72666	hypothetical prote
532	8	2.2	1882	1	GNVUTR	genome polyprotein	605	7	2.0	110	2	T37490	hypothetical prote
533	8	2.2	1901	2	F70806	hypothetical glyci	606	7	2.0	110	2	T01565	acidic ribosomal p
534	8	2.2	1958	2	B40505	hypothetical prote	607	7	1.9	110	2	T26817	hypothetical prote
535	8	2.2	2783	1	A41948	alpha-fetoprotein	608	7	2.0	111	2	E72524	probable ribosomal
536	8	2.2	3119	2	I49729	HD protein - mouse	609	7	2.0	111	2	S08438	vxp protein - huma
537	8	2.2	3190	2	T13828	CREB-binding prote	610	7	2.0	111	2	G70772	hypothetical prote
538	8	2.2	3472	2	T31308	hypothetical 367K	611	7	1.9	111	2	S41504	12RNP1 protein - S
539	8	2.2	5327	2	T13564	hypothetical prote	612	7	2.0	112	1	R5PF2E	acidic ribosomal p
540	7	1.9	12	2	A58375	microtubule-associ	613	7	2.0	112	1	ASLJX3	vxp protein - simi
541	7	2.0	15	2	P70037	microcin B17 - Esc	614	7	2.0	112	1	ASLJCX	vxp protein - huma
542	7	2.0	25	2	A35545	light harvesting (C	615	7	2.0	112	1	ASLJGH	vxp protein - huma
543	7	2.0	26	2	A38839	T-kininogenase (C	616	7	2.0	112	1	ASLJST	vxp protein - simi
544	7	2.0	37	2	S23145	histone H2B - sea	617	7	2.0	112	1	ASLJSX	vxp protein - huma
545	7	2.0	38	2	S50764	tissue kallikrein-	618	7	2.0	112	1	ASLJX2	vxp protein - huma
546	7	1.9	40	2	A40128	ribosomal protein	619	7	2.0	112	2	T10267	ribosomal protein
547	7	1.9	40	2	F45095	probable antigen 1	620	7	2.0	112	2	S12155	vxp protein - huma
548	7	2.0	43	2	S35379	photosystem I ligh	621	7	2.0	112	2	S53094	vxp protein - huma
549	7	1.9	53	2	H84319	cadherin-related p	622	7	2.0	112	2	T11562	vxp protein - simi
550	7	2.0	57	2	S10782	hypothetical prote	623	7	2.0	112	2	S07990	vxp protein - simi
551	7	1.9	60	2	T16886	salivary protein P	624	7	2.0	112	2	S03066	gene X protein - h
552	7	1.9	60	2	T00005	hypothetical prote	625	7	1.9	113	2	S44577	C064.3 protein -
553	7	2.0	64	2	A30981	pepJ protein - Aci	626	7	2.0	114	2	T52357	related to ribosom
554	7	1.9	64	2	S53051	prostatic arginine	627	7	2.0	115	2	A25924	Ig kappa chain pre
555	7	2.0	66	2	I52972	glycine rich prote	628	7	1.9	115	2	A84676	60S acidic ribosom
556	7	1.9	69	1	M1EC77	kallikrein - mouse	629	7	1.9	115	2	B84676	60S acidic ribosom
557	7	2.0	70	2	A56784	microcin B17 precu	630	7	2.0	117	2	T46322	hypothetical prote
558	7	2.0	70	2	A96650	kallikrein-like se	631	7	2.0	118	2	T15621	hypothetical prote
559	7	2.0	72	2	D70683	protein F2401.6 [l	632	7	1.9	118	2	D72524	hypothetical prote
560	7	2.0	75	2	S76586	hypothetical prote	633	7	1.9	119	2	E72744	hypothetical prote
561	7	2.0	76	2	B96809	hypothetical prote	634	7	1.9	119	2	T04243	acidic ribosomal p
562	7	2.0	78	2	I35783	protein F28K19.18	635	7	1.9	120	2	T07888	protein kinase (EC
563	7	1.9	78	2	E84686	H+-transporting tw	636	7	2.0	120	2	A72761	hypothetical prote
564	7	2.0	78	2	S31008	hypothetical prote	637	7	1.9	121	2	S18751	hypothetical prote
565	7	2.0	79	1	PJHUSB	gene 63 protein -	638	7	2.0	122	1	R3NT12	ribosomal protein
566	7	2.0	80	2	A05324	proline-rich pep1	639	7	2.0	122	2	E85751	hypothetical prote
567	7	2.0	80	2	PQ0477	gamma-tenin (EC 3.	640	7	2.0	122	2	D90867	hypothetical prote
568	7	1.9	80	2	T10550	pistil extensin-li	641	7	2.0	123	2	S39501	ribosomal protein
569	7	2.0	82	2	T46510	hypothetical prote	642	7	2.0	123	2	A26574	ribosomal protein
570	7	1.9	82	2	S19774	hypothetical prote	643	7	2.0	123	2	G70969	ribosomal protein
571	7	1.9	82	2	S00265	glycine-rich prote	644	7	1.9	124	2	S78400	hypothetical prote
572	7	2.0	85	2	S4461	dipteridin A - nes	645	7	2.0	125	2	H81392	ribosomal protein
573	7	2.0	88	2	C86200	elastase (EC 3.4.2	646	7	2.0	125	2	A34630	50S ribosomal prot
574	7	2.0	90	2	T18068	hypothetical prote	647	7	1.9	126	2	S04577	kinase-related tra
575	7	2.0	91	2	T11554	hypothetical prote	648	7	2.0	127	2	S13069	Ig kappa chain pre
576	7	1.9	91	2	G96614	vxp protein - simi	649	7	2.0	128	2	S13069	ribosomal protein
577	7	1.9	91	2	T47456	probable phosphogl	650	7	1.9	128	2	S12900	hypothetical prote
578	7	2.0	94	2	D82498	hypothetical prote	651	7	2.0	129	2	D49094	phycocerythrin alph
579	7	2.0	96	2	A05308	conserved hypothet	652	7	2.0	130	2	T08534	methylmalonyl-CoA
580	7	2.0	99	1	R6MXL2	tissue kallikrein	653	7	2.0	130	2	S22996	traj protein - Ent
581	7	1.9	100	2	T49621	ribosomal protein	654	7	2.0	131	2	B39303	hypothetical prote
582	7	1.9	100	2	S20482	hypothetical prote	655	7	1.9	131	2	T05837	hypothetical prote
583	7	1.9	101	2	S04634	dipteridin D precu	656	7	1.9	132	2	S14977	glycine-rich prote
584	7	1.9	102	2	C75520	hypothetical prote	657	7	2.0	132	2	T50779	copper chaperone h
585	7	1.9	102	2	D71415	hypothetical prote	658	7	2.0	134	2	AF3280	SSU ribosomal prot
586	7	1.9	102	2	H95992	hypothetical prote	659	7	2.0	134	2	D84672	hypothetical prote
587	7	2.0	104	2	S15395	hypothetical prote	660	7	1.9	134	2	F75582	hypothetical prote
588	7	1.9	104	2	T02612	tissue kallikrein-	661	7	2.0	135	2	S34815	nifU protein - Rh
589	7	2.0	105	2	F72658	hypothetical prote	662	7	1.9	135	2	G72601	hypothetical prote
590	7	2.0	105	2	E82613	hypothetical prote	663	7	1.9	135	2	T01322	aluminum-induced p
591	7	2.0	105	2	T22564	hypothetical prote	664	7	2.0	136	2	A56062	Alu RNA-binding pr
592	7	1.9	105	2	AH2094	RNA-binding protei	665	7	2.0	136	2	S34196	signal recognition
593	7	2.0	106	1	R6D092	acidic ribosomal p	666	7	1.9	137	1	CCR2C	cytochrome C2 prec
594	7	2.0	106	2	C69436	LSU ribosomal prot	667	7	1.9	137	2	T16485	hypothetical prote
595	7	1.9	106	2	T52147	ribosomal protein	668	7	2.0	137	2	S55364	serine proteinase
596	7	1.9	106	2	F84797	hypothetical prote	669	7	2.0	139	2	T46186	hypothetical prote
597	7	2.0	106	2	A30996	orf-X protein - si	670	7	2.0	141	2	A34043	hypothetical proli
598	7	2.0	106	2	B72490	hypothetical prote	671	7	1.9	141	2	B82845	hypothetical prote

c 672	1.9	142	2	AG0327	probable membrane	745	7	2.0	174	2	A31989	sarcoplasmic calci
c 673	2.0	142	2	B41132	collagen-related p	746	7	2.0	174	2	D83309	probable transcrip
c 674	2.0	143	2	S05543	dehydrin 9 - barle	c 747	7	1.9	176	2	S30147	glycine-rich RNA b
c 675	2.0	143	2	T04524	photosystem I chai	c 748	7	1.9	176	2	G69163	hypothetical prote
c 676	2.0	145	2	T48552	glutaredoxin-like	749	7	2.0	177	1	RGYGI	regulatory protein
c 677	1.9	145	2	T01356	glycine-rich RNA b	c 750	7	2.0	177	2	S23505	chymase (EC 3.4.21
c 678	1.9	147	2	F95346	Azul pseudourin	c 751	7	1.9	177	2	C88115	protein F53C3.3 (i
c 679	2.0	147	2	S37485	gene msg1 protein	c 752	7	2.0	178	2	E75340	conserved hypotet
c 680	2.0	148	2	S39206	proline-rich prote	c 753	7	1.9	178	2	E88637	protein W09G12.6 (
c 681	2.0	149	1	KQWSM	tissue kallikrein	c 754	7	1.9	179	2	S28280	transcription fact
c 682	2.0	149	2	A41132	collagen-related p	c 755	7	1.9	179	2	A85217	hypothetical prote
c 683	2.0	150	2	C82994	conserved hypotet	c 756	7	1.9	179	2	B84792	hypothetical prote
c 684	1.9	150	2	C86224	hypothetical prote	c 757	7	1.9	180	2	C72676	hypothetical prote
c 685	2.0	150	2	C73697	hypothetical prote	c 758	7	1.9	180	2	T49530	related to glycine
c 686	1.9	151	2	S43296	bone morphogenetic	c 759	7	2.0	181	2	JC5233	spermatophorin Sp2
c 687	2.0	151	2	H88480	protein C16A3.8 (i	c 760	7	2.0	182	2	A44157	spermatophorin Sp2
c 688	1.9	151	2	AB0331	sigma E factor reg	c 761	7	1.9	183	2	PN0109	keratin-like prote
c 689	2.0	151	2	S10084	hypothetical 16K p	c 762	7	1.9	183	2	S29004	virion protein j13
c 690	1.9	151	2	T04553	hypothetical prote	c 763	7	2.0	183	2	F75086	hypothetical prote
c 691	2.0	152	2	S35209	serine proteinase	c 764	7	1.9	183	2	T02974	probable DNA bindi
c 692	2.0	152	2	S35206	serine proteinase	c 765	7	2.0	184	2	S78091	endocuticular prot
c 693	2.0	152	2	S35203	serine proteinase	c 766	7	2.0	184	2	B84259	hypothetical prote
c 694	2.0	153	2	T31654	hypothetical prote	c 767	7	2.0	185	2	S76361	hypothetical prote
c 695	2.0	154	2	T41831	AcMNPV orf91 - Bom	c 768	7	1.9	185	2	S29003	virion protein j13
c 696	2.0	154	2	PQ0476	pistil extensin-l1	c 769	7	2.0	186	2	C41132	collagen-related p
c 697	1.9	155	2	S20846	glycine-rich prote	c 770	7	1.9	186	2	T35736	hypothetical prote
c 698	1.9	155	2	A86320	hypothetical prote	c 771	7	1.9	187	2	C97095	probable P-loop AT
c 699	1.9	155	2	T03463	hypothetical prote	c 772	7	2.0	188	2	B32340	tissue kallikrein
c 700	2.0	156	2	C86206	hypothetical prote	c 773	7	1.9	188	2	T15651	hypothetical prote
c 701	2.0	156	2	B23863	tissue kallikrein	c 774	7	1.9	189	2	S52902	virion protein j13
c 702	1.9	156	2	S41771	glycine-rich RNA-b	c 775	7	1.9	189	2	S52907	virion protein j13
c 703	2.0	156	2	C84556	probable bZIP tran	c 776	7	1.9	189	2	A53329	pallidipin precurs
c 704	1.9	157	2	T15064	hypothetical prote	c 777	7	2.0	189	2	B90234	hypothetical prote
c 705	2.0	158	2	S35201	serine proteinase	c 778	7	2.0	191	2	B86937	hypothetical prote
c 706	1.9	159	2	F86429	protein F26G16.9 (	c 779	7	2.0	191	2	H83151	hypothetical prote
c 707	1.9	160	2	T04346	glycine-rich RNA-b	c 780	7	1.9	193	2	A71415	hypothetical prote
c 708	2.0	160	2	S58759	ezrin - rat (fragm	c 781	7	2.0	194	1	MOHUA1	myosin alkali ligh
c 709	2.0	160	2	D48232	cysteine-rich exte	c 782	7	2.0	194	2	A38203	proline-rich prote
c 710	2.0	160	2	T49661	hypothetical prote	c 783	7	1.9	195	2	A28201	cytochrome b-245 a
c 711	1.9	160	2	H88114	protein F53C3.6 (i	c 784	7	2.0	196	2	B48232	cysteine-rich exte
c 712	2.0	161	2	E48232	cysteine-rich exte	c 785	7	1.9	196	2	S49194	GCR 17 protein - f
c 713	1.9	161	2	G71407	transcription fact	c 786	7	1.9	197	2	T03442	glycine-rich prote
c 714	1.9	162	2	T10479	glycine-rich RNA-b	c 787	7	1.9	197	2	T18918	hypothetical prote
c 715	1.9	162	2	C85356	glycine-rich prote	c 788	7	2.0	198	2	T35915	hypothetical prote
c 716	1.9	163	2	T47394	hypothetical prote	c 789	7	2.0	198	2	E86261	F13K23.6 protein -
c 717	2.0	163	2	T33130	hypothetical prote	c 790	7	1.9	199	2	T48099	hypothetical prote
c 718	1.9	163	2	T33130	hypothetical prote	c 791	7	1.9	199	2	T49450	hypothetical prote
c 719	1.9	165	2	S59529	RNA-binding glycin	c 792	7	1.9	199	2	S16063	acp-22 protein - y
c 720	1.9	165	2	S41773	glycine-rich RNA-b	c 793	7	1.9	199	2	S32224	splicing factor 9G
c 721	1.9	165	2	T03583	glycine-rich RNA-b	c 794	7	1.9	200	2	T05112	hypothetical prote
c 722	2.0	165	2	C48232	cysteine-rich exte	c 795	7	1.9	201	2	T00799	hypothetical prote
c 723	2.0	165	2	B87702	ribosomal protein	c 796	7	1.9	201	2	F84596	glycine-rich prote
c 724	2.0	165	2	C71717	hypothetical prote	c 797	7	1.9	201	2	F86250	hypothetical prote
c 725	1.9	165	2	T02933	Mov34 protein homo	c 798	7	1.9	201	2	JQ1094	hypothetical prote
c 726	2.0	165	2	T24470	hypothetical prote	c 799	7	1.9	202	2	C71084	hypothetical prote
c 727	1.9	165	2	T24470	hypothetical prote	c 800	7	1.9	203	1	TVHUC2	GTP-binding protei
c 728	1.9	166	2	T10463	glycine-rich prote	c 801	7	1.9	203	2	B71411	hypothetical prote
c 729	1.9	167	2	S71779	glycine-rich RNA-b	c 802	7	1.9	203	2	H75102	hypothetical prote
c 730	1.9	167	2	S21359	keratin, type I, c	c 803	7	2.0	204	2	T07679	protein import rec
c 731	1.9	167	2	AB1109	hypothetical prote	c 804	7	2.0	204	2	T36466	multif domain-contai
c 732	1.9	167	2	AD1470	hypothetical prote	c 805	7	2.0	205	2	F87623	hypothetical prote
c 733	1.9	168	2	T02036	early light-induce	c 806	7	1.9	206	2	D72323	conserved hypotet
c 734	1.9	168	2	A03864	hypothetical 17.7K	c 807	7	1.9	206	2	T32854	hypothetical prote
c 735	2.0	169	1	KTHOB	choriogonadotropin	c 808	7	1.9	206	2	I53066	gene M-twist prote
c 736	1.9	169	2	T10465	glycine-rich prote	c 809	7	1.9	207	2	T07381	glycine-rich prote
c 737	1.9	170	2	C82599	hypothetical prote	c 810	7	1.9	207	2	T38961	hypothetical prote
c 738	1.9	170	2	B82797	hypothetical prote	c 811	7	2.0	208	2	C85035	hypothetical prote
c 739	1.9	170	2	B85359	hypothetical prote	c 812	7	2.0	209	2	F69839	conserved hypotet
c 740	2.0	172	2	D41132	collagen-related p	c 813	7	1.9	209	2	D86399	protein F17L21.18
c 741	2.0	172	2	T27505	hypothetical prote	c 814	7	1.9	209	2	G75181	hypothetical prote
c 742	2.0	173	2	S35568	sex-determining pr	c 815	7	2.0	210	2	JC4244	heat-shock 27K pro
c 743	2.0	173	2	T28299	hypothetical prote	c 816	7	2.0	210	2	I55609	insulin receptor -
c 744	2.0	174	1	DNBPWU	DNA-binding protei	c 817	7	1.9	210	2	B84775	probable harpin-in



818	7	2.0	210	2	T28771	hypothetical prote	891	7	1.9	243	2	T46221	PRE-MRNA SPLICING
C 819	7	1.9	210	2	I49294	CD7 antigen - mous	892	7	2.0	244	1	LNRTMC	mannose-binding le
C 820	7	1.9	211	2	T04098	CBP20 preproteol	893	7	2.0	244	1	A44284	tissue kallikrein
C 821	7	1.9	211	2	A85098	hypothetical prote	894	7	2.0	244	2	S44822	F44E2.3 protein -
C 822	7	1.9	211	2	C84775	probable harpin-in	895	7	2.0	245	1	W4WL5	E4 protein - human
C 823	7	2.0	211	2	S55129	transcription fact	896	7	2.0	245	1	W4WL5	E4 protein - human
C 824	7	2.0	211	2	T25931	hypothetical prote	897	7	2.0	246	1	A46504	chymase (EC 3.4.21
C 825	7	1.9	211	2	S28304	hypothetical prote	898	7	1.9	246	1	C48492	3-deoxy-manno-octu
C 826	7	1.9	212	2	S41581	probable phosphoes	899	7	2.0	246	2	B38678	mast cell proteina
C 827	7	1.9	212	2	A83680	spore germination	900	7	2.0	246	2	A38678	mast cell proteina
C 828	7	2.0	213	2	T03931	DNA binding protei	901	7	2.0	246	2	T46446	hypothetical prote
C 829	7	1.9	213	2	AB0433	probable stringent	902	7	1.9	246	2	T49305	hypothetical prote
C 830	7	2.0	213	2	S27736	hypothetical prote	903	7	2.0	247	1	KYHUCM	chymase (EC 3.4.21
C 831	7	2.0	214	2	S65052	histil-specific pr	904	7	2.0	247	1	PRRTG	mast cell proteina
C 832	7	2.0	215	2	T22572	hypothetical prote	905	7	2.0	247	2	S23504	chymase (EC 3.4.21
C 833	7	1.9	215	2	E72736	probable DNA polym	906	7	2.0	247	2	S59135	mast cell proteina
C 834	7	2.0	215	2	S34163	homeotic protein H	907	7	2.0	247	2	T06721	hypothetical prote
C 835	7	1.9	215	2	AH3215	hypothetical prote	908	7	2.0	248	2	A33412	cytotoxic T-lympho
C 836	7	2.0	216	2	T20186	hypothetical prote	909	7	2.0	248	2	A33412	hypothetical prote
C 837	7	2.0	217	2	T04353	DNA binding protei	910	7	2.0	249	1	A35842	hypothetical prote
C 838	7	2.0	217	2	T15873	hypothetical prote	911	7	1.9	249	2	T04436	ankyrin 3 homolog
C 839	7	1.9	217	2	T47175	hypothetical prote	912	7	2.0	250	1	A31757	homeotic protein H
C 840	7	1.9	218	2	B85021	hypothetical prote	913	7	2.0	250	2	A10416	conserved hypotet
C 841	7	2.0	219	2	T27105	hypothetical prote	914	7	2.0	250	2	T08908	hypothetical prote
C 842	7	1.9	220	2	T14441	glycine-rich prote	915	7	2.0	250	2	T16342	hypothetical prote
C 843	7	2.0	220	2	S52005	nodulin-30 (NpV30)	916	7	2.0	251	1	B60492	homeotic protein H
C 844	7	1.9	220	2	A44805	eggshell protein p	917	7	1.9	252	1	S01821	chymase (EC 3.4.21
C 845	7	2.0	220	2	B82642	hypothetical prote	918	7	1.9	253	2	H36145	glycine-rich prote
C 846	7	2.0	220	2	A95399	hypothetical prote	919	7	1.9	253	2	T04642	cobM protein - Pse
C 847	7	2.0	221	2	T37165	probable transcrip	920	7	1.9	253	2	A33144	hypothetical prote
C 848	7	2.0	221	2	H82857	TonB protein XF000	921	7	2.0	254	2	S49329	homeotic protein U
C 849	7	2.0	222	2	T43500	hypothetical prote	922	7	2.0	254	2	B84901	trypsin-like prote
C 850	7	1.9	222	2	F86480	hypothetical prote	923	7	2.0	255	2	C36222	hypothetical prote
C 851	7	2.0	223	1	S29224	translation elonga	924	7	2.0	255	2	A27122	phosphoprotein pho
C 852	7	2.0	224	2	T07006	L-lactate dehydrog	925	7	2.0	256	1	PRHU3	cathepsin G (EC 3.
C 853	7	2.0	225	2	T09964	extensin CXC15 pre	926	7	1.9	256	2	T03371	proteinase 3 (EC 3
C 854	7	1.9	225	2	A24016	heterogeneous ribo	927	7	1.9	257	2	B84346	glycine-rich prote
C 855	7	2.0	226	1	KCUF	brachyurin (EC 3.4	928	7	2.0	259	1	KQRTN	hypothetical prote
C 856	7	2.0	226	2	T29460	hypothetical prote	929	7	2.0	259	2	D23863	tonin (EC 3.4.21.-
C 857	7	1.9	226	2	H84237	hypothetical prote	930	7	2.0	259	2	B31136	tissue kallikrein
C 858	7	2.0	226	2	S41032	hypothetical prote	931	7	1.9	259	2	T15126	tissue kallikrein
C 859	7	1.9	228	2	D86416	probable beta-1,3	932	7	2.0	259	2	H83616	hypothetical prote
C 860	7	2.0	228	2	T20219	hypothetical prote	933	7	1.9	259	2	S26043	probable transcrip
C 861	7	2.0	229	1	W4WL8	E4 protein - human	934	7	2.0	260	2	S26043	hypothetical prote
C 862	7	1.9	229	1	WMAD51	late 33K protein -	935	7	2.0	261	2	S45303	chymase (EC 3.4.21
C 863	7	1.9	229	2	B87431	hypothetical prote	936	7	2.0	261	2	A31136	tissue kallikrein
C 864	7	1.9	229	2	B72700	hypothetical prote	937	7	2.0	261	2	A34079	tissue kallikrein
C 865	7	2.0	231	1	RDCUP	ubiquinol-cytochro	938	7	1.9	262	1	TLAPM1	tissue kallikrein
C 866	7	2.0	231	2	T06258	superoxide dismuta	939	7	1.9	262	2	S00275	tail fiber protein
C 867	7	2.0	231	2	A60468	venombin A (EC 3.4	940	7	1.9	263	2	A34466	calpain (EC 3.4.22
C 868	7	2.0	231	2	S37108	cuticlin 2 - Caeno	941	7	2.0	263	2	A84385	hypothetical prote
C 869	7	2.0	231	2	T50853	response regulator	942	7	2.0	264	2	A28942	pancreatic elastas
C 870	7	2.0	231	2	S07475	early light-induce	943	7	1.9	264	2	T52104	GATA-binding trans
C 871	7	2.0	231	2	T31231	traw protein homol	944	7	1.9	264	2	JC6125	U2 small nuclear r
C 872	7	2.0	231	2	T45579	hypothetical prote	945	7	2.0	264	2	B89005	protein T24A6.18 l
C 873	7	1.9	231	2	T21119	hypothetical prote	946	7	2.0	265	1	KQRTP	tissue kallikrein
C 874	7	2.0	233	1	JG0169	venombin A (EC 3.4	947	7	1.9	265	2	A40649	hypothetical prote
C 875	7	1.9	233	2	H75359	hypothetical prote	948	7	1.9	266	1	CIPGL	calpain (EC 3.4.22
C 876	7	2.0	233	2	T28914	hypothetical prote	949	7	1.9	266	1	CIRBL	calpain (EC 3.4.22
C 877	7	1.9	234	2	H71443	hypothetical prote	950	7	1.9	266	1	TLBP2X	tail fiber protein
C 878	7	1.9	234	2	E87692	conserved hypotet	951	7	2.0	266	2	C75613	probable molybdenu
C 879	7	2.0	235	2	T47432	hypothetical prote	952	7	1.9	267	1	CTPGP	corticotropin / li
C 880	7	2.0	235	2	AF3209	hypothetical prote	953	7	1.9	267	2	B87578	hypothetical prote
C 881	7	2.0	236	2	T02577	transcription regu	954	7	2.0	267	2	A13458	urease accessory p
C 882	7	2.0	236	2	A70808	probable AP2 domai	955	7	2.0	267	2	T15645	hypothetical prote
C 883	7	1.9	237	2	F95271	hypothetical prote	956	7	1.9	268	1	CIHUL	calpain (EC 3.4.22
C 884	7	1.9	237	2	G83327	hypothetical prote	957	7	2.0	268	2	S68825	pancreatic elastas
C 885	7	1.9	238	2	T05344	hypothetical prote	958	7	2.0	268	2	S68826	pancreatic elastas
C 886	7	2.0	240	1	CPBOA3	procarboxypeptidas	959	7	2.0	268	2	JQ1473	pancreatic elastas
C 887	7	2.0	240	2	T25814	hypothetical prote	960	7	2.0	268	2	T51066	hypothetical prote
C 888	7	1.9	240	2	D71272	hypothetical prote	961	7	1.9	268	2	S09860	hypothetical prote
C 889	7	1.9	240	2	F84722	hypothetical prote	962	7	2.0	269	2	C84707	hypothetical prote
C 890	7	2.0	240	2	D70894	probable pra prote	963	7	2.0	270	2	AI2598	dihydrodipicolinat

964	7	2.0	270	2	A29934	pancreatic elastase	c1037	7	1.9	303	2	T29383	hypothetical prote
965	7	2.0	270	2	B29934	pancreatic elastase	1038	7	2.0	303	2	QJ1386	hypothetical 33K p
c 966	7	1.9	270	2	G84728	hypothetical prote	1039	7	2.0	304	1	W4WL47	E4 protein - human
c 967	7	1.9	270	2	T35365	hypothetical prote	1040	7	2.0	304	2	A32993	transcription fact
c 968	7	1.9	271	2	S34666	hypothetical prote	1041	7	2.0	304	2	T48281	hypothetical prote
969	7	2.0	271	2	T26640	glycine-rich prote	1042	7	2.0	304	2	H86332	T2H2.26 protein -
c 970	7	1.9	272	2	T45256	probable indole-3-	c1043	7	1.9	305	2	T20906	hypothetical prote
c 971	7	2.0	272	2	T02745	nucleic acid bindi	c1044	7	1.9	306	2	F87677	hypothetical prote
c 972	7	1.9	272	2	F36802	IR6 protein - equi	c1045	7	1.9	306	2	S08607	chorion protein s3
c 973	7	1.9	272	2	E70862	hypothetical prote	c1046	7	1.9	307	2	T27609	hypothetical prote
c 974	7	1.9	273	1	TVZMMB	anthocyanin biosyn	c1047	7	1.9	307	2	T48305	hypothetical prote
c 975	7	1.9	273	2	T51145	nucleic acid bindi	c1048	7	1.9	307	2	T26907	hypothetical prote
c 976	7	1.9	273	2	T01985	zinc-finger protei	1049	7	2.0	308	2	A86246	hypothetical prote
c 977	7	1.9	273	2	T52385	zinc finger protei	1050	7	2.0	308	2	AI2993	hypothetical prote
c 978	7	1.9	274	2	A84617	homeodomain transc	1051	7	2.0	309	1	S09257	homeotic protein H
c 979	7	1.9	274	2	T52371	homeobox protein H	c1052	7	1.9	309	2	A39169	myristylated alani
c 980	7	1.9	274	2	T52372	homeobox protein H	c1053	7	1.9	309	2	A39773	probable RNA bindi
c 981	7	1.9	275	2	S28749	NADH2 dehydrogenas	c1054	7	1.9	309	2	T47685	probable oxidoredu
982	7	2.0	275	2	D83626	transcription regu	1055	7	2.0	310	2	T35825	probable PE protei
983	7	2.0	276	2	T03823	probable myb-relat	1056	7	2.0	310	2	A70620	hypothetical prote
984	7	2.0	277	2	H87552	hypothetical prote	1057	7	2.0	310	2	T45873	hypothetical prote
c 985	7	1.9	277	2	T04441	hypothetical prote	c1058	7	1.9	311	2	T07838	chitinase (EC 3.2.
c 986	7	1.9	278	2	A49067	transcription init	c1059	7	1.9	311	2	F86341	hypothetical prote
987	7	2.0	278	2	A49266	fas ligand - rat	1060	7	2.0	311	2	T02783	probable homeotic
988	7	2.0	278	2	H82769	cell division prot	1061	7	2.0	312	2	I48303	collagen alpha 4(I
989	7	2.0	279	2	B97381	dihydrodipicolinat	1062	7	2.0	312	2	A56911	TRADD protein - hu
990	7	2.0	279	2	A53062	Fas ligand - mouse	c1063	7	1.9	312	2	T25048	hypothetical prote
c 991	7	1.9	280	2	A42424	chitinase (EC 3.2.	1064	7	2.0	313	2	T33010	hypothetical prote
c 992	7	1.9	280	2	D70685	hypothetical prote	c1065	7	1.9	314	2	G85529	2,3-dihydroxypheny
c 993	7	1.9	280	2	A35872	steroid hormone re	c1066	7	1.9	314	2	C90679	2,3-dihydroxypheny
994	7	2.0	281	2	S65692	E4 protein - human	c1067	7	1.9	314	2	D64762	paired type homeob
995	7	2.0	281	2	T29150	hypothetical prote	c1068	7	1.9	314	2	JC5273	hypothetical prote
996	7	2.0	282	2	T51013	related to calmodu	1069	7	2.0	315	2	E75382	hypothetical prote
997	7	2.0	283	2	S13383	hydroxyproline-ric	1070	7	2.0	315	2	B99607	hypothetical prote
c 998	7	1.9	284	2	F84590	probable heat choc	c1071	7	1.9	316	1	A38743	loricrin - human
c 999	7	1.9	284	2	G72662	hypothetical prote	c1072	7	1.9	316	2	T01637	gene R protein - A
1000	7	2.0	284	2	S39581	IPF1 protein - mou	c1073	7	1.9	316	2	T20497	hypothetical prote
c1001	7	1.9	284	2	T17563	RNA-binding protei	c1074	7	1.9	317	2	JE0175	frezzled protein-1
1002	7	2.0	285	2	T27458	hypothetical prote	1075	7	2.0	318	2	C70840	probable dehydroge
c1003	7	1.9	285	2	T31503	hypothetical prote	1076	7	2.0	318	2	JC6115	gamma-glutamyl hyd
c1004	7	1.9	285	2	T18689	hypothetical prote	1077	7	2.0	318	2	T29479	hypothetical prote
c1005	7	1.9	285	2	S69312	probable membrane	1078	7	2.0	319	2	A98140	glycosyl transfera
1006	7	2.0	285	2	T03395	CAR-binding facto	1079	7	2.0	319	2	AB3148	glycosyltransferas
1007	7	2.0	287	2	H83306	hypothetical prote	1080	7	2.0	320	2	AE2842	conserved hypotet
c1008	7	1.9	287	2	A06043	antigen 5401 - Eim	c1081	7	1.9	321	2	S13550	anther-specific pr
1009	7	2.0	287	2	T34397	hypothetical prote	1082	7	2.0	322	2	A70661	hypothetical prote
1010	7	2.0	288	2	H95274	probable ABC trans	c1083	7	1.9	322	2	A45036	single-stranded-DN
c1011	7	1.9	288	2	F48423	homeotic protein e	1084	7	2.0	322	2	T22403	hypothetical prote
1012	7	2.0	289	2	T03395	probable lipase -	c1085	7	1.9	323	2	S20099	transforming prote
1013	7	2.0	289	2	T52354	hypothetical prote	1086	7	2.0	323	2	AB0362	glucokinase (EC 2.
c1014	7	1.9	290	2	T23416	hypothetical prote	c1087	7	1.9	323	2	T48160	transcription fact
c1015	7	1.9	290	2	AD1849	hypothetical prote	c1088	7	1.9	323	2	S16318	homeotic protein H
1016	7	2.0	292	2	S24169	mucin - rat	1089	7	2.0	324	2	T10802	chitinase (EC 3.2.
1017	7	2.0	294	2	B87210	hypothetical prote	1090	7	2.0	324	2	D87725	protein M01D7.2 [i
c1018	7	1.9	294	2	T08408	transcription fact	1091	7	2.0	324	2	T15283	hypothetical prote
1019	7	2.0	294	2	A55477	survival motor neu	c1092	7	1.9	325	2	I48765	siah-2 protein - m
1020	7	2.0	295	2	A44984	collagen - nematod	c1093	7	1.9	325	2	G96718	unknown protein, 5
c1021	7	1.9	297	2	G69525	formylmethanofuran	c1094	7	1.9	326	2	A41732	heterogeneous ribo
c1022	7	1.9	297	2	AC2380	hypothetical prote	c1095	7	1.9	326	2	E84178	hypothetical prote
c1023	7	1.9	298	2	C96690	unknown protein F2	c1096	7	1.9	327	2	T00797	hypothetical prote
1024	7	2.0	299	1	PR3MBG	streptogrisin B (E	c1097	7	1.9	327	2	B84781	hypothetical prote
c1025	7	1.9	299	2	T03494	glycine-rich prote	c1098	7	1.9	327	2	C42756	hypothetical prote
1026	7	1.9	299	2	T00837	glycine-rich prote	1099	7	2.0	328	2	C42756	hypothetical prote
1027	7	2.0	299	2	G70784	probable mmp3 pro	1100	7	2.0	328	2	S57128	hypothetical prote
c1028	7	1.9	301	2	B31219	collagen 2 - Caeno	c1101	7	1.9	328	2	G02469	homeotic protein D
1029	7	2.0	301	2	T50001	hypothetical prote	c1102	7	1.9	328	2	A44192	heterogeneous nucl
c1030	7	1.9	302	2	S35526	homeotic protein H	c1103	7	1.9	329	2	E90839	alanine racemase 2
1031	7	2.0	302	2	G87538	MotA/TolQ/ExbB pro	1104	7	2.0	329	2	D72669	hypothetical prote
c1032	7	1.9	302	2	S59853	DNA-binding protei	c1105	7	1.9	329	2	T04244	hypothetical prote
1033	7	2.0	302	2	C86480	33-2K hypothetical	c1106	7	1.9	329	2	T32783	hypothetical prote
1034	7	2.0	303	1	TVRHJD	transforming prote	c1107	7	1.9	330	2	T02525	probable DQF zinc
c1035	7	1.9	303	1	TVRHJD	transforming prote	1108	7	2.0	330	2	B98290	hypothetical prote
c1036	7	1.9	303	2	S52841	protein kinase (EC	1109	7	2.0	331	2	T27906	hypothetical prote

cl110	7	1.9	331	2	T22648	hypothetical prote	1183	7	2.0	358	2	E87309	hypothetical prote
cl111	7	1.9	331	2	A36358	T-cell acute lymph	cl184	7	1.9	358	2	H72666	hypothetical prote
cl112	7	1.9	331	2	T26807	hypothetical prote	cl185	7	1.9	358	2	T26281	hypothetical prote
cl113	7	1.9	332	2	F81053	D-lactate dehydrog	1186	7	2.0	359	2	T13478	hypothetical prote
cl114	7	1.9	332	2	F81022	D-lactate dehydrog	1187	7	2.0	359	2	F97619	hypothetical prote
cl115	7	2.0	332	2	A38873	myristylated alani	cl188	7	1.9	360	2	G86435	protein F17p8.7 [i
cl116	7	1.9	332	2	C30768	hypothetical prote	cl189	7	1.9	360	2	G86187	hypothetical prote
cl117	7	1.9	332	2	D70716	hypothetical prote	cl190	7	1.9	361	1	F64355	conserved hypothet
cl118	7	2.0	333	2	T15257	hypothetical prote	1191	7	2.0	361	2	S19552	potassium channel
cl119	7	2.0	333	2	C46984	indole-3-pyruvate	cl192	7	1.9	361	2	H82105	flagellar P-ring p
cl120	7	2.0	333	2	S84398	probable transcrip	1193	7	2.0	363	2	T16755	hypothetical prote
cl121	7	1.9	333	2	C86353	protein F2E2.8 [im	1194	7	2.0	363	2	JC7820	alpha-N-arabinoxur
cl122	7	1.9	333	2	T28808	hypothetical prote	cl195	7	1.9	364	2	C87455	alanine racemase [
cl123	7	2.0	333	2	D72492	probable ABC trans	cl196	7	1.9	365	2	A26459	helix-destabilizin
cl124	7	1.9	333	2	C48423	homeotic protein e	1197	7	2.0	365	2	T04718	hypothetical prote
cl125	7	2.0	334	2	T04572	hypothetical prote	1198	7	2.0	365	2	T24955	hypothetical prote
cl126	7	2.0	334	2	G02409	protein kinase C-b	cl199	7	1.9	366	2	T39192	probable GTP-bindi
cl127	7	1.9	334	2	T29061	probable integral	cl200	7	1.9	366	2	T42381	probable GTP-bindi
cl128	7	1.9	335	2	S08341	myristylated alani	1201	7	2.0	366	2	B75481	periplasmic serine
cl129	7	2.0	335	2	I61746	pheromone receptor	1202	7	2.0	367	2	I33172	cyclin-dependent k
cl130	7	1.9	335	2	T50600	acetylglucan estera	cl203	7	1.9	367	2	JC6087	helix-loop-helix t
cl131	7	1.9	336	1	S18750	chitinase (EC 3.2.	1204	7	2.0	368	2	T03828	myb protein - rice
cl132	7	2.0	336	2	A87300	TPR domain protein	1205	7	2.0	368	2	T03580	probable transcrip
cl133	7	1.9	337	2	G84590	probable heat shoc	1206	7	2.0	368	2	T51200	hypothetical prote
cl134	7	1.9	338	1	KNWU	glycine-rich cell	cl207	7	1.9	368	2	T26269	hypothetical prote
cl135	7	1.9	338	2	T16221	homeobox protein c	cl208	7	1.9	369	1	TVFVAF	transforming prote
cl136	7	1.9	339	2	B71869	hypothetical prote	1209	7	2.0	370	2	C84846	hypothetical prote
cl137	7	1.9	339	2	T06612	hypothetical prote	1210	7	2.0	370	2	T04664	hypothetical prote
cl138	7	1.9	339	2	S20880	homeotic protein H	1211	7	2.0	370	2	B88455	hypothetical prote
cl139	7	1.9	340	1	B46345	gene V protein - p	cl212	7	1.9	370	2	AG3192	hypothetical prote
cl140	7	2.0	340	2	S53763	homeotic protein H	cl213	7	1.9	371	2	E88633	hypothetical prote
cl141	7	1.9	342	2	S14432	heterogeneous ribo	cl214	7	1.9	371	2	B39625	T-cell receptor al
cl142	7	1.9	342	2	S18649	homeotic protein H	cl215	7	1.9	371	2	I46089	thyroid transcript
cl143	7	2.0	343	1	RGBPP1	recombinase - phag	1216	7	2.0	372	2	T10472	G-box binding prot
cl144	7	1.9	343	2	T29547	hypothetical prote	1217	7	2.0	372	2	AD0860	probable secreted
cl145	7	1.9	344	1	VWV2J	coat protein VP2 -	cl218	7	1.9	372	2	AG2827	HPLK protein limpo
cl146	7	2.0	345	2	S12788	transcription fact	cl219	7	1.9	372	2	S53724	thyroid-specific
cl147	7	1.9	346	1	S35500	heterogeneous ribo	cl220	7	1.9	372	2	S12002	thyroid nuclear fa
cl148	7	2.0	346	2	T07005	L-lactate dehydrog	cl221	7	1.9	373	2	S40777	heterogeneous ribo
cl149	7	1.9	346	2	T48049	hypothetical prote	1222	7	2.0	373	2	A70856	probable lppz prot
cl150	7	2.0	346	2	S19129	proline-rich prote	cl223	7	1.9	373	2	T02976	probable DNA bindi
cl151	7	2.0	346	2	S76923	hypothetical prote	cl224	7	1.9	373	2	E97605	proteinase chain h
cl152	7	1.9	347	2	AF0344	probable phosphori	cl225	7	1.9	374	2	T03875	probable homeobox
cl153	7	2.0	347	2	A43815	transforming prote	1226	7	2.0	375	2	E64674	carbamoyl-phosphat
cl154	7	1.9	347	2	A43815	transforming prote	cl227	7	1.9	375	2	T41885	ODV-E56 orf148 - B
cl155	7	1.9	347	2	T35013	probable membrane	cl228	7	1.9	375	2	T03874	probable homeobox
cl156	7	2.0	347	2	A84403	dipeptide ABC tran	1229	7	2.0	376	2	JC5228	actin 2 - earthwor
cl157	7	1.9	347	2	H84608	probable RNA-bind	cl230	7	1.9	376	2	T48714	hypothetical prote
cl158	7	2.0	348	2	AB3260	hypothetical membr	1231	7	2.0	377	2	JC4368	protein farnesyltr
cl159	7	2.0	348	2	S52720	homeobox protein g	1232	7	2.0	377	2	A41625	protein farnesyltr
cl160	7	2.0	349	2	T06207	cysteine proteinas	1233	7	2.0	377	2	C88710	protein C43G2.5 [i
cl161	7	2.0	349	2	G84852	hypothetical prote	cl234	7	1.9	377	2	T04213	heat shock transcr
cl162	7	2.0	350	2	T07061	L-lactate dehydrog	cl235	7	1.9	378	2	A55735	G protein-coupled
cl163	7	2.0	350	2	AG2379	hypothetical prote	1236	7	2.0	378	2	T21651	hypothetical prote
cl164	7	2.0	350	2	JC7213	Cre recombinase pr	cl237	7	2.0	379	2	S31719	proline-rich prote
cl165	7	1.9	351	1	VWV2B	coat protein VP2 -	1239	7	2.0	379	2	T19069	proline-rich prote
cl166	7	1.9	351	1	VWV2B	coat protein VP2 -	cl238	7	2.0	380	2	S73845	hypothetical prote
cl167	7	2.0	351	2	I54347	rod outer segment	1240	7	2.0	382	2	E70719	probable fadE13 pr
cl168	7	1.9	351	2	S60653	synapse associated	cl241	7	1.9	382	2	D84766	hypothetical prote
cl169	7	1.9	352	2	T24279	hypothetical prote	cl242	7	1.9	382	2	G90751	probable transport
cl170	7	2.0	352	2	C96643	hypothetical prote	cl243	7	1.9	382	2	E85082	hypothetical prote
cl171	7	1.9	353	2	B70358	hydrogenase (EC 1.	1244	7	2.0	382	2	T14186	hypothetical prote
cl172	7	1.9	355	2	T24938	hypothetical prote	1245	7	2.0	382	2	E85615	probable transport
cl173	7	2.0	355	2	A41285	coat protein - swe	cl246	7	1.9	382	2	A13406	permease [imported
cl174	7	1.9	356	1	A29519	alanine racemase (	cl247	7	1.9	382	2	A64829	membrane protein y
cl175	7	1.9	356	1	C53383	alanine racemase [	cl248	7	1.9	383	1	T74423	phosphate-binding
cl176	7	1.9	356	2	AC0723	alanine racemase 2	cl249	7	1.9	383	2	T50775	probable translati
cl177	7	1.9	356	2	E85697	nuclear factor 1 f	cl250	7	2.0	383	2	AE2295	hypothetical prote
cl178	7	2.0	357	2	PC4293	hypothetical prote	1251	7	1.9	384	1	A26099	glycine-rich cell
cl179	7	2.0	357	2	T47367	CCAAT/enhancer bin	cl252	7	1.9	384	2	A81212	fatty acid efflux
cl180	7	2.0	358	2	JC4311	CCAAT/enhancer bin	1253	7	2.0	384	2	S25771	gasl protein - mou
cl181	7	2.0	358	2	A54265	CCAAT/enhancer-bin	cl254	7	1.9	384	2	S51796	vasodilator-stimul
cl182	7	1.9	358	2	A54265	CCAAT/enhancer-bin	1255	7	2.0	384	2	S51796	vasodilator-stimul

c1256	1.9	385	2	S40778	7	1.9	416	2	S50342	homeotic protein S
1257	2.0	385	2	H70503	7	2.0	417	2	S47539	homeotic protein H
c1258	1.9	385	2	T20410	7	2.0	417	2	T15174	hypothetical prote
c1259	1.9	385	2	A92717	7	2.0	418	2	I52968	colligin-2 - human
c1260	1.9	385	2	H97498	7	2.0	419	2	F72866	alkaline exonuclea
c1261	1.9	386	1	S22315	7	1.9	419	2	G70602	hypothetical prote
c1262	1.9	386	2	T05691	7	1.9	420	1	QB8E44	BDLF2 protein - hu
c1263	1.9	387	2	B83080	7	2.0	420	2	T46910	hypothetical prote
1264	2.0	387	2	A93335	7	2.0	420	2	JC4716	zinc finger DNA-bi
c1265	1.9	388	2	H98321	7	1.9	420	2	I59234	octamer binding tr
c1266	1.9	388	2	AF2961	7	1.9	420	2	A49642	transcription fact
c1267	1.9	388	2	T23173	7	1.9	422	2	T09742	drough-induced pr
1268	2.0	388	2	T26922	7	1.9	422	2	T51199	hypothetical prote
1269	2.0	388	2	JC5437	7	2.0	423	2	S60939	GTP-binding protei
1270	2.0	389	2	T03411	7	2.0	423	2	A45363	somatoliberin rece
c1271	1.9	389	2	T26995	7	2.0	423	2	A49772	cuticle protein cu
1272	2.0	390	2	G01936	7	2.0	424	2	T20032	hypothetical prote
c1273	1.9	391	1	E64465	7	2.0	424	2	D75330	probable beta-lact
1274	2.0	392	1	A30100	7	1.9	425	1	KRXL2A	keratin, 64K type
1275	2.0	392	2	JC4553	7	1.9	425	2	T03605	probable DNA bindi
1276	2.0	392	2	A86206	7	2.0	426	2	JQ1696	pistil extensin-li
1277	2.0	392	2	T48360	7	2.0	427	2	T48159	hypothetical prote
c1278	1.9	392	2	T48360	7	1.9	427	2	A32372	female-specific do
c1279	1.9	393	1	XXALAE	7	2.0	427	2	I49603	transcription regu
1280	2.0	393	2	T33103	7	2.0	430	2	JC2301	hypothetical 47.8K
1281	2.0	393	2	PQ0479	7	1.9	430	2	S66671	neuron-derived rec
c1282	1.9	393	2	T00647	7	1.9	431	1	WJHU2G	homeotic protein H
c1283	1.9	393	2	T20268	7	2.0	431	2	T12450	hypothetical prote
1284	2.0	393	2	JC5614	7	2.0	432	1	S18932	u-plasminogen acti
1285	2.0	394	2	F81789	7	2.0	432	2	S96515	hypothetical prote
1286	2.0	395	2	I49575	7	2.0	433	1	FOLJH2	gag polyprotein -
1287	2.0	396	1	JH0633	7	2.0	433	2	S20963	homeotic protein H
1288	2.0	396	2	A36339	7	1.9	433	2	C88594	protein V48A6B.10
c1289	1.9	396	2	S56820	7	2.0	433	2	E70768	hypothetical glyci
c1290	1.9	397	2	T17008	7	2.0	434	2	G97610	hypothetical metab
c1291	1.9	398	2	T17009	7	2.0	434	2	AC2833	hypothetical prote
1292	2.0	399	2	S34681	7	2.0	434	2	T47772	hypothetical prote
c1293	1.9	399	2	A39625	7	1.9	435	2	T15143	hypothetical prote
c1294	1.9	399	2	I49754	7	1.9	435	2	B55452	cartilage-derived
1295	2.0	400	2	D75331	7	2.0	436	2	JC5599	cholesterol kinase-A
c1296	1.9	400	2	T10476	7	1.9	436	2	JC5599	transcription fact
c1297	1.9	401	2	G02321	7	1.9	437	2	A54595	hypothetical prote
1298	2.0	401	2	A48423	7	2.0	438	2	T12494	conserved hypothet
c1299	1.9	402	1	CGB02S	7	2.0	438	2	C69337	Batten disease-rel
1300	2.0	402	2	E86185	7	2.0	438	2	A57219	3-phosphohikimate
c1301	2.0	403	2	D96961	7	1.9	439	2	G84432	probable C2H2-type
1302	2.0	403	2	S52796	7	1.9	439	2	G84432	probable DNA-bind
c1303	1.9	403	2	A53662	7	1.9	439	2	S52291	chitinase (EC 3.2.
c1304	1.9	405	2	T29167	7	2.0	440	2	H86312	F2H15.2 protein -
c1305	1.9	405	2	T12317	7	2.0	440	2	S71795	transcription fact
c1306	1.9	405	2	T10630	7	2.0	440	2	S71795	transcription fact
c1307	1.9	405	2	A95880	7	1.9	440	2	A56693	receptor protein k
1308	2.0	407	1	A40150	7	1.9	440	2	A56693	conserved hypothet
c1309	1.9	407	2	H71857	7	2.0	441	2	C83318	transcription fact
c1310	1.9	407	2	F64658	7	2.0	443	1	S29334	transcription fact
1311	2.0	408	2	T31254	7	1.9	443	1	S29334	transcription fact
1312	2.0	408	2	S50899	7	1.9	443	2	E96495	hypothetical prote
c1313	1.9	408	2	S57483	7	2.0	444	2	T09474	forkhead protein F
1314	2.0	408	2	G96707	7	2.0	445	1	A49447	transcription fact
c1315	1.9	409	2	S44346	7	1.9	445	1	A49447	transcription fact
c1316	1.9	410	2	T38502	7	2.0	445	1	S31224	transcription fact
1317	2.0	411	2	B41398	7	1.9	445	1	S31224	transcription fact
c1318	1.9	411	2	I58156	7	2.0	445	2	S19990	alpha-amylase (EC
c1319	1.9	411	2	A49127	7	2.0	445	2	S41741	N-acetylmuramoyl-L
1320	2.0	411	2	S34164	7	2.0	445	2	A86113	N-acetylmuramoyl-L
c1321	1.9	414	2	G69536	7	2.0	445	2	A91272	Krox-20 protein -
1322	2.0	414	2	C86301	7	2.0	446	2	S00256	hypothetical prote
1323	2.0	414	2	T50010	7	2.0	446	2	T26988	hydroxyproline-ric
c1324	1.9	415	2	F84393	7	2.0	446	2	T07907	hypothetical prote
1325	2.0	415	2	T13435	7	2.0	446	2	T20416	cysteine proteinas
c1326	1.9	416	2	T44423	7	2.0	447	2	S37048	gag-like polypote
1327	1.9	416	2	T32458	7	1.9	447	2	S42805	hypothetical prote
1328	2.0	416	2	T34279	7	2.0	447	2	A84718	

1402	7	2.0	448	2	S33926	Wilms' tumor prote
1403	7	2.0	449	2	A38080	Wilms tumor suscep
1404	7	2.0	449	2	A39692	Wilms' tumor prote
1405	7	2.0	449	2	D87682	OmpA family protei
1406	7	2.0	450	2	S07051	cysteine proteinas
1407	7	2.0	450	2	S12099	cysteine proteinas
1408	7	1.9	451	2	A36646	probable tartrate
1409	7	1.9	452	2	H96710	hypothetical prote
1410	7	2.0	454	2	A96803	probable mitotic c
1411	7	1.9	455	1	TVCRGG	phosphoglycerate k
1412	7	1.9	455	2	A10599	probable ATP-depen
1413	7	1.9	455	2	T05081	hypothetical prote
1414	7	1.9	455	2	B86427	hypothetical prote
1415	7	2.0	456	2	A40492	early growth respo
1416	7	1.9	456	2	S55661	hypothetical prote
1417	7	2.0	457	2	E88456	protein W03A5.3 [i
1418	7	1.9	457	2	E88456	protein W03A5.3 [i
1419	7	2.0	457	2	AF2975	aminotransferase,
1420	7	2.0	457	2	E98307	probable aminotran
1421	7	1.9	458	2	A30775	dihydrolipoamide a
1422	7	2.0	458	2	T02804	hypothetical prote
1423	7	2.0	458	2	H87624	peptidase, M23/M37
1424	7	1.9	458	2	I48690	homeotic protein N
1425	7	2.0	459	2	F71257	hypothetical prote
1426	7	1.9	460	2	D84396	signal recognition
1427	7	1.9	460	2	T21626	hypothetical prote
1428	7	1.9	460	2	G70803	hypothetical prote
1429	7	2.0	461	1	A45077	steroid hormone re
1430	7	1.9	461	1	D64701	thiophene and fura
1431	7	1.9	461	2	G71818	probable thiophene
1432	7	1.9	461	2	F82819	D-lactate dehydrog
1433	7	2.0	461	2	S45568	nuclear factor I-A
1434	7	2.0	462	1	A56120	steroid hormone re
1435	7	2.0	462	1	A40716	steroid hormone re
1436	7	2.0	463	2	A48375	cellulase (EC 3.2.
1437	7	2.0	463	2	T45565	hypothetical prote
1438	7	1.9	463	2	T36810	probable integral
1439	7	2.0	464	2	JC7143	endoglucoanase I -
1440	7	1.9	464	2	A55660	intermediate filam
1441	7	1.9	464	2	A87675	carboxyl-terminal
1442	7	1.9	464	2	T21628	hypothetical prote
1443	7	2.0	464	2	T50955	hypothetical prote
1444	7	2.0	464	2	S75831	hypothetical prote
1445	7	2.0	464	2	S22697	extensin - Volvox
1446	7	1.9	465	1	S01820	glycine-rich cell
1447	7	2.0	465	1	W2BEB4	51.3K capsid prote
1448	7	2.0	465	2	A42128	embryonal long ter
1449	7	2.0	465	2	G02738	PREAC-4 - human
1450	7	1.9	465	2	G02738	delta-1-crystallin
1451	7	1.9	466	1	CYDKD1	argininosuccinate
1452	7	1.9	466	2	JN0486	argininosuccinate
1453	7	1.9	466	2	S29247	hypothetical prote
1454	7	1.9	466	2	T45585	keratin type I - 9
1455	7	1.9	467	2	I50476	hypothetical prote
1456	7	2.0	467	2	A41318	efflux system prot
1457	7	2.0	467	2	C87349	hypothetical prote
1458	7	1.9	467	2	T18744	hypothetical prote
1459	7	2.0	467	2	S35782	serine/threonine p
1460	7	1.9	468	1	CYDKD2	delta-2-crystallin
1461	7	1.9	469	2	T02325	probable selenium-
1462	7	1.9	470	2	T31602	hypothetical prote
1463	7	2.0	470	2	A30136	developmental cont
1464	7	2.0	471	2	S09110	hypothetical prote
1465	7	1.9	472	1	WMADP6	early B1B 52K prot
1466	7	2.0	474	2	A35732	protective protein
1467	7	1.9	474	2	F83550	serine proteinase
1468	7	2.0	474	2	A43312	hypothetical ATP-b
1469	7	2.0	474	2	S57239	gene forked protei
1470	7	2.0	474	2	T10271	capsid-associated
1471	7	1.9	474	2	I38240	transcription fact
1472	7	1.9	475	2	C84384	hypothetical prote
1473	7	1.9	475	2	A43915	homeotic protein e
1474	7	2.0	476	2	S60927	hypothetical prote

## RESULT 1

DBHU

Complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)

N:Alternate names: adipsin; C3 convertase activator

C:Species: Homo sapiens (man)

C&gt;Date: 28-Aug-1985 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C:Accession: A40197; A00936; A60571; S86645

R:White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;

J. Biol. Chem. 267, 9210-9213, 1992

A:Title: Human adipsin is identical to complement factor D and is expressed at high level

A:Reference number: A40197; MUID:92250520; PMID:1374388

A:Accession: A40197

A:Molecule type: mRNA

A:Residues: 1-246 &lt;WHI&gt;

R:Niemann, M.A.; Brown, A.S.; Bennett, J.C.; Volanakis, J.E.

Biochemistry 23, 2482-2486, 1984

A:Title: Amino acid sequence of human D of the alternative complement pathway.

A:Reference number: A00936; MUID:85000441; PMID:6383466

A:Accession: A00936

A:Molecule type: protein

A:Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITTE',90-172,86-91,185-235,'J

A:Note: a few residues were assigned from the previously published sequence of Reid et al

R:Miya, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Yan

Mol. Immunol. 27, 637-644, 1990

A:Title: Molecular and functional identification and purification of complement component

A:Reference number: A60571; MUID:90370044; PMID:2395435

A:Accession: A60571

A:Molecule type: protein

A:Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 &lt;MIY&gt;

R:Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.

FEBS Lett. 371, 300-302, 1995

A:Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement

A:Reference number: S66645; MUID:96013156; PMID:7556615

A:Accession: S66645

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 19-44,'C',46-48 &lt;BAL&gt;

C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activa

C:Genetics:

A:Gene: GDB:DP

A:Cross-references: GDB:132645; OMIM:134350

A:Map position: Xpter-Xqter

C:Superfamily: trypsin; trypsin homology  
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>  
F:19-241/Domain: trypsin homology <TRY>  
F:44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted  
F:59,105,201/Active site: His, Asp, Ser #status predicted

Alignment Scores:  
Pred. No.: 0.00139 Length: 246  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x DBHU (1-246)

QY 712 GGTGATCTCGGGGCCCTGTGTGGGGAGTCCTT 750  
|||||  
Db 199 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 211  
|||||

RESULT 2

JS0600  
t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat  
N/Alternate names: tissue plasminogen activator  
C:Species: Desmodus rotundus (common vampire bat)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JS0600  
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dorf  
Gene 105, 229-237, 1991  
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des  
A:Reference number: JS0597; MUID:92039036; PMID:1937019  
A:Accession: JS0600  
A:Molecule type: mRNA  
A:Residues: 1-394 <KRA>  
A:Cross-references: UNIPROT:P49150; GB:M63990; NID:gl66078; PIDN:AAA31595.1; PID:gl66079  
A:Note: the authors translated the codon ATC for residue 75 as Thr  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-36/Domain: propeptide #status predicted <PRO>  
F:37-394/Product: plasminogen activator gamma #status predicted <PLA>  
F:45-126/Domain: kringle homology <KRG>  
F:143-388/Domain: trypsin homology <TRY>  
F:145-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:  
F:142-143/Cleavage site: His-Ser (plasmin) #status predicted  
F:189,238,345/Active site: His, Asp, Ser #status predicted  
F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 0.00125 Length: 394  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x JS0600 (1-394)

QY 700 GATGCTCCAGGTGATTCGGGGCCCCCTGGTGTT 738  
|||||  
Db 339 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 351  
|||||

RESULT 3

JS0599  
t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat  
N/Alternate names: tissue plasminogen activator  
C:Species: Desmodus rotundus (common vampire bat)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JS0599  
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dorf  
Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des  
A:Reference number: JS0597; MUID:92039036; PMID:1937019  
A:Accession: JS0599  
A:Molecule type: mRNA  
A:Residues: 1-431 <KRA>  
A:Cross-references: UNIPROT:P98121; GB:M63989; NID:gl66076; PIDN:AAA31594.1; PID:gl66077  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-36/Domain: propeptide #status predicted <PRO>  
F:37-431/Product: plasminogen activator beta #status predicted <PLA>  
F:41-74/Domain: EGF homology <EGF>  
F:82-163/Domain: kringle homology <KRG>  
F:180-425/Domain: trypsin homology <TRY>  
F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bonds:  
F:139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:179-180/Cleavage site: His-Ser (plasmin) #status predicted  
F:226,275,382/Active site: His, Asp, Ser #status predicted  
F:345-361,378-406/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 0.00122 Length: 431  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x JS0599 (1-431)

QY 700 GATGCTCCAGGTGATTCGGGGCCCCCTGGTGTT 738  
|||||  
Db 376 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 388  
|||||

RESULT 4

A34369  
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)  
C:Species: Megaderma lyra  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A34369  
R:Gardelli, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacobs  
J. Biol. Chem. 264, 17947-17952, 1989  
A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin  
A:Reference number: A34369; MUID:90036867; PMID:2509450  
A:Accession: A34369  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-477 <GAR>  
A:Cross-references: UNIPROT:P15638; GB:J05082; NID:gl66080; PIDN:AAA31596.1; PID:gl66081  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-36/Domain: propeptide #status predicted <PRO>  
F:37-477/Product: plasminogen activator #status predicted <PLA>  
F:42-79/Domain: fibronectin type I repeat homology <1FA>  
F:87-120/Domain: EGF homology <EGF>  
F:128-209/Domain: kringle homology <KRG>  
F:226-471/Domain: trypsin homology <TRY>  
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4  
F:272,321,428/Active site: His, Asp, Ser #status predicted

Alignment Scores:  
Pred. No.: 0.0012 Length: 477  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x A34369 (1-477)

QY 700 GATGCTCCAGGTGATTCGGGGCCCCCTGGTGTT 738  
|||||

Db 422 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 434

## RESULT 5

JS0597  
t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat  
N:Alternate names: tissue plasminogen activator  
C:Species: Desmodus rotundus (common vampire bat)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JS0597  
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor  
Gene 105, 229-237, 1991  
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des  
A:Reference number: JS0597; MUID:92039036; PMID:1937019  
A:Accession: JS0597  
A:Molecule type: mRNA  
A:Residues: 1-477 <KRA>  
A:Cross-references: UNIPROT:P98119; GB:M63987; NID:G166070; PIDN:AAA31593.1; PID:G166071  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-36/Domain: propeptide #status predicted <PRO>  
F:37-477/Product: plasminogen activator alpha-1 #status predicted <PLA>  
F:42-79/Domain: fibronectin type I repeat homology <IFA>  
F:87-120/Domain: EGF homology <EGF>  
F:128-209/Domain: kringle homology <KRG>  
F:226-471/Domain: trypsin homology <TRY>  
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4  
F:153,398/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:225-226/Cleavage site: His-Ser (plasmin) #status predicted  
F:272,321,428/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.:	0.0012	Length:	477
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x JS0597 (1-477)

QY 700 GATGCTGCCAGGTCATTCTGGGGCCCCCTGGTGTTGT 738

Db 422 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 434

## RESULT 6

JS0598  
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat  
N:Alternate names: tissue plasminogen activator  
C:Species: Desmodus rotundus (common vampire bat)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JS0598  
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor  
Gene 105, 229-237, 1991  
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des  
A:Reference number: JS0597; MUID:92039036; PMID:1937019  
A:Accession: JS0598  
A:Molecule type: mRNA  
A:Residues: 1-477 <KRA>  
A:Cross-references: UNIPROT:P15638; GB:M63988; NID:G166074; PIDN:AAA31593.1; PID:G166075  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-36/Domain: propeptide #status predicted <PRO>  
F:37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>  
F:42-79/Domain: fibronectin type I repeat homology <IFA>  
F:87-120/Domain: EGF homology <EGF>  
F:128-209/Domain: kringle homology <KRG>  
F:226-471/Domain: trypsin homology <TRY>  
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4  
F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:225-226/Cleavage site: His-Ser (plasmin) #status predicted  
F:272,321,428/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.:	0.0012	Length:	477
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x JS0598 (1-477)

QY 700 GATGCTGCCAGGTCATTCTGGGGCCCCCTGGTGTTGT 738

Db 422 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 434

## RESULT 7

A29941  
t-plasminogen activator (EC 3.4.21.68) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A29941; S48205; S48207; S48206  
R:Rickles, R.J.; Darrow, A.L.; Strickland, S.  
J. Biol. Chem. 263, 1563-1569, 1988  
A:Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mR  
A:Reference number: A29941; MUID:88087303; PMID:2826484  
A:Accession: A29941  
A:Molecule type: mRNA  
A:Residues: 1-559 <RIC>  
A:Cross-references: UNIPROT:P11214; GB:J03520; NID:G202109; PIDN:AAA40470.1; PID:G202110  
R:Liijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.  
Eur. J. Biochem. 224, 863-871, 1994  
A:Title: Characterization of the murine plasma fibrinolytic system.  
A:Reference number: S48202; MUID:95010076; PMID:7523120

A:Accession: S48205

A:Molecule type: protein

A:Residues: 33-37, X', 39-40 <LIJ>

A:Accession: S48207

A:Molecule type: protein

A:Residues: 309-316 <LI2>

A:Accession: S48206

A:Molecule type: protein

A:Residues: 33-37, X', 39-40 <LIW>

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-29/Domain: propeptide #status predicted <PRO>

F:30-559/Product: t-plasminogen activator #status predicted <MAT>

F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>

F:38-75/Domain: fibronectin type I repeat homology <IF1>

F:83-116/Domain: EGF homology <EGF>

F:124-205/Domain: kringle homology <KR1>

F:213-294/Domain: kringle homology <KR2>

F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>

F:309-553/Domain: trypsin homology <TRY>

F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4

F:149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted

F:355,404,510/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.:	0.00115	Length:	559
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	1	Gaps:	0

US-10-015-385A-193 (1-1091) x A29941 (1-559)

QY 700 GATGCTGCCAGGTCATTCTGGGGCCCCCTGGTGTTGT 738

Db 504 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 516

## RESULT 8

A35029  
t-plasminogen activator (EC 3.4.21.68) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A35029; A31597  
R:Feng, P.; Ohlsson, M.; Ny, T.  
J. Biol. Chem. 265, 2022-2027, 1990  
A:Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec  
A:Reference number: A35029; MUID:90130448; PMID:2105315  
A:Accession: A35029  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-559 <FEN>  
A:Cross-references: UNIPROT:P19637; GB:M31197; NID:G207429; PIDN:AAA42261.1; PID:G207431  
R:Ny, T.; Leonardsson, G.; Hsueh, A.J.W.  
DNA 7, 671-677, 1988  
A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activator  
A:Reference number: A31597; MUID:89170114; PMID:3148445  
A:Accession: A31597  
A:Molecule type: mRNA  
A:Residues: 1-379, 'K', 381-559 <NVT>  
A:Cross-references: GB:M23697; NID:G530159; PIDN:AAA41812.1; PID:G530160  
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-29/Domain: propeptide #status predicted <PRO>  
F:30-559/Product: t-plasminogen activator #status predicted <WAT>  
F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>  
F:38-75/Domain: fibronectin type I repeat homology <IF1>  
F:83-116/Domain: EGF homology <EGF>  
F:124-205/Domain: kringle homology <KR1>  
F:213-294/Domain: kringle homology <KR2>  
F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>  
F:309-553/Domain: trypsin homology <TRY>  
F:38-68, 66-75, 83-94, 88-105, 107-116, 124-205, 145-187, 176-200, 213-294, 234-276, 265-289, 297-4  
F:149, 481/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted  
F:355, 404, 510/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.:	0.00115	Length:	559
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.64%	Indels:	0
DB:	1	Gaps:	0

US-10-015-385A-193 (1-1091) x A35029 (1-559)

QY 700 GATGCTGCACGGTGATTCGGGGCCCGCTGGTGTTGT 738  
|||||  
DB 504 AspAlaCyGlnGlyAspSerGlyGlyProLeuValCys 516  
|||||

## RESULT 9

UKHUT  
t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human  
N:Alternate names: t-PA; tissue plasminogen activator  
C:Species: Homo sapiens (man)  
C:Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 09-Jul-2004  
C:Accession: A94004; A23529; J0562; A93293; S02125; A91343; A93951; A91322; A54645; 160  
R:Ny, T.; Eligh, F.; Lund, B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984  
A:Title: The structure of the human tissue-type plasminogen activator gene: correlation  
A:Reference number: A94004; MUID:84298137; PMID:6089198  
A:Accession: A94004  
A:Molecule type: DNA  
A:Residues: 1-562 <NVT>  
A:Cross-references: UNIPROT:P00750; GB:L00141  
A:Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translati  
R:Friezner Degen, S.J.; Rajput, B.; Reich, E.  
J. Biol. Chem. 261, 6972-6985, 1986  
A:Title: The human tissue plasminogen activator gene.

A:Reference number: A23529; MUID:86196143; PMID:3009482  
A:Accession: A23529  
A:Molecule type: DNA  
A:Residues: 1-562 <DEG>  
A:Cross-references: GB:K03021; NID:G339817; PIDN:AAA98809.1; PID:G339818  
R:Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.  
Agric. Biol. Chem. 55, 1225-1232, 1991  
A:Title: Purification and characterization of tissue plasminogen activator secreted by h  
A:Reference number: J0562; MUID:91291340; PMID:1368681  
A:Accession: J0562  
A:Molecule type: mRNA  
A:Residues: 31-562 <ITA>  
A:Cross-references: DBJ:D01096; NID:G220128; PIDN:BAA00881.1; PID:G441174  
A:Experimental source: embryonic lung fibroblast IMR-90 cells  
A:Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vohar, G.A.; Ward, C.A.; Bennett,  
Nature 301, 214-221, 1983  
A:Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Escher  
A:Reference number: A93293; MUID:83115262; PMID:6337343  
A:Accession: A93293  
A:Molecule type: mRNA  
A:Residues: 1-562 <PEN>  
A:Cross-references: GB:L00141  
A:Experimental source: melanoma cells  
R:Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.  
Nucleic Acids Res. 16, 5695, 1988  
A:Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fet  
A:Reference number: S02125; MUID:88262579; PMID:3133640  
A:Accession: S02125  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-562 <SAS>  
A:Cross-references: EMBL:X07393; NID:G37243; PIDN:CAA30302.1; PID:G37244  
A:Experimental source: fetal lung cells  
R:Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Mat  
FEBS Lett. 189, 145-149, 1985  
A:Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen  
A:Reference number: A91343; MUID:85285620; PMID:3896853  
A:Accession: A91343  
A:Molecule type: mRNA  
A:Residues: 1-38, 'G', 86-433, 'E', 435-562 <KAG>  
A:Experimental source: Detroit 562 cells; ATCC 138  
R:Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983  
A:Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activa  
A:Reference number: A93951; MUID:83169656; PMID:6572897  
A:Accession: A93951  
A:Molecule type: mRNA  
A:Residues: 251-358 <BDL>  
A:Experimental source: melanoma cells  
R:Pohl, G.; Kallstrom, M.; Bergedorf, H.  
Biochemistry 23, 3701-3707, 1984  
A:Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived am  
differences.  
A:Reference number: A90488; MUID:85000468; PMID:6433976  
A:Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and i  
R:Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.  
FEBS Lett. 168, 29-32, 1984  
A:Title: Differences between uterine and melanoma forms of tissue plasminogen activator.  
A:Reference number: A91322; MUID:84158956; PMID:6538514  
A:Accession: A91322  
A:Molecule type: protein  
A:Residues: 33-45; 311-320 <POH>  
A:Experimental source: uterus  
A:Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln  
R:van Zonneveld, A.J.; Veerman, H.; Pamnekoek, H.  
J. Biol. Chem. 261, 14214-14218, 1986  
A:Reference number: A37567; MUID:87033611; PMID:3021732  
R:Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger-  
EMBO J. 5, 3525-3530, 1986  
A:Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen act  
A:Reference number: A37568; MUID:87161761; PMID:3030730



A:Contents: annotation; fibrin binding site  
R:Dodd, I.; Nunn, B.; Robinson, J.H.  
Thromb. Haemost. 59, 523-528, 1988  
A:Title: Isolation, identification and pharmacokinetic properties of human tissue-type plasminogen activator; fibrinolytic activity; PMD:3142086  
A:Reference number: A60902; MUID:89044681; PMD:3142086  
A:Contents: annotation; novel forms of expressed recombinant t-PA  
R:Haris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.; Mol. Biol. Med. 3, 279-292, 1986  
A:Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expression; PMD:3090401  
A:Reference number: A54645; MUID:86284200; PMD:3090401  
A:Accession: A54645  
A:Molecule type: mRNA  
A:Residues: 1-562 <HAR>  
A:Cross-references: GB:M15518; NID:G190031; PIDN:AAA60111.1; PID:G190032  
A:Note: parts of this sequence were confirmed by peptide sequencing  
R:Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.  
DNA 6, 461-472, 1987  
A:Title: Expression of human uterine tissue-type plasminogen activator in mouse cells using a plasmid vector; PMD:2824147  
A:Reference number: I60110; MUID:88054470; PMD:2824147  
A:Accession: I60110  
A:Molecule type: mRNA  
A:Status: translated from GB/EMBL/DBJ  
A:Residues: 1-562 <RES>  
A:Cross-references: GB:M18182; NID:G340176; PIDN:AAA36800.1; PID:G340177  
R:Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.  
J. Biol. Chem. 260, 11223-11230, 1985  
A:Title: Isolation and characterization of the human tissue-type plasminogen activator gene; PMD:3161893  
A:Reference number: I55232; MUID:85289338; PMD:3161893  
A:Accession: I55232  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-36 <RE2>  
A:Cross-references: GB:M11890; NID:G339837; PIDN:AAA61213.1; PID:G339839  
A:Comment: Cleavage by plasmin or trypsin produces two chains held together by a single disulfide bond  
C:Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It cleaves plasminogen to plasmin and the fibrinogen type I repeat.  
C:Genetics:  
A:Gene: GDB:PLAT  
A:Cross-references: GDB:119496; OMIM:173370  
A:Map position: 8p12-8p12  
A:Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510/1  
A:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homology  
C:Keywords: fibrinolysis; glycoprotein; kringle; plasma; serine proteinase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-32/Domain: propeptide #status predicted <PRO>  
F:33-562/Product: t-plasminogen activator #status experimental <MAT>  
F:33-310/Product: t-plasminogen activator chain A #status experimental <ACH>  
F:41-78/Domain: fibronectin type I repeat homology <FI1>  
F:86-119/Domain: EGF homology <EGF>  
F:127-208/Domain: kringle homology <KR1>  
F:215-296/Domain: kringle homology <KR2>  
F:311-562/Product: t-plasminogen activator chain B #status experimental <BCH>  
F:311-556/Domain: trypsin homology <TRY>  
F:41-71, 69-78, 86-97, 91-108, 110-119, 127-208, 148-190, 179-203, 215-296, 236-278, 267-291, 299-421, 483-562/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:152, 483/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:310-311/Cleavage site: Arg-Tle (plasmin, trypsin) #status experimental  
F:357, 406/Active site: His, Asp #status predicted  
F:513/Active site: Ser #status experimental

Alignment Scores:  
Pred. No.: 0.00115 Length: 562  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x UKHUT (1-562)

QY 700 GATGCTGCAGGTGATCTGGGGCCCCCTGGTGTGT 738  
|||||  
DB 507 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 519  
|||||

## RESULT 10

S45281  
coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)  
N:Alternate names: Hageman factor (activated)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Apr-1995 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C:Accession: S45281; A61329  
R:Shibuya, Y.; Samba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.  
Biochim. Biophys. Acta 1206, 63-70, 1994  
A:Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human factor XII; MUID:94242782; PMID:81866251  
A:Reference number: S45281; MUID:94242782; PMID:81866251  
A:Accession: S45281  
A:Molecule type: mRNA  
A:Residues: 1-593 <SHI>  
A:Cross-references: UNIPROT:P98140; GB:S70164  
A:Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as Leu, and ATC for residue 505 as Leu  
R:Fujikawa, K.; Walsh, K.A.; Davie, E.W.  
Biochemistry 16, 2270-2278, 1977  
A:Title: Isolation and characterization of bovine factor XII (Hageman factor).  
A:Reference number: A61329; MUID:77182112; PMID:861210  
A:Accession: A61329  
A:Molecule type: protein  
A:Residues: 10-16, 'X', 18-19; 525-550 <FUJ>  
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;  
C:Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; serine proteinase  
F:37-78/Domain: fibronectin type II repeat homology <1F2>  
F:88-120/Domain: EGF homology <EGF>  
F:125-160/Domain: fibronectin type I repeat homology <FB1>  
F:207-287/Domain: kringle homology <KR>  
F:350-587/Domain: trypsin homology <TRY>  
F:541/Active site: Ser #status predicted

Alignment Scores:  
Pred. No.: 0.00114 Length: 593  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x S45281 (1-593)

QY 700 GATGCTGCAGGTGATCTGGGGCCCCCTGGTGTGT 738  
|||||

DB 535 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 547  
|||||

## RESULT 11

S28941  
coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)  
N:Alternate names: Hageman factor  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 25-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S28941  
R:Samba, U.; Yamamoto, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.  
Biochim. Biophys. Acta 1159, 113-121, 1992  
A:Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage site  
A:Reference number: S28941; MUID:93003367; PMID:1390917  
A:Accession: S28941  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-603 <SEM>  
A:Cross-references: UNIPROT:Q04962; EMBL:X68615; NID:949578; PIDN:CAA48600.1; PID:949578  
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;  
C:Keywords: hydrolase; serine proteinase  
F:46-87/Domain: fibronectin type II repeat homology <1F2>  
F:134-169/Domain: fibronectin type I repeat homology <FB1>  
F:177-208/Domain: EGF homology <EGF>  
F:216-294/Domain: kringle homology <KR>  
F:359-597/Domain: trypsin homology <TRY>

Alignment Scores:  
Pred. No.: 0.00115 Length: 562  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x UKHUT (1-562)

QY 700 GATGCTGCAGGTGATCTGGGGCCCCCTGGTGTGT 738  
|||||

DB 507 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 519  
|||||

## Alignment Scores:

Pred. No.: 0.00113 Length: 603  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x S28941 (1-603)

QY 700 GATGCTGCCAGGCTGATTCGGGGCCCCCTGGTGTGT 738

Db 545 AspAlaCysGlnGlyAspSerGlyProLeuValCys 557

## RESULT 12

KFHUI2

coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human

N;Alternate names: Hageman factor (activated)

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence revision 30-Jun-1991 #text change 09-Jul-2004

C;Accession: A29411; A26814; A00930; A25191; A22248; A21037

R;Cool, D.E.; MacGillivray, R.T.A.

J. Biol. Chem. 262, 13662-13673, 1987

A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon ge

A;Reference number: A29411; MUID:88007593; PMID:2888762

A;Accession: A29411

A;Molecule type: DNA

A;Residues: 1-615 &lt;COO&gt;

A;Cross-references: UNIPROT:P00748; GB:M17466; GB:J02807; NID:g180355; PIDN:AA859490.1;

R;Trippodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.

Nucleic Acids Res. 14, 3146, 1986

A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).

A;Reference number: A26814; MUID:86176794; PMID:3754331

A;Accession: A26814

A;Molecule type: mRNA

A;Residues: 4-615 &lt;TRI&gt;

A;Cross-references: GB:M31315; NID:g182291; PIDN:AAA70225.1; PID:g182292

R;Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.T.

J. Biol. Chem. 260, 13666-13676, 1985

A;Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the

A;Reference number: A00930; MUID:86033830; PMID:3877053

A;Accession: A00930

A;Molecule type: mRNA

A;Residues: 14-332, 'S', '334-615 &lt;CO2&gt;

A;Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359

R;Que, B.G.; Davie, E.W.

Biochemistry 25, 1525-1528, 1986

A;Title: Characterization of a cDNA coding for human factor XII (Hageman factor).

A;Reference number: A25191; MUID:86216049; PMID:3011063

A;Accession: A25191

A;Molecule type: mRNA

A;Residues: 146-378, 'G', '380-615 &lt;QUE&gt;

A;Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361

R;McMullen, B.A.; Fujikawa, K.

J. Biol. Chem. 260, 5328-5341, 1985

A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Ha

A;Reference number: A22248; MUID:85182674; PMID:3886654

A;Accession: A22248

A;Molecule type: protein

A;Residues: 20-379 &lt;MCM&gt;

R;Fujikawa, K.; McMullen, B.A.

J. Biol. Chem. 258, 10924-10933, 1983

A;Title: Amino acid sequence of human beta-factor XIIa.

A;Reference number: A21037; MUID:83291041; PMID:6604055

A;Accession: A21037

A;Molecule type: protein

A;Residues: 354-362;373-615 &lt;FUI&gt;

R;Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A;Title: O-linked fucose is present in the first epidermal growth factor domain of facto

A;Reference number: A44606; MUID:92184750; PMID:1544894

A;Contents: annotation; carbohydrate binding site

C;Genetics:

A;Gene: GDB:F12

A;Cross-references: GDB:119892; OMIM:234000

A;Map position: 5q34-qter

A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/1

C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic s

C;Function:

A;Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma pr

ikrein

A;Pathway: blood coagulation; fibrinolysis

C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;

C;Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma; s

F;1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F;20-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental &lt;A12&gt;

F;47-88/Domain: fibronectin type II repeat homology &lt;FB2&gt;

F;98-130/Domain: EGF homology &lt;EG1&gt;

F;135-170/Domain: fibronectin type I repeat homology &lt;IF1&gt;

F;178-209/Domain: EGF homology &lt;EG2&gt;

F;217-295/Domain: kringle homology &lt;KR2&gt;

F;298-356/Region: proline-rich

F;354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental &lt;B12&gt;

F;373-609/Domain: trypsin homology &lt;TRY&gt;

F;98-110,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-290,

F;109/Binding site: carbohydrate (Thr) (covalent) #status experimental

F;249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted

F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;412,461,563/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.: 0.00113 Length: 615

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0

DB: 1 Gaps: 0

US-10-015-385A-193 (1-1091) x KFHUI2 (1-615)

QY 700 GATGCTGCCAGGCTGATTCGGGGCCCCCTGGTGTGT 738

Db 557 AspAlaCysGlnGlyAspSerGlyProLeuValCys 569

## RESULT 13

T30337

polyprotein - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T30337

R;Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.

submitted to the EMBL Data Library, March 1998

A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer

A;Reference number: Z20829

A;Accession: T30337

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-1524 &lt;YAN&gt;

A;Cross-references: UNIPROT:Q91674; EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAAC2471;

C;Superfamily: trypsin related polyprotein; trypsin homology

## Alignment Scores:

Pred. No.: 0.000923 Length: 1524

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0

DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x T30337 (1-1524)

QY 700 GATGCTGCCAGGCTGATTCGGGGCCCCCTGGTGTGT 738

Db 762 AspAlaCysGlnGlyAspSerGlyProLeuValCys 774

Search completed: March 5, 2005, 23:49:08  
Job time : 70 secs

## RESULT 14

S54115  
complement factor D (EC 3.4.21.46) - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S54115

R:Nicolas, N.

submitted to the EMBL Data Library, April 1995

A:Reference number: S54115

A:Accession: S54115

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-191 <NIC>

A:Cross-references: UNIPROT:P51779; EMBL:Z49058; NID:g773264; PIDN:CAA88844.1; PID:g7732

C:Superfamily: trypsin; trypsin homology

C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase

F:1-181/Domain: trypsin homology (fragment) <TRY>

## Alignment Scores:

Pred. No.:	0.013	Length:	191
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x S54115 (1-191)

QY 712 GGTGATTCGGGGCCCCCTGTGTGGGGAGTC 747

DB 139 GlyAspSerGlyGlyProLeuValCysGlyGlyVal 150

## RESULT 15

S65465

trypsin-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)

C:Species: Sarcophaga bullata

C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S65465; S65403

R:Botovskiy, D.; Janssen, I.; Vanden Broeck, J.; Huybrechts, R.; Verhaert, P.; de Bondt,

Eur. J. Biochem. 237, 279-287, 1996

A:Title: Molecular sequencing and modeling of Neobellieria bullata trypsin. Evidence for

A:Reference number: S65403; MUID:96203936; PMID:8620885

A:Accession: S65465

A:Molecule type: mRNA

A:Residues: 1-254 <BOR>

A:Cross-references: UNIPROT:P51588; EMBL:X94691; NID:g1177315; PIDN:CAA64354.1; PID:g117

A:Accession: S65403

A:Molecule type: protein

A:Residues: 27-36 <BOW>

A>Note: 27-Leu, 35-Leu were also found

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-26/Domain: propeptide #status predicted <PRO>

F:27-254/Product: trypsin #status experimental <MAT>

F:27-247/Domain: trypsin homology <TRY>

F:53-69,154-158,195-238,204-228/Disulfide bonds: #status predicted

F:68,113,208/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.:	0.0122	Length:	254
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.36%	Indels:	0
DB:	2	Gaps:	0

US-10-015-385A-193 (1-1091) x S65465 (1-254)

QY 700 GATGCTGCAGGTGATTCGGGGCCCCCTGGTG 735

DB 202 AspAlaCysGlnGlyAspSerGlyProLeuVal 213



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 5, 2005, 23:39:31 ; Search time 220.5 Seconds  
(without alignments)  
5067.378 Million cell updates/sec

Title: US-10-015-385a-193

Perfect score: 357

Sequence: 1 caagcaggtcatcccttgg.....aggggcaaaaaaaaaa 1091

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp  
-Q=/cn2\_1/USPTO spool p/US10015385/runat 05032005 173711 18178/app query.faeta\_1.1287  
-DB=UniProt\_03 -QFWT=fastan -SUFFIX=olin2p.rup -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=1500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10015385 @CGN 1.1 244 @runat 05032005 173711 18178 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

- 1: uniprot\_sprot.\*
- 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	69.5	248	1 KLKC HUMAN	Q9ukr0 homo sapien
2	65	18.2	111	2 Q9UKR2	Q9ukr2 homo sapien
3	31	8.7	234	2 Q9CV76	Q9cv76 mus musculus
4	14	3.9	681	2 Q7ZT70	Q7zt70 lampetra ja
5	13	3.6	200	2 Q924U6	Q924u6 mus musculus
6	13	3.6	228	2 Q6FWH3	Q6fhw3 homo sapien
7	13	3.6	235	2 Q8N4E0	Q8n4e0 homo sapien
8	13	3.6	242	2 Q8OV54	Q8ov54 mus musculus
9	13	3.6	243	2 Q86VJ5	Q86vj5 homo sapien
10	13	3.6	246	2 Q88J01	Q88j01 mus musculus
11	13	3.6	247	2 Q66PG9	Q66pg9 fugu rubrip
12	13	3.6	247	2 Q9W7Q5	Q9w7q5 paralichthy
13	13	3.6	249	2 Q6QX59	Q6qx59 lepeophthei
14	13	3.6	250	2 Q8CGR5	Q8cgr5 mus musculus
15	13	3.6	251	2 O54854	O54854 rattus norv
16	13	3.6	253	1 CFAD_HUMAN	P00746 homo sapien

Q8wzb4	homo sapien	253	3.6	13	17
Q91y82	mus musculus	253	3.6	13	18
Q9mz26	macaca fasc	267	3.6	13	19
Q96899	scelopendra	277	3.6	13	20
Q96ef3	homo sapien	300	3.6	13	21
Q7q619	anopheles g	317	3.6	13	22
Q7t0x2	xenopus lae	320	3.6	13	23
Q6nv7	xenopus tro	330	3.6	13	24
Q9vcj16	rattus norv	371	3.6	13	25
Q9pvx7	xenopus lae	389	3.6	13	26
P49150	desmodus ro	394	3.6	13	27
Q9bzv1	homo sapien	395	3.6	13	28
P98121	desmodus ro	431	3.6	13	29
Q8cj17	rattus norv	445	3.6	13	30
Q9er04	mus musculus	455	3.6	13	31
Q8cdro	mus musculus	455	3.6	13	32
P98119	desmodus ro	477	3.6	13	34
P15638	desmodus ro	477	3.6	13	35
Q9bu99	homo sapien	543	3.6	13	36
P11214	mus musculus	559	3.6	13	37
P19637	rattus norv	559	3.6	13	38
Q6p7u0	mus musculus	559	3.6	13	39
P00750	homo sapien	562	3.6	13	40
Q8sq23	sus scrofa	562	3.6	13	41
Q8mb1	oryzotolagus	564	3.6	13	42
Q28198	bos taurus	566	3.6	13	43
Q6pja5	homo sapien	589	3.6	13	44
P98140	bos taurus	593	3.6	13	45
O35727	mus musculus	597	3.6	13	46
Q6per0	mus musculus	597	3.6	13	47
Q04962	cavia porce	603	3.6	13	48
Q80vc5	mus musculus	609	3.6	13	49
P00748	homo sapien	615	3.6	13	50
O81z25	homo sapien	615	3.6	13	51
Q97507	sus scrofa	616	3.6	13	52
Q9r098	mus musculus	653	3.6	13	53
Q8vc84	mus musculus	653	3.6	13	54
Q6pf94	mus musculus	799	3.6	13	55
Q6uxd8	homo sapien	802	3.6	13	56
O81u80	homo sapien	811	3.6	13	57
Q9dbi0	mus musculus	811	3.6	13	58
Q6ic22	homo sapien	824	3.6	13	59
Q7rtv7	homo sapien	834	3.6	13	60
Q91674	xenopus lae	1524	3.6	13	61
Q6jvs2	sus scrofa	83	3.4	12	62
Q8mvl1	boltenia vi	85	3.4	12	63
Q6gz6	drosophila	141	3.4	12	64
Q9ylx4	anopheles g	155	3.4	12	65
O45045	scirpophaga	187	3.4	12	66
Q6xi43	drosophila	220	3.4	12	67
Q6xhu4	drosophila	226	3.4	12	68
Q7ps50	anopheles g	230	3.4	12	69
Q7q344	anopheles g	240	3.4	12	70
Q92876	homo sapien	244	3.4	12	71
P54625	drosophila	253	3.4	12	72
P42626	drosophila	253	3.4	12	73
P4277	drosophila	253	3.4	12	74
Q8mz41	drosophila	253	3.4	12	75
Q8sz4	drosophila	253	3.4	12	76
P51588	sarcophaga	254	3.4	12	77
O76520	stomoxys ca	254	3.4	12	78
Q9xyy0	rhizopertha	254	3.4	12	79
Q9v7a9	metarhizium	255	3.4	12	80
P35588	hypoderma 1	256	3.4	12	81
P54624	drosophila	256	3.4	12	82
P04814	drosophila	256	3.4	12	83
P54627	drosophila	256	3.4	12	84
P35005	drosophila	256	3.4	12	85
O18599	drosophila	256	3.4	12	86
Q25081	hypoderma 1	256	3.4	12	87
Q9xyy1	rhizopertha	256	3.4	12	88
		256	3.4	12	89

90	12	3.4	258	1	TRYU DROER	P54629 drosophila	163	11	3.1	237	2	Q29464	Q29464 bos taurus
91	12	3.4	258	2	Q6NLM5	Q6nlm5 drosophila	164	11	3.1	241	2	Q7PQB3	Q7pqb3 anopheles g
92	12	3.4	258	2	Q9W5U8	Q9w5u8 drosophila	165	11	3.1	242	2	Q6NTB8	Q6ntb8 homo sapien
93	12	3.4	258	2	Q6JUF3	Q6juf3 neodiprion	166	11	3.1	245	2	Q7Q2Q8	Q7q2q8 anopheles g
94	12	3.4	259	1	CFAD_PIG	P51779 sus scrofa	167	11	3.1	249	2	Q9QYN4	Q9qyn4 mus musculus
95	12	3.4	260	2	Q9V6P6	Q9v6p6 drosophila	168	11	3.1	249	2	Q6DIW2	Q6diw2 xenopus tro
96	12	3.4	261	2	Q962G7	Q962g7 culx pipie	169	11	3.1	250	1	KLK9 HUMAN	Q9ubx7 homo sapien
97	12	3.4	261	2	Q6IDF4	Q6idf4 drosophila	170	11	3.1	250	1	KLKB HUMAN	Q9uk9 homo sapien
98	12	3.4	262	1	TRYU DROME	P42279 drosophila	171	11	3.1	250	2	Q632F2	Q632f2 rattus norv
99	12	3.4	262	2	Q9V5X9	Q9v5x9 drosophila	172	11	3.1	251	2	KLKE HUMAN	Q9p0g3 homo sapien
100	12	3.4	263	2	Q02570	Q02570 culx quinq	173	11	3.1	251	2	Q6B089	Q6b089 homo sapien
101	12	3.4	264	1	VDP_BOMMO	Q07943 bombyx mori	174	11	3.1	254	2	Q8CGR4	Q8cgr4 mus musculus
102	12	3.4	264	1	Q02569	Q02569 culx quinq	175	11	3.1	254	2	Q96RQ0	Q96rq0 homo sapien
103	12	3.4	267	1	TRY7 ANOGA	P35041 anopheles g	176	11	3.1	255	2	Q6ISIO	Q6isi0 homo sapien
104	12	3.4	271	2	Q54213	Q54213 streptomyce	177	11	3.1	255	2	Q7JIG6	Q7jig6 saguinus oe
105	12	3.4	272	2	Q9V5X6	Q9v5x6 drosophila	178	11	3.1	256	1	KLKF HUMAN	Q9h2r5 homo sapien
106	12	3.4	272	2	Q82XG0	Q82xg0 streptomyce	179	11	3.1	257	2	Q8R560	Q8r560 ostrinia nu
107	12	3.4	274	1	TRY1 ANOGA	P35035 anopheles g	180	11	3.1	257	2	Q7Z0G1	Q7z0g1 phlebotomus
108	12	3.4	274	2	Q16133	Q16133 anopheles g	181	11	3.1	258	2	Q632F4	Q632f4 rattus norv
109	12	3.4	275	1	Q17086	Q17086 anopheles s	182	11	3.1	260	1	KLK8 HUMAN	Q60259 homo sapien
110	12	3.4	275	1	TRY3 ANOGA	P35037 anopheles g	183	11	3.1	260	1	NRPN_MOUSE	Q61955 mus musculus
111	12	3.4	275	1	TRY4 ANOGA	P35038 anopheles g	184	11	3.1	260	1	NRPN_MOUSE	Q61955 mus musculus
112	12	3.4	275	2	Q7PNF7	Q7pnf7 anopheles g	185	11	3.1	260	2	Q8IW69	Q8iww9 mus musculus
113	12	3.4	276	2	P91894	P91894 arenicola m	186	11	3.1	260	2	Q9U4I4	Q9u4i4 plodia inte
114	12	3.4	276	2	Q16133	Q16133 anopheles s	187	11	3.1	261	2	Q66HW9	Q66hw9 brachydano
115	12	3.4	278	2	P91893	P91893 arenicola m	188	11	3.1	261	2	Q9W7Q4	Q9w7q4 paralichthy
116	12	3.4	278	2	Q7PNF6	Q7pnf6 anopheles g	189	11	3.1	261	2	TRYT DROER	P54628 drosophila
117	12	3.4	279	2	Q7TNX3	Q7tnx3 mus musculus	190	11	3.1	262	1	TRYT DROME	P42278 drosophila
118	12	3.4	279	2	Q9QZ74	Q9qz74 rattus norv	191	11	3.1	262	2	Q8SZQ7	Q8szq7 drosophila
119	12	3.4	280	2	Q7Q494	Q7q494 anopheles g	192	11	3.1	262	2	Q9NB91	Q9nb91 agrotis ips
120	12	3.4	281	1	TRYZ DROER	P54630 drosophila	193	11	3.1	262	2	Q9V5Y0	Q9v5y0 drosophila
121	12	3.4	285	2	Q69997	Q69997 streptomyce	194	11	3.1	263	2	Q9NB92	Q9nb92 agrotis ips
122	12	3.4	416	2	Q8BZ13	Q8bz13 mus musculus	195	11	3.1	264	1	CTRL_HUMAN	P40313 homo sapien
123	12	3.4	416	2	Q8BZ30	Q8bz30 mus musculus	196	11	3.1	264	1	Q9D7B8	Q9d7b8 mus musculus
124	12	3.4	417	2	Q8VHJ4	Q8vhj4 rattus norv	197	11	3.1	264	2	Q9D960	Q9d960 mus musculus
125	12	3.4	417	2	Q8VHK8	Q8vhk8 mus musculus	198	11	3.1	264	2	Q9EQZ8	Q9eqz8 rattus norv
126	12	3.4	417	2	Q8VHD1	Q8vdv1 mus musculus	199	11	3.1	264	2	Q9ER05	Q9er05 mus musculus
127	12	3.4	418	1	HATT_HUMAN	O60235 homo sapien	200	11	3.1	266	2	Q24091	Q24091 drosophila
128	12	3.4	418	2	Q61E15	Q6ie15 rattus norv	201	11	3.1	266	2	Q8WR10	Q8wr10 paralithode
129	12	3.4	420	2	Q61E14	Q6ie14 rattus norv	202	11	3.1	267	2	Q9VLF5	Q9vlf5 drosophila
130	12	3.4	422	1	DES1_HUMAN	Q9ul52 homo sapien	203	11	3.1	267	2	Q640E1	Q640e1 xenopus lae
131	12	3.4	423	2	Q6UW31	Q6uw31 homo sapien	204	11	3.1	267	2	Q7Z0G0	Q7z0g0 phlebotomus
132	12	3.4	423	2	Q8BM10	Q8bm10 mus musculus	205	11	3.1	268	2	Q8IUW0	Q8iuvw0 homo sapien
133	12	3.4	423	2	Q7PN85	Q7pn85 anopheles g	206	11	3.1	269	2	Q921N4	Q921n4 mus musculus
134	11	3.1	54	2	Q6JD13	Q6jdi3 canis fami	207	11	3.1	270	1	TRYT MERUN	P50342 meriones un
135	11	3.0	68	2	Q8RH77	Q8rh77 oryza sativ	208	11	3.1	271	2	Q8HYJ2	Q8hyj2 bos taurus
136	11	3.0	73	2	Q9TV90	Q9tv90 equus cabal	209	11	3.1	273	1	MCT7_MOUSE	Q22844 mus musculus
137	11	3.1	87	2	Q9CQ78	Q9cq78 m mus muscu	210	11	3.1	273	1	TRYT_SHEEP	P27435 rattus norv
138	11	3.1	119	2	Q9NR68	Q9nr68 homo sapien	211	11	3.1	273	2	Q9XSM1	Q9xsm1 ovis aries
139	11	3.1	126	2	Q7W325	Q7w325 sus scrofa	212	11	3.1	273	2	Q6P6W8	Q6p6w8 rattus norv
140	11	3.0	139	2	Q942T9	Q942t9 oryza sativ	213	11	3.1	273	2	Q921N4	Q921n4 mus musculus
141	11	3.1	148	2	Q25069	Q25069 haematobia	214	11	3.1	273	2	Q921N4	P05524 mus musculus
142	11	3.1	156	2	Q16007	Q16007 schistosoma	215	11	3.0	274	1	FGF3_MOUSE	P50343 rattus norv
143	11	3.1	163	2	Q6GH01	Q6gh01 xenopus lae	216	11	3.1	274	1	MCT6_RAT	P50343 rattus norv
144	11	3.1	164	2	Q9DC82	Q9dc82 mus musculus	217	11	3.1	275	1	TRB1_HUMAN	Q15661 homo sapien
145	11	3.1	171	2	Q6T3V9	Q6t3v9 helicoverpa	218	11	3.1	275	1	TRB2_HUMAN	P20231 homo sapien
146	11	3.1	176	2	Q6SL22	Q6sl22 canis fami	219	11	3.1	275	1	TRYT_CANFA	P15944 canis fami
147	11	3.1	176	2	Q8K5D7	Q8k5d7 mus musculus	220	11	3.1	275	1	TRYT_PIG	Q8ixd7 mus scrofa
148	11	3.1	176	2	Q91VQ8	Q91vq8 mus musculus	221	11	3.1	275	2	Q8IXD7	Q8ixd7 homo sapien
149	11	3.1	182	2	Q9NB87	Q9nb87 agrotis ips	222	11	3.1	275	2	Q96RZ6	Q96rz6 homo sapien
150	11	3.1	197	2	Q45043	Q45043 helicoverpa	223	11	3.1	275	2	Q8E051	Q8e051 homo sapien
151	11	3.1	197	2	Q9NB80	Q9nb80 heliothis z	224	11	3.1	275	2	Q6FHB8	Q6fhb8 homo sapien
152	11	3.1	197	2	Q9NB89	Q9nb89 agrotis ips	225	11	3.1	275	2	Q8ETM8	Q8etm8 homo sapien
153	11	3.1	202	2	Q9NB90	Q9nb90 agrotis ips	226	11	3.1	275	2	Q7YS62	Q7ys62 equus cabal
154	11	3.1	203	2	Q9NB77	Q9nb77 heliothis z	227	11	3.1	276	1	MCT6_MOUSE	P21845 mus musculus
155	11	3.1	210	2	Q6BDS2	Q6bds2 homo sapien	228	11	3.1	276	2	Q86UA5	Q86ua5 homo sapien
156	11	3.1	211	2	Q6ZNH3	Q6znh3 homo sapien	229	11	3.1	276	2	Q9QYN3	Q9qyn3 m hippostas
157	11	3.1	211	2	Q9NB81	Q9nb81 heliothis z	230	11	3.1	277	2	Q8OWM7	Q8owm7 mus musculus
158	11	3.1	227	2	Q7PHB4	Q7phb4 anopheles g	231	11	3.1	280	1	TRYZ_DROME	P42280 drosophila
159	11	3.1	228	2	Q7Q153	Q7q153 anopheles g	232	11	3.1	280	2	Q8N171	Q8n171 homo sapien
160	11	3.1	235	1	TRYD_HUMAN	Q9bzj3 homo sapien	233	11	3.1	280	2	Q9V5X8	Q9v5x8 drosophila
161	11	3.1	236	2	Q9TVH3	Q9tvh3 schistosoma	234	11	3.1	282	2	Q6NZY1	Q6nzy1 homo sapien
162	11	3.1	237	2	Q17035	Q17035 anopheles g	235	11	3.1	284	2	Q8NF86	Q8nf86 homo sapien

236	11	3.1	299	2	Q61Y8	Q6yly8 lygus lineo	309	11	3.1	845	2	Q9DGR1	Q9dgr1 xenopus lae
237	11	3.1	304	1	DISP_RAT	P83748 rattus norv	310	11	3.1	845	2	Q63ZQ6	Q63zq6 xenopus lae
238	11	3.1	309	2	Q27083	Q27083 tachyleus	311	11	3.1	855	2	Q7Z410	Q7z410 xenopus lae
239	11	3.1	310	1	DISP_MOUSE	Q9gyz9 mus musculu	312	11	3.1	1004	2	P79953	P79953 xenopus lae
240	11	3.1	314	2	Q9VR15	Q9vr15 drosophila	313	11	3.1	1059	2	Q7Z411	Q7z411 homo sapien
241	11	3.1	315	2	Q81RR3	Q81rr3 drosophila	314	11	3.1	1089	2	Q8T3A0	Q8t3a0 ciona intes
242	11	3.1	317	2	Q8DGR3	Q8dgr3 xenopus lae	315	11	3.1	1379	2	Q9V4N6	Q9v4n6 drosophila
243	11	3.1	321	2	Q6GNK3	Q6gnk3 xenopus lae	316	11	3.1	1397	2	Q7KQ99	Q7kq99 drosophila
244	11	3.1	325	2	Q15944	Q15944 sarcophaga	317	11	3.1	1801	2	Q8WSJ2	Q8wsj2 bombyx mori
245	11	3.1	328	2	Q61RA4	Q61ra4 xenopus lae	318	11	3.1	2616	1	NDL_DROME	P81559 drosophila
246	11	3.1	329	2	Q70B72	Q7qb72 anopheles g	319	11	3.1	4548	1	APOA_HUMAN	P08519 homo sapien
247	11	3.1	329	2	Q42272	Q42272 xenopus lae	320	10	2.8	43	2	Q7M3N4	P07m3n4 antheraea p
248	11	3.1	333	1	PLMN_CANFA	P80009 canis famli	321	10	2.8	50	2	Q9CTK6	Q9gk6 culex quinq
249	11	3.1	334	2	Q46507	Q46507 papio hamad	322	10	2.8	110	2	Q9JRW7	Q9jrw7 mus musculu
250	11	3.1	338	1	PLMN_HORSE	P80010 equus cabal	323	10	2.8	116	2	Q7JMX5	Q7jmx5 helicoverpa
251	11	3.1	339	2	Q8BLV6	Q8blv6 mus musculu	324	10	2.8	122	2	Q7NKT6	Q7nkt6 gloeobacter
252	11	3.1	340	2	Q8BTV6	Q8biv6 mus musculu	325	10	2.8	154	2	O18448	Q18448 helicoverpa
253	11	3.1	342	1	PS8_MOUSE	Q9ead1 mus musculu	326	10	2.8	159	2	Q28286	Q28286 canis famli
254	11	3.1	342	1	PS8_RAT	Q9es87 rattus norv	327	10	2.8	160	2	Q6XGZ1	Q6xgz1 homo sapien
255	11	3.1	343	1	PLMN_SHEEP	P81286 ovis aries	328	10	2.8	161	2	Q28511	Q28511 macaca mula
256	11	3.1	343	1	PS8_HUMAN	Q16651 homo sapien	329	10	2.8	161	2	Q60546	Q60546 mesocricetu
257	11	3.1	344	2	Q640F8	Q640f8 xenopus lae	330	10	2.8	161	2	Q63109	Q63109 rattus norv
258	11	3.1	376	1	FA10_HOPST	P83370 hoplocephal	331	10	2.8	165	1	TRV3_LUCCU	P35043 lucilia cup
259	11	3.1	376	1	FA10_TROCA	P81428 tropidechis	332	10	2.8	186	2	Q6X655	P35043 lucilia cup
260	11	3.1	378	2	Q8SY50	Q8sy50 drosophila	333	10	2.8	205	2	O45046	O45046 scirpophaga
261	11	3.1	388	2	O44330	O44330 manduca sex	334	10	2.8	210	2	Q63Z11	Q63z11 xenopus lae
262	11	3.1	388	2	Q81926	Q81926 hyphantria	335	10	2.8	211	2	Q8CH29	Q8ch29 mus musculu
263	11	3.1	390	2	Q81927	Q81927 hyphantria	336	10	2.8	238	1	TRY5_AEDAE	P29787 aedes aegyp
264	11	3.1	390	2	Q8MPJ8	Q8mpj8 bombyx mori	337	10	2.8	244	1	MCT2_MOUSE	P15119 mus musculu
265	11	3.1	391	2	Q7FAX5	Q7pxj5 anopheles g	338	10	2.8	244	2	Q8MWR5	Q8mwr5 dermatophag
266	11	3.1	400	2	Q27081	Q27081 tachyleus	339	10	2.8	245	2	Q9XI60	Q9xy60 ctenoccephal
267	11	3.1	404	2	Q64ID3	Q64id3 anthonomus	340	10	2.8	247	2	O18458	Q18458 heterodera
268	11	3.1	411	2	Q9VUF0	Q9avb0 drosophila	341	10	2.8	248	1	GRZ1_RAT	Q06605 rattus norv
269	11	3.1	429	2	O8AVB0	Q8avb0 brachydanio	342	10	2.8	248	1	NKP1_RAT	P18291 rattus norv
270	11	3.1	431	1	UROK_HUMAN	P00749 homo sapien	343	10	2.8	248	2	Q9XYX9	Q9xyx9 rhyzopertha
271	11	3.1	433	1	UROK_BOVIN	Q05589 bos taurus	344	10	2.8	253	1	TRYB_DROME	P35004 drosophila
272	11	3.1	433	1	UROK_PAPCY	P16227 papio cynoc	345	10	2.8	253	2	Q6W741	Q6w741 pediculus h
273	11	3.1	433	2	Q8MHY7	P16227 papio cynoc	346	10	2.8	253	2	Q9V5Y3	Q9vsy3 drosophila
274	11	3.1	433	2	Q8MIL0	Q8mly7 oryctolagus	347	10	2.8	254	1	CTRL_HALRU	P35003 haliotis ru
275	11	3.1	442	1	UROK_PIG	Q8mly7 oryctolagus	348	10	2.8	254	1	TRY3_AEDAE	P29786 aedes aegyp
276	11	3.1	449	2	Q9VDU8	P04185 sus scrofa	349	10	2.8	254	2	Q8MMK9	Q8mmk9 aedes aegyp
277	11	3.1	453	1	TMS3_MOUSE	Q8kto mus musculu	350	10	2.8	254	2	Q8T637	Q8t637 aedes aegyp
278	11	3.1	453	2	Q6ZMC3	Q6zmc3 homo sapien	351	10	2.8	255	1	TRY4_LUCCU	Q8t637 aedes aegyp
279	11	3.1	453	2	Q812A6	Q812a6 mus musculu	352	10	2.8	256	1	HYFA_HYPLI	P35587 hypoderma 1
280	11	3.1	454	1	TMS3_HUMAN	P57727 homo sapien	353	10	2.8	256	2	Q25082	Q25082 hypoderma 1
281	11	3.1	467	2	Q6IT09	Q6it09 pseudonaja	354	10	2.8	256	2	Q9XY51	Q9xy51 ctenoccephal
282	11	3.1	471	2	Q8CFE0	Q8cfe0 mus musculu	355	10	2.8	256	2	Q6MJY6	Q6mly6 bdellovibri
283	11	3.1	488	2	Q9TYH4	Q9tyh4 schistosoma	356	10	2.8	257	1	GRAM_HUMAN	P51124 homo sapien
284	11	3.1	492	2	Q7Z155	Q7z155 chiromantes	357	10	2.8	257	2	Q8IT49	Q8it49 pyrocoelia
285	11	3.1	537	2	Q9BYE1	Q9bye1 homo sapien	358	10	2.8	257	2	Q27440	Q27440 aedes aegyp
286	11	3.1	540	2	Q800Y7	Q800y7 meleagris g	359	10	2.8	257	2	Q86PL8	Q86pl8 aedes aegyp
287	11	3.1	556	2	Q803D5	Q803d5 brachydanio	360	10	2.8	257	2	Q9NB49	Q9nb49 aedes aegyp
288	11	3.1	558	2	Q86YM4	Q86ym4 homo sapien	361	10	2.8	258	1	GRAM_RAT	Q03238 rattus norv
289	11	3.1	569	2	Q8QGV1	Q8qgv1 cyprinus ca	362	10	2.8	259	2	Q9XY61	Q9xy61 ctenoccephal
290	11	3.1	575	2	Q8IRB8	Q8irb8 drosophila	363	10	2.8	259	2	Q6JPG5	Q6jpg5 neodiprion
291	11	3.1	581	2	Q9BYE2	Q9bye2 homo sapien	364	10	2.8	261	2	Q00344	Q00344 cochliobolu
292	11	3.1	581	2	Q81925	Q81925 hyphantria	365	10	2.8	261	2	Q8IRE1	Q8ire1 drosophila
293	11	3.1	581	2	Q9XZM7	Q9xzm7 strongyloce	366	10	2.8	261	2	Q6OX60	Q6ox60 lepeophthei
294	11	3.1	654	2	Q6QNF4	Q6qnf4 canis famli	367	10	2.8	263	1	CFAD_RAT	P32038 rattus norv
295	11	3.1	655	1	HGFA_HUMAN	Q04756 homo sapien	368	10	2.8	263	2	O08643	O08643 mus musculu
296	11	3.0	677	2	Q8TEJ7	Q8tej7 homo sapien	369	10	2.8	265	2	Q9XY55	Q9xy55 ctenoccephal
297	11	3.1	681	2	Q70554	Q7q554 anopheles g	370	10	2.8	266	2	Q81916	Q81916 blomia trop
298	11	3.1	707	2	Q8QGV0	Q8qgv0 cyprinus ca	371	10	2.8	267	2	Q9V942	Q9v942 drosophila
299	11	3.1	766	2	Q8NBY4	Q8nby4 homo sapien	372	10	2.8	269	2	Q7PWT2	Q7pwt2 anopheles g
300	11	3.1	790	1	PLMN_PIG	P06867 sus scrofa	373	10	2.8	269	2	Q9V929	Q9v929 drosophila
301	11	3.1	810	1	PLMN_ERIEU	Q29485 erinaceus e	374	10	2.8	271	2	Q7Z0G2	Q7z0g2 phlebotomus
302	11	3.1	810	1	PLMN_HUMAN	P00747 homo sapien	375	10	2.8	272	1	SER3_DROME	P17207 drosophila
303	11	3.1	810	1	PLMN_MACMU	P12545 macaca mula	376	10	2.8	272	2	Q7Q483	Q7q483 anopheles g
304	11	3.1	812	1	PLMN_BOVIN	P06868 bos taurus	377	10	2.8	275	2	Q66UD0	Q66ud0 culicoides
305	11	3.1	812	1	PLMN_MOUSE	P20918 mus musculu	378	10	2.8	276	2	O18443	O18443 helicoverpa
306	11	3.1	812	1	PLMN_RAT	Q01177 rattus norv	379	10	2.8	277	2	Q81Q10	Q81q10 drosophila
307	11	3.1	818	2	Q6PBA6	Q6pba6 brachydanio	380	10	2.8	277	2	Q7PN79	Q7pn79 anopheles g
308	11	3.1	845	2	Q6GR54	Q6gr54 xenopus lae	381	10	2.8	291	2	Q8WPE4	Q8wpe4 lygus lineo

382	10	2.8	291	2	Q95P15	Q95p15 lygus hespe	455	9	2.5	157	2	Q95W21	Q95w21 anthonomus
383	10	2.8	291	2	Q6V1Y7	Q6vly7 lygus lineo	456	9	2.5	158	2	Q9VYD8	Q9vyd8 drosophila
384	10	2.8	291	2	Q6V1Y9	Q6vly9 lygus lineo	457	9	2.5	162	2	Q95W27	Q95w27 anthonomus
385	10	2.8	291	2	Q6T1Z0	Q6t1z0 lygus lineo	458	9	2.5	169	2	Q8CER7	Q8cer7 mus musculus
386	10	2.8	292	2	O18444	O18444 helicoverpa	c 459	9	2.5	170	2	Q7PXR0	Q7pxr0 anopheles g
387	10	2.8	295	2	O18445	O18445 helicoverpa	c 460	9	2.5	170	2	Q6AUV4	Q6auv4 oryza sativ
388	10	2.8	295	2	O18450	O18450 helicoverpa	461	9	2.5	174	2	Q9GSL5	Q9gsl5 chrysomya b
389	10	2.8	295	2	Q9N6C6	Q9n6c6 heliothis z	462	9	2.5	174	2	Q9GSM2	Q9gsm2 chrysomya b
390	10	2.8	295	2	Q9NH07	Q9nh07 heliothis z	c 463	9	2.5	174	2	Q67VL2	Q67vl2 oryza sativ
391	10	2.8	297	2	Q86M89	Q86m89 spodoptera	464	9	2.5	175	2	Q6PLJ9	Q6plj9 squilla ora
392	10	2.8	298	2	Q9NH06	Q9nh06 heliothis z	465	9	2.5	175	2	Q9GN96	Q9gn96 chrysomya b
393	10	2.8	300	2	Q9NH08	Q9nh08 agrotis ips	466	9	2.5	175	2	Q9GSL6	Q9gsl6 chrysomya b
394	10	2.8	302	2	Q8SYZ7	Q8syz7 drosophila	467	9	2.5	175	2	Q9GSM0	Q9gsm0 chrysomya b
395	10	2.8	302	2	Q9W586	Q9w586 drosophila	468	9	2.5	175	2	Q9GSM1	Q9gsm1 chrysomya b
396	10	2.8	302	2	Q7E900	Q7e900 drosophila	469	9	2.5	175	2	Q9GSM4	Q9gsm4 chrysomya b
397	10	2.8	305	2	Q7QJ37	Q7qj37 anopheles g	c 470	9	2.5	175	2	Q9LSN6	Q9lsn6 arabidopsis
398	10	2.8	308	2	Q9W454	Q9w454 drosophila	471	9	2.5	176	2	Q66TN7	Q66tn7 bufo arenar
399	10	2.8	335	2	Q8VIF2	Q8vif2 mus musculus	472	9	2.5	181	2	Q8NFV7	Q8nfv7 homo sapien
400	10	2.8	374	2	Q9VUG2	Q9vug2 drosophila	473	9	2.5	181	2	Q9GSM6	Q9gsm6 chrysomya b
401	10	2.8	375	1	PCE TACTR	P21902 tachypleus	474	9	2.5	182	2	Q6PLJ6	Q6plj6 penaeus jap
402	10	2.8	382	2	Q75HL1	Q75hl1 mus musculus	475	9	2.5	182	2	Q8PLJ8	Q8plj8 procamburus
403	10	2.8	385	2	Q25101	Q25101 herdmania m	476	9	2.5	183	2	Q7PLJ7	Q7plj7 fenneropena
404	10	2.8	417	1	HEPS_HUMAN	P05981 homo sapien	c 477	9	2.5	191	2	Q7EYGS	Q7eygs oryza sativ
405	10	2.8	436	1	HEPS_MOUSE	O35453 mus musculus	478	9	2.5	192	2	Q9NB79	Q9nb79 heliothis z
406	10	2.8	462	2	Q6PAG2	Q6pag2 xenopus lae	479	9	2.5	195	2	Q40627	Q40627 oryza sativ
407	10	2.8	463	2	Q6T1T0	Q6t1t0 pseudonaja	480	9	2.5	202	2	Q6XGZ3	Q6xgz3 homo sapien
408	10	2.8	469	2	Q9GMD9	Q9gmd9 ornithorhyn	c 481	9	2.5	203	2	Q6L4Q2	Q6l4q2 oryza sativ
409	10	2.8	474	2	Q8JHC8	Q8jhc8 brachydanio	482	9	2.5	204	2	Q86V17	Q86v17 homo sapien
410	10	2.8	475	1	FA10_CHICK	P25155 gallus galli	c 483	9	2.5	209	2	Q8GRT1	Q8grt1 oryza sativ
411	10	2.8	475	2	Q804W9	Q804w9 fugu rubrip	c 484	9	2.5	209	2	Q9FPF3	Q9fpf3 oryza sativ
412	10	2.8	481	1	FA10_MOUSE	O88947 mus musculus	c 485	9	2.5	213	1	ACH1_LONAC	P23604 lonomia ach
413	10	2.8	482	1	FA10_RAT	Q63207 rattus norv	c 486	9	2.5	213	2	Q83CL2	Q83cl2 coxiella bu
414	10	2.8	488	1	FA10_HUMAN	P00742 homo sapien	487	9	2.5	214	1	ACH2_LONAC	P23605 lonomia ach
415	10	2.8	490	1	FA10_RABIT	O19045 oryctolagus	488	9	2.5	214	2	Q9XYW2	Q9xyw2 schistosoma
416	10	2.8	490	1	TMS2_MOUSE	Q9J1q8 mus musculus	489	9	2.5	220	2	Q8NCW4	Q8ncw4 homo sapien
417	10	2.8	490	2	Q920K3	Q920k3 rattus norv	490	9	2.5	223	2	Q9VBY4	Q9vby4 drosophila
418	10	2.8	490	2	Q6P7D7	Q6p7d7 rattus norv	491	9	2.5	223	2	Q9XY58	Q9xy58 ctenocephal
419	10	2.8	490	2	Q7TN04	P07n04 bos taurus	492	9	2.5	226	1	DDN1_BOVIN	P80219 bos taurus
420	10	2.8	492	1	FA10_BOVIN	P00743 homo sapien	493	9	2.5	229	2	Q7PV13	Q7pv13 anopheles g
421	10	2.8	492	1	TMS2_HUMAN	O15393 homo sapien	494	9	2.5	232	1	ACRL_HUMAN	P58840 homo sapien
422	10	2.8	492	2	Q96T73	Q96t73 homo sapien	495	9	2.5	232	2	Q9TXE6	Q9txe6 bombyx mori
423	10	2.8	503	2	Q8AYE4	Q8aye4 brachydanio	496	9	2.5	234	2	Q6ZLH1	Q6zlh1 oryza sativ
424	10	2.8	504	2	Q6PGW7	Q6pgw7 brachydanio	497	9	2.5	234	2	Q9R048	Q9r048 mus musculus
425	10	2.8	505	2	Q7Q9W3	Q7q9w3 anopheles g	498	9	2.5	235	2	Q6XGZ4	Q6xgz4 homo sapien
c 426	10	2.8	575	2	Q7Q9W3	Q7q9w3 anopheles g	499	9	2.5	235	2	Q7PSC7	Q7psc7 anopheles g
c 427	10	2.8	597	2	Q8LQW9	Q8lqw9 oryza sativ	500	9	2.5	235	2	Q28731	Q28731 oryctolagus
428	10	2.8	702	2	Q96PX1	Q96px1 homo sapien	501	9	2.5	235	2	Q8B4R4	Q8b4r4 bos taurus
429	10	2.8	705	1	C1R_HUMAN	P00736 homo sapien	502	9	2.5	235	2	Q90387	Q90387 cynops pyr
430	10	2.8	706	2	Q8CFG9	Q8cfg9 mus musculus	503	9	2.5	236	2	Q90387	Q90387 cynops pyr
431	10	2.8	707	1	C1R_MOUSE	Q8cg16 mus musculus	504	9	2.5	236	2	Q921H1	Q921h1 mus musculus
432	10	2.8	721	2	Q7ZT69	Q7zt69 lampetra ja	505	9	2.5	237	1	TRYP_ASTFL	P00765 astacus flu
433	10	2.8	722	2	Q6NUF5	Q6nuf5 xenopus lae	506	9	2.5	239	2	Q8T4E3	Q8t4p3 lepeophthei
434	10	2.8	767	2	Q9DGR2	Q9dgr2 xenopus lae	507	9	2.5	239	2	Q8LCU4	Q8lcu4 lepeophthei
435	10	2.8	833	2	Q96442	Q96442 strongyloce	508	9	2.5	241	2	Q9GQ02	Q9gg02 biomphalari
436	10	2.8	974	2	Q9OWD8	Q9owd8 bufo japoni	509	9	2.5	241	2	Q63637	Q63637 rattus norv
c 437	10	2.8	1282	2	Q86A78	Q86a78 dictyosteli	510	9	2.5	243	2	Q7M4I3	Q7m4i3 megabombus
438	9	2.5	1430	2	Q7QJ48	P37358 equus cabal	511	9	2.5	244	2	O6LAW0	Q6lam0 homo sapien
439	9	2.5	73	1	EL2B_HORSE	Q73158 equus cabal	512	9	2.5	245	1	CTRA_BOVIN	P00766 bos taurus
440	9	2.5	86	2	Q8LFO1	Q8lflq1 arabidopsis	513	9	2.5	245	1	CTRB_BOVIN	P00767 bos taurus
441	9	2.5	103	2	Q95T80	Q95t80 drosophila	514	9	2.5	245	1	CTRB_GADMO	P80646 gadus morhu
442	9	2.5	115	2	Q6XGZ0	Q6xgz0 homo sapien	515	9	2.5	245	1	GILX_HELHO	P43685 heloderma h
443	9	2.5	122	2	Q9NIU1	Q9niul drosophila	516	9	2.5	245	1	MCT1_SHEEP	P80931 ovis aries
c 444	9	2.5	124	2	Q84SN4	Q84sn4 oryza sativ	517	9	2.5	245	2	O6DKQ3	Q6dkq3 eisenia foe
445	9	2.5	125	2	Q86V18	Q86v18 homo sapien	518	9	2.5	245	2	Q9BLI8	Q9bli8 lumbricus r
446	9	2.5	139	2	Q95VU4	Q95vu4 homarus ame	519	9	2.5	245	2	Q8DF10	Q8df10 xenopus tro
447	9	2.5	142	2	Q95W34	Q95w34 anthonomus	520	9	2.5	246	1	GRAH_HUMAN	P20718 homo sapien
448	9	2.5	145	2	Q8C1J4	Q8c1j4 mus musculus	521	9	2.5	246	1	MCT1_MERUN	P50340 meriones un
449	9	2.5	146	2	Q8IVY7	Q8ivy7 homo sapien	522	9	2.5	246	1	MCT4_RAT	P97592 rattus norv
450	9	2.5	147	2	Q95W31	Q95w31 anthonomus	523	9	2.5	246	2	Q8I7P0	Q8i7p0 lumbricus b
451	9	2.5	148	2	Q95W23	Q95w23 anthonomus	524	9	2.5	246	2	O6DKQ2	Q6dkq2 eisenia foe
452	9	2.5	148	2	Q9UB93	Q9ub93 helicoverpa	525	9	2.5	246	2	Q7QAM2	Q7qam2 anopheles g
453	9	2.5	149	2	Q25237	Q25237 lucilia cup	526	9	2.5	246	2	Q9BLI7	Q9bli7 lumbricus r
454	9	2.5	150	2	Q66784	Q66784 haematobia	527	9	2.5	246	2	Q6IE10	Q6ie10 rattus norv
455	9	2.5	152	2	Q6XGZ2	Q6xgz2 homo sapien							



528	9	2.5	247	1	GRAB_HUMAN	P10144 h granzyme	601	9	2.5	259	2	Q6AZC2	Q6azc2 brachydanio
529	9	2.5	247	1	GRAB_MOUSE	P04187 mus musculus	602	9	2.5	260	1	MC11_RAT	P09650 rattus norv
530	9	2.5	247	1	MCT2_MERUN	P50341 meriones un	603	9	2.5	260	1	VG38_BPK3	P07876 bacterioph
531	9	2.5	247	1	TRYP_SIMVI	P35048 simulum vi	604	9	2.5	260	2	Q8T4P5	Q8t4p5 lepeophthei
532	9	2.5	247	2	O8N1D2	Q8nid2 homo sapien	605	9	2.5	260	2	Q8T4P6	Q8t4p6 lepeophthei
533	9	2.5	247	2	Q17039	Q17039 anopheles g	606	9	2.5	260	2	Q9U4I6	Q9u4i6 plodia inte
534	9	2.5	247	2	Q6T376	Q6t376 eisenia foe	607	9	2.5	260	2	Q9U4I7	Q9u4i7 plodia inte
535	9	2.5	248	1	GRAD_MOUSE	P11033 mus musculus	608	9	2.5	260	2	Q6P2V9	Q6p2v9 xenopus tro
536	9	2.5	248	1	GRAE_MOUSE	P08884 mus musculus	609	9	2.5	260	2	Q7T229	Q7t229 bothrops ja
537	9	2.5	248	1	GRAF_MOUSE	P08883 mus musculus	610	9	2.5	260	2	Q9W7Q3	Q9w7q3 paralichthy
538	9	2.5	248	1	TRV1_CHICK	Q90627 gallus gall	611	9	2.5	261	1	CATG_MOUSE	P28293 mus musculus
539	9	2.5	248	1	TRV2_CHICK	Q90628 gallus gall	612	9	2.5	261	1	KLK2_HUMAN	P20151 homo sapien
540	9	2.5	248	2	Q8T4P2	Q8t4p2 lepeophthei	613	9	2.5	261	1	KLK3_HUMAN	P07888 homo sapien
541	9	2.5	248	2	Q920S1	Q920s1 mus musculus	614	9	2.5	261	1	KLK3_MACMU	P33619 macaca mula
542	9	2.5	248	2	Q63224	Q63224 rattus norv	615	9	2.5	261	2	Q62598	I622598 plodia inte
543	9	2.5	248	2	Q66105	Q66105 xenopus lae	616	9	2.5	261	2	Q8T4P1	Q8t4p1 lepeophthei
544	9	2.5	249	2	Q6OX62	Q6ox62 lepeophthei	617	9	2.5	261	2	Q6DT45	Q6dt45 macaca fasc
545	9	2.5	249	2	Q91VE3	Q91ve3 m thymopsin	618	9	2.5	261	2	Q6DHD9	Q6dhd9 brachydanio
546	9	2.5	249	2	Q9W7Q1	Q9w7q1 paralichthy	619	9	2.5	262	2	Q8T4P7	Q8t4p7 lepeophthei
547	9	2.5	250	2	Q8T4P4	Q8t4p4 lepeophthei	620	9	2.5	262	2	Q720G5	Q720g5 phlebotomus
548	9	2.5	250	2	Q7PWE3	Q7pwe3 anopheles g	621	9	2.5	262	2	Q721D6	Q721d6 lepeophthei
549	9	2.5	250	2	Q61E07	Q6ie07 rattus norv	622	9	2.5	263	1	CTR2_CANFA	P04813 canis famil
550	9	2.5	250	2	Q8BX01	Q8bx01 mus musculus	623	9	2.5	263	1	CTRA_GADMO	P47796 gadus morhu
551	9	2.5	251	1	MCT3_SHEEP	Q46683 ovis aries	624	9	2.5	263	1	CTRB_HUMAN	P17538 homo sapien
552	9	2.5	251	2	Q7Q9W2	Q7q9w2 anopheles g	625	9	2.5	263	1	CTRB_RAT	P07338 rattus norv
553	9	2.5	251	2	Q9GLN2	Q9gln2 bos taurus	626	9	2.5	263	2	Q6GP11	Q6gpl1 homo sapien
554	9	2.5	251	2	Q9D9G7	Q9d9g7 m mus muscu	627	9	2.5	263	2	Q62562	O62562 penaeus van
555	9	2.5	252	2	Q61388	Q61388 mus musculus	628	9	2.5	263	2	Q721D5	Q721d5 lepeophthei
556	9	2.5	253	1	KLK7_HUMAN	P49862 homo sapien	629	9	2.5	263	2	Q9TV16	Q9tv16 penaeus van
557	9	2.5	253	2	Q8NSN9	Q8nsn9 homo sapien	630	9	2.5	263	2	Q821H6	Q821h6 streptomyc
558	9	2.5	253	2	O18440	O18440 helicoverpa	631	9	2.5	263	2	Q9CR35	Q9cr35 m mus muscu
559	9	2.5	253	2	O18442	O18442 helicoverpa	632	9	2.5	263	2	Q9D8X8	Q9d8x8 mus musculus
560	9	2.5	253	2	Q9NB82	Q9nb82 heliothis z	633	9	2.5	263	2	Q9DC86	Q9dc86 mus musculus
561	9	2.5	253	2	Q9NGY5	Q9ngy5 heliothis v	634	9	2.5	263	2	Q6GNF7	Q6gnf7 xenopus lae
562	9	2.5	254	2	O18434	O18434 helicoverpa	635	9	2.5	263	2	Q6P9S4	Q6p9s4 xenopus lae
563	9	2.5	254	2	O18436	O18436 helicoverpa	636	9	2.5	263	2	Q7SX97	Q7sxs7 brachydanio
564	9	2.5	254	2	O18447	O18447 helicoverpa	637	9	2.5	263	2	Q7SYS4	Q7sys4 xenopus lae
565	9	2.5	254	2	Q76954	Q76954 laccanobia o	638	9	2.5	263	2	Q9FWQ6	Q9fwq6 gadus morhu
566	9	2.5	255	2	O18435	O18435 helicoverpa	639	9	2.5	263	2	Q632K0	Q632k0 xenopus lae
567	9	2.5	255	2	O44332	O44332 manduca sex	640	9	2.5	264	2	O62561	O62561 penaeus van
568	9	2.5	255	2	Q961Y0	Q961y0 galleria me	641	9	2.5	264	2	O81PY7	O81py7 drosophila
569	9	2.5	255	2	Q7PF16	Q7pf16 anopheles g	642	9	2.5	264	2	Q7XSS9	Q7xss9 lepeophthei
570	9	2.5	255	2	Q75H82	Q75h82 oryza sativ	643	9	2.5	264	2	Q8QGF6	Q8qgf6 xenopus lae
571	9	2.5	256	1	TRVX_MANSE	P35045 manduca sex	644	9	2.5	264	2	Q6GPF5	Q6gpy5 xenopus lae
572	9	2.5	256	1	TRVC_MANSE	P35046 manduca sex	645	9	2.5	265	2	Q7QCB3	Q7qcb3 anopheles g
573	9	2.5	256	1	TRVC_MANSE	P35047 manduca sex	646	9	2.5	265	2	O61515	O61515 mus musculus
574	9	2.5	256	1	TRIP_CHOFU	P35042 choristoneu	647	9	2.5	265	2	Q6P326	Q6p326 xenopus tro
575	9	2.5	256	2	O18441	O18441 helicoverpa	648	9	2.5	266	1	ELI_BOVIN	Q28153 bos taurus
576	9	2.5	256	2	Q27540	Q27540 choristoneu	649	9	2.5	266	1	ELI_PIG	P00772 sus scrofa
577	9	2.5	256	2	Q6R561	Q6r561 ostrinia nu	650	9	2.5	266	1	ELI_RAT	P00773 rattus norv
578	9	2.5	257	1	VSPC_TRIGA	O13062 trimeresuru	651	9	2.5	266	2	Q27761	Q27761 penaeus van
579	9	2.5	257	2	Q6LDS3	Q6lds3 homo sapien	652	9	2.5	266	2	O46644	O46644 macaca fasc
580	9	2.5	257	2	Q97099	Q97099 anopheles d	653	9	2.5	266	2	Q91X79	Q91x79 mus musculus
581	9	2.5	257	2	Q8T639	Q8t639 aedes aegypt	654	9	2.5	266	2	Q9D936	Q9d936 mus musculus
582	9	2.5	257	2	Q71QH5	Q71qh5 trimeresuru	655	9	2.5	266	2	Q6AZC0	Q6azc0 brachydanio
583	9	2.5	257	2	Q71QI5	Q71qi5 trimeresuru	656	9	2.5	268	2	O46151	O46151 pacifastacu
584	9	2.5	257	2	Q71QI7	Q71q17 trimeresuru	657	9	2.5	269	2	Q7Q5I5	Q7q5i5 anopheles g
585	9	2.5	257	2	Q71QJ0	Q71qj0 trimeresuru	658	9	2.5	270	2	O96871	O96871 trichinella
586	9	2.5	257	2	Q71QJ1	Q71qj1 trimeresuru	659	9	2.5	270	2	Q819P2	Q8i9p2 aplysina fi
587	9	2.5	257	2	Q71QJ3	Q71qj3 trimeresuru	660	9	2.5	270	2	Q9VRS4	Q9vrs4 drosophila
588	9	2.5	258	1	CTR2_ANOGA	Q17025 anopheles g	661	9	2.5	271	1	S24D_ANOGA	Q17004 anopheles g
589	9	2.5	258	1	EL1_HUMAN	Q9unil1 homo sapien	662	9	2.5	271	2	Q7PIA2	Q7pia2 anopheles g
590	9	2.5	258	2	Q6ISM6	Q6ism6 homo sapien	663	9	2.5	272	2	Q7Q9W5	Q7q9w5 anopheles g
591	9	2.5	258	2	Q9NGY6	Q9ngy6 aedes aegypt	664	9	2.5	272	2	Q9VRS3	Q9vrs3 drosophila
592	9	2.5	258	2	Q867B0	Q867b0 canis famil	665	9	2.5	273	2	Q7JYN3	Q7jyn3 drosophila
593	9	2.5	258	2	Q9GME1	Q9gme1 ornithorhyn	666	9	2.5	274	2	Q924N9	Q924n9 mus musculus
594	9	2.5	258	2	O80270	O80270 bacterioph	667	9	2.5	275	1	TRYA_HUMAN	P15157 homo sapien
595	9	2.5	258	2	Q8W678	Q8w678 entërobacte	668	9	2.5	275	2	Q8ZWL5	Q8zwl5 pyrobaculum
596	9	2.5	258	2	Q71QI2	Q71qi2 trimeresuru	669	9	2.5	277	1	KLKD_HUMAN	Q9ukr3 homo sapien
597	9	2.5	259	1	CTR1_ANOGA	Q27289 anopheles g	670	9	2.5	277	2	Q6GS52	Q6gs52 oikopleura
598	9	2.5	259	2	Q69EZ7	Q69ez7 homo sapien	671	9	2.5	277	2	Q8SQ44	Q8sq44 sus scrofa
599	9	2.5	259	2	O97097	O97097 anopheles a	672	9	2.5	277	2	Q6WQB3	Q6mqb3 bdellovibri
600	9	2.5	259	2	Q7PF17	Q7pf17 anopheles g	673	9	2.5	277	2	Q7T0T6	Q7t0t6 xenopus lae

c 674	9	2.5	278	2	Q8W374	Q8W374 oryza sativ	c 747	9	2.5	368	2	Q6MFG1	Q6mfg1 neurospora
c 675	9	2.5	278	2	Q7XD89	Q7xd89 oryza sativ	748	9	2.5	369	2	Q6AXZ6	Q6axz6 rattus norv
c 676	9	2.5	279	2	Q99MS4	Q99ms4 mus musculus	749	9	2.5	370	2	Q7PVB6	Q7pvb6 anopheles g
677	9	2.5	280	2	Q64ID5	Q64id5 anthonomus	750	9	2.5	371	2	Q8MRV3	Q8mrv3 drosophila
678	9	2.5	281	2	Q67BC3	Q67bc3 homo sapien	751	9	2.5	371	2	Q8MS52	Q8ms52 drosophila
679	9	2.5	281	2	Q46137	Q46137 lumbricus r	752	9	2.5	372	2	Q9W2C8	Q9w2c8 drosophila
680	9	2.5	282	2	Q25395	Q25395 lumbricus r	753	9	2.5	374	2	Q7QCS5	Q7qcs5 anopheles g
681	9	2.5	282	2	Q7PT16	Q7pt16 anopheles g	754	9	2.5	374	2	Q8QYD5	Q8qyd5 mus musculus
682	9	2.5	282	2	Q8WJD1	Q8wjd1 canis famil	755	9	2.5	377	2	P79343	P79343 bos taurus
683	9	2.5	282	2	Q8DA13	Q8da13 mus musculus	756	9	2.5	377	1	RUI7_MOUSE	Rui7 mouse
684	9	2.5	283	2	Q25394	Q25394 lumbricus r	757	9	2.5	378	2	Q90WP0	Q90wp0 trachemys s
685	9	2.5	283	2	Q8ITU7	Q8itu7 lumbricus r	758	9	2.5	380	2	Q9YIK5	Q9yik5 anopheles g
686	9	2.5	283	2	Q9SV22	Q9sv22 lumbricus b	759	9	2.5	383	1	NTRB_RHILP	Ntrb rhizobium l
687	9	2.5	284	2	O18437	O18437 helicoverpa	c 760	9	2.5	383	2	Q6YX93	Q6yvx9 oryza sativ
688	9	2.5	284	2	Q8MLV8	Q8mlv8 drosophila	761	9	2.5	384	2	Q9YX63	Q9yx63 ctenocephal
689	9	2.5	288	2	Q8T9T5	Q8t9t5 aedes aegyp	762	9	2.5	385	2	Q90WS2	Q90ws2 elaphe sp.
690	9	2.5	289	2	Q9NH09	Q9nh09 agrotis ips	763	9	2.5	386	2	Q8DEX8	Q8dex8 vibrio vuln
691	9	2.5	290	1	PR27_HUMAN	Q9bqr3 homo sapien	764	9	2.5	387	2	Q9XY57	Q9xy57 ctenocephal
692	9	2.5	293	2	Q23528	Q23528 caenorhabdi	765	9	2.5	388	2	Q966V2	Q966v2 halocynthia
693	9	2.5	293	2	Q95UB0	Q95ub0 creontiaades	766	9	2.5	392	2	Q9VMZ3	Q9vmz3 drosophila
694	9	2.5	293	2	Q7Q8F9	Q7q8f9 anopheles g	767	9	2.5	393	2	Q9W3D7	Q9w3d7 drosophila
695	9	2.5	295	2	Q69EZ8	Q69ez8 homo sapien	768	9	2.5	398	2	Q8MS90	Q8ms90 drosophila
c 696	9	2.5	295	2	Q9LSZ8	Q9lsz8 arabidopsis	769	9	2.5	400	2	Q7MNH3	Q7mnh3 vibrio vuln
697	9	2.5	296	2	Q9VDV1	Q9vdv1 drosophila	770	9	2.5	402	2	Q7QB73	Q7qb73 anopheles g
698	9	2.5	298	2	Q8T4N4	Q8t4n4 rhipicephal	771	9	2.5	405	2	Q7QAC0	Q7qac0 anopheles g
699	9	2.5	305	2	Q8WRL2	Q8wrl2 drosophila	772	9	2.5	408	2	Q9VM19	Q9vm19 drosophila
700	9	2.5	307	2	Q6ZND6	Q6znd6 homo sapien	773	9	2.5	413	2	Q6K712	Q6k712 oryza sativ
701	9	2.5	308	1	RAD_HUMAN	P55042 homo sapien	774	9	2.5	415	1	ACRO_PIG	P08001 sus scrofa
702	9	2.5	308	2	Q92788	Q92788 homo sapien	775	9	2.5	415	2	Q90I55	Q90i55 sus sp. pre
703	9	2.5	309	2	Q6DHH4	Q6dhh4 brachydanio	776	9	2.5	416	1	HEPS_RAT	Q05511 rattus norv
704	9	2.5	312	2	Q6MPY2	Q6mpy2 bdellovibri	777	9	2.5	418	2	Q7Q529	Q7q529 anopheles g
705	9	2.5	313	2	Q9BMQ7	Q9bmq7 bombyx mori	c 778	9	2.5	420	2	Q9LFX8	Q9lfx8 arabidopsis
c 706	9	2.5	313	2	Q9LC81	Q9lc81 arthrobacte	779	9	2.5	421	1	ACRO_HUMAN	P10323 homo sapien
707	9	2.5	318	2	Q7RTY9	Q7rty9 homo sapien	780	9	2.5	421	2	Q6ICK2	Q6ick2 homo sapien
708	9	2.5	318	2	Q9XY10	Q9xy10 bombyx mori	781	9	2.5	421	2	Q6Q491	Q6q491 cavia porce
709	9	2.5	320	2	Q7QAM3	Q7qam3 anopheles g	782	9	2.5	422	2	Q8WVC1	Q8wvc1 homo sapien
710	9	2.5	321	2	Q6IE60	Q6ie60 rattus norv	c 783	9	2.5	422	2	Q803K3	Q803k3 brachydanio
711	9	2.5	321	2	Q80Y38	Q80y38 mus musculus	784	9	2.5	428	2	Q8WPM7	Q8wpm7 oikopleura
712	9	2.5	322	2	Q920S2	Q920s2 mus musculus	c 785	9	2.5	429	2	Q655Y0	Q655y0 oryza sativ
713	9	2.5	323	2	Q76920	Q76920 drosophila	786	9	2.5	430	2	Q6RUJ3	Q6ruj3 trichinella
c 714	9	2.5	324	1	TEST_MOUSE	Q9jhj7 mus musculus	787	9	2.5	431	1	ACRO_RABIT	P48038 oryctolagus
c 715	9	2.5	324	2	Q6XT10	Q6xt10 oryza sativ	c 788	9	2.5	431	2	Q7RZH7	Q7rzh7 neurospora
716	9	2.5	326	2	Q7RTY6	Q7rty6 homo sapien	789	9	2.5	432	2	Q6UX37	Q6ux37 homo sapien
717	9	2.5	326	2	Q9D9M0	Q9d9m0 mus musculus	c 790	9	2.5	432	2	Q9SV57	Q9sv57 arabidopsis
718	9	2.5	326	2	Q7Z280	Q7z280 brachydanio	791	9	2.5	433	2	Q8T3A2	Q8t3a2 ciona intes
719	9	2.5	327	2	Q7Q530	Q7q530 anopheles g	792	9	2.5	433	2	Q9QWF2	Q9qwf2 rattus sp.
720	9	2.5	327	2	Q7QAM4	Q7qam4 anopheles g	793	9	2.5	434	2	Q9V7S7	Q9v7s7 drosophila
721	9	2.5	328	2	Q6BEA2	Q6bea2 rattus norv	794	9	2.5	435	1	TMS4_MOUSE	Q8vca5 mus musculus
722	9	2.5	328	2	Q80Z40	Q80z40 rattus norv	795	9	2.5	435	2	Q9NFI2	Q9nfy2 anopheles g
723	9	2.5	328	2	Q8BJR6	Q8bjr6 mus musculus	796	9	2.5	436	1	ACRO_MOUSE	P23578 mus musculus
724	9	2.5	329	2	Q9GL10	Q9gl10 ovis aries	797	9	2.5	437	1	ACRO_RAT	P29293 rattus norv
725	9	2.5	331	2	Q8RIAG	Q8ria6 mus musculus	798	9	2.5	437	1	TMS4_HUMAN	Q9nrs4 homo sapien
726	9	2.5	331	2	Q8OX17	Q8ox17 mus musculus	799	9	2.5	445	2	Q7Q956	Q7q956 anopheles g
727	9	2.5	333	2	Q7S019	Q7s019 neurospora	800	9	2.5	452	2	Q7Y195	Q7y195 oryza sativ
728	9	2.5	336	2	Q80YD8	Q80yd8 mus musculus	801	9	2.5	456	1	FXD1_MOUSE	Q61345 mus musculus
729	9	2.5	337	2	Q9ET75	Q9et75 rattus norv	802	9	2.5	456	2	Q7QC30	Q7qc30 anopheles g
730	9	2.5	340	2	Q8CK32	Q8ck32 streptomyce	803	9	2.5	459	2	Q67ME8	Q67me8 symbiobacte
731	9	2.5	346	2	Q7P243	Q7p243 anopheles g	804	9	2.5	460	2	Q9VFZ6	Q9vzf6 drosophila
732	9	2.5	346	2	Q8FR92	Q8fr92 xanthomonas	805	9	2.5	461	2	Q8T4N2	Q8t4n2 rhipicephal
733	9	2.5	346	2	Q826Z4	Q826z4 streptomyce	806	9	2.5	464	2	Q6L7Z5	Q6l7z5 haemaphysal
734	9	2.5	348	2	Q8GWS5	Q8gws5 homo sapien	807	9	2.5	465	2	Q9BJL7	Q9bjl7 trichinella
c 735	9	2.5	350	2	Q7S4S4	Q7s4s4 neurospora	c 808	9	2.5	466	2	Q6AVV5	Q6avv5 oryza sativ
736	9	2.5	351	2	Q7QCUB	Q7qcu8 anopheles g	809	9	2.5	468	2	Q9U0G3	Q9u0g3 pacifastacu
737	9	2.5	352	2	Q6UWB4	Q6uwb4 homo sapien	810	9	2.5	472	2	Q7Q182	Q7q182 anopheles g
c 738	9	2.5	356	2	Q8MZC1	Q8mzcl drosophila	c 811	9	2.5	473	2	Q94D54	Q94d54 oryza sativ
c 739	9	2.5	356	2	Q9VH98	Q9vh98 drosophila	812	9	2.5	485	2	Q7PKK0	Q7pkk0 anopheles g
740	9	2.5	358	2	Q45029	Q45029 drosophila	813	9	2.5	486	2	Q7PX74	Q7px74 anopheles g
741	9	2.5	362	2	Q9W453	Q9w453 drosophila	814	9	2.5	499	2	Q9SH37	Q9sh37 arabidopsis
742	9	2.5	365	2	Q7QGL1	Q7qgl1 anopheles g	815	9	2.5	501	2	Q7QCV0	Q7qcv0 anopheles g
c 743	9	2.5	365	2	Q6VYG5	Q6vyg5 oryza sativ	816	9	2.5	505	2	Q966V4	Q966v4 halocynthia
744	9	2.5	366	2	Q70170	Q70170 mus musculus	817	9	2.5	506	2	Q7PR64	Q7pr64 anopheles g
c 745	9	2.5	367	1	MURG_XYLFA	Q9pf81 xyliella fas	c 818	9	2.5	506	2	Q9SXS5	Q9sxs5 antirrhinum
746	9	2.5	367	2	O70169	Q70169 mus musculus	819	9	2.5	511	2	Q9VZH5	Q9vzh5 drosophila

820	9	2.5	515	2	Q7PW75	Q7pw75 anopheles g	893	9	2.5	1019	1	ENTK_HUMAN	P98073 homo sapien
821	9	2.5	516	2	Q8BZQ8	Q8bzq8 mus musculus	894	9	2.5	1034	1	ENTK_PIG	P98074 sus scrofa
822	9	2.5	517	2	Q8K0D2	Q8k0d2 mus musculus	895	9	2.5	1035	1	ENTK_BOVIN	P98072 bos taurus
823	9	2.5	528	2	Q03536	Q03536 plasmid rp4	896	9	2.5	1042	1	CORI_HUMAN	Q629q5 homo sapien
824	9	2.5	535	2	Q7XKK4	Q7xkk4 oryza sativ	897	9	2.5	1058	1	Q62G2C	Q62g2c oryza sativ
825	9	2.5	536	2	Q7PX72	Q7px72 anopheles g	898	9	2.5	1069	1	ENTK_MOUSE	P97435 mus musculus
826	9	2.5	538	2	Q7XJY2	Q7xjy2 oryza sativ	899	9	2.5	1079	1	Q7RWQ1	Q7rwq1 neurospora
827	9	2.5	540	2	Q7NL21	Q7nl21 gloeobacter	900	9	2.5	1099	2	Q8WZM9	Q8wz49 neurospora
828	9	2.5	544	2	Q46171	Q46171 nephila cla	901	9	2.5	1099	2	Q7XM40	Q7xm40 oryza sativ
829	9	2.5	546	2	Q8SXG6	Q8sxg6 drosophila	902	9	2.5	1108	2	Q7XVP2	Q7xvp2 oryza sativ
830	9	2.5	553	2	Q6P7I9	Q6p7i9 xenopus lae	903	9	2.5	1111	2	Q80YN4	Q80yn4 rattus norv
831	9	2.5	558	2	Q6L711	Q6l711 rattus norv	904	9	2.5	1113	1	CORI_MOUSE	Q92319 mus musculus
832	9	2.5	560	2	Q14520	Q14520 homo sapien	905	9	2.5	1186	2	Q7T401	Q7t401 cercopithec
833	9	2.5	564	2	Q7RTZ1	Q7rtz1 homo sapien	906	9	2.5	1190	2	Q7S867	Q7s867 neurospora
834	9	2.5	564	2	Q9V369	Q9v369 drosophila	907	9	2.5	1234	2	Q7P1Q7	Q7p1q7 anopheles g
835	9	2.5	567	2	Q7S7E5	Q7s7e5 ashbya goss	908	9	2.5	1322	2	Q7PNN7	Q7pnr7 anopheles g
836	9	2.5	573	2	Q9V516	Q9v516 drosophila	909	9	2.5	1322	2	Q9NAT0	Q9nat0 anopheles g
837	9	2.5	574	2	Q7RW61	Q7rw61 neurospora	910	9	2.5	1322	2	Q9NJS5	Q9nj55 anopheles g
838	9	2.5	583	1	CPAI_HUMAN	P05156 homo sapien	911	9	2.5	1374	2	Q9VSU0	Q9vau0 drosophila
839	9	2.5	600	2	Q7ZTR2	Q7ztr2 xenopus lae	912	9	2.5	1449	2	Q9ULI2	Q9ul12 drosophila
840	9	2.5	603	1	CPAI_MOUSE	Q61129 mus musculus	913	9	2.5	1450	2	Q8IQB8	Q8iqb8 drosophila
841	9	2.5	604	1	CPAI_RAT	Q9wuw3 rattus norv	914	9	2.5	1462	2	Q9ULI3	Q9ul13 drosophila
842	9	2.5	607	2	Q6DFJ5	Q6dfj5 xenopus lae	915	9	2.5	1673	2	Q6C2Q2	Q6c2q2 yarrowia li
843	9	2.5	609	2	Q7M761	Q7m761 mus musculus	916	9	2.5	1787	2	Q9M4X9	Q9m4x9 chlamydomon
844	9	2.5	613	2	Q03711	Q03711 xenopus lae	917	9	2.5	2382	2	Q9B1I9	Q9b1i9 drosophila
845	9	2.5	615	2	Q6GNK4	Q6gnk4 xenopus lae	918	9	2.5	2409	2	Q960G6	Q960g6 drosophila
846	9	2.5	617	1	THRB_RAT	P18292 rattus norv	919	9	2.5	2481	2	Q9WJD3	Q9wj33 venezuelan
847	9	2.5	617	2	Q8JIS1	Q8jis1 triakis scy	920	9	2.5	2786	2	Q9VSU2	Q9vau2 drosophila
848	9	2.5	618	1	THRB_MOUSE	P19221 mus musculus	921	9	2.5	3848	2	Q76737	Q76737 dictyosteli
849	9	2.5	622	1	THRB_HUMAN	P00734 homo sapien	922	9	2.5	4218	2	Q7W7M5	Q7w7m5 bordetella
850	9	2.5	622	2	Q7Z7P3	Q7z7p3 homo sapien	923	9	2.5	4218	2	Q7WL14	Q7wl14 bordetella
851	9	2.5	625	1	THRB_BOVIN	P00735 bos taurus	924	9	2.5	30	2	Q6R7S1	Q6r7s1 pectinaria
852	9	2.5	629	2	Q6AZS7	Q6azs7 xenopus lae	925	8	2.2	36	2	Q74P28	Q74p28 bacillus ce
853	9	2.5	635	2	Q6ZG11	Q6zgi1 oryza sativ	926	8	2.2	39	2	Q9BR93	Q9br93 homo sapien
854	9	2.5	638	1	KAL_HUMAN	P03952 homo sapien	927	8	2.2	40	2	P78341	P78341 homo sapien
855	9	2.5	638	1	KAL_MOUSE	P26262 mus musculus	928	8	2.2	40	2	P78342	P78342 homo sapien
856	9	2.5	638	1	KAL_RAT	P14272 rattus norv	929	8	2.2	41	2	Q9INZ5	Q9inz5 rattus norv
857	9	2.5	638	2	Q8R0P5	Q8rop5 mus musculus	930	8	2.2	44	2	Q9S562	Q9s562 rattus norv
858	9	2.5	667	2	Q9BJM1	Q9bjm1 trichinella	931	8	2.2	46	2	Q6C1W4	Q6c1w4 yarrowia li
859	9	2.5	669	2	Q7PWE1	Q7pwe1 anopheles g	932	8	2.2	59	2	Q76768	Q76768 hydra atten
860	9	2.5	674	2	Q7QPM7	Q7qpm7 anopheles g	933	8	2.2	61	2	O08549	O08549 mus musculus
861	9	2.5	676	2	Q6PEI2	Q6pei2 brachydanio	934	8	2.2	62	2	O81F78	O81f78 trypanosoma
862	9	2.5	683	2	Q8MRH5	Q8mrh5 drosophila	935	8	2.2	63	2	Q943G6	Q943g6 oryza sativ
863	9	2.5	685	2	Q9DGC0	Q9dgc0 cyprinus ca	936	8	2.2	65	2	Q654A1	Q654a1 oryza sativ
864	9	2.5	685	2	Q9DGC1	Q9dgc1 cyprinus ca	937	8	2.2	65	2	Q8QTC1	Q8qtc1 white spot
865	9	2.5	686	2	Q9DGC2	Q9dgc2 cyprinus ca	938	8	2.2	65	2	O8VAQ0	O8vaq0 white spot
866	9	2.5	719	2	Q6DJ90	Q6dj90 xenopus tro	939	8	2.2	73	2	Q7XIW2	Q7xiw2 oryza sativ
867	9	2.5	733	1	HIC1_HUMAN	Q14526 homo sapien	940	8	2.2	73	2	Q6MK36	Q6mk36 bdellovibri
868	9	2.5	733	2	Q9VTX9	Q9vtx9 drosophila	941	8	2.2	75	2	Q8P4K1	Q8pak1 xanthomonas
869	9	2.5	741	2	Q75IA9	Q75ia9 oryza sativ	942	8	2.2	75	2	Q7LZF5	Q7lzf5 crotalus at
870	9	2.5	742	2	Q8LN55	Q8ln55 oryza sativ	943	8	2.2	77	2	Q7SG98	Q7sg98 neurospora
871	9	2.5	761	1	NETR_MOUSE	O08762 mus musculus	944	8	2.2	78	2	Q6ETC1	Q6etc1 oryza sativ
872	9	2.5	761	2	Q99JC8	Q99jc8 rattus norv	945	8	2.2	82	1	ANPA_PSEAM	P04002 pseudopleur
873	9	2.5	777	2	Q8CAN9	Q8can9 mus musculus	946	8	2.2	82	2	Q9TH51	Q9th51 pseudopleur
874	9	2.5	778	2	Q9V519	Q9v519 drosophila	947	8	2.2	83	2	Q9VNV8	Q9vnr8 drosophila
875	9	2.5	786	1	STUB_DROME	Q05319 drosophila	948	8	2.2	83	2	Q6VSH9	Q6vsh9 oryza sativ
876	9	2.5	787	2	Q9VEY6	Q9vey6 drosophila	949	8	2.2	84	2	Q64827	Q64827 human adeno
877	9	2.5	807	2	Q8LQY2	Q8lqy2 oryza sativ	950	8	2.2	85	2	Q67WG5	Q67wg5 oryza sativ
878	9	2.5	804	2	Q8IQ14	Q8iq14 drosophila	951	8	2.2	89	2	Q7WXL8	Q7wxl8 alcaligenes
879	9	2.5	806	1	FLMN_MACEU	O18783 macropus eu	952	8	2.2	90	2	Q9AX99	Q9ax99 oryza sativ
880	9	2.5	829	2	Q9VQV7	Q9vqv7 drosophila	953	8	2.2	90	2	Q99PM8	Q99pm8 mus musculus
881	9	2.5	850	2	Q6K322	Q6k322 oryza sativ	954	8	2.2	94	2	Q7M0B4	Q7m0b4 mus musculus
882	9	2.5	855	1	ST14_HUMAN	Q9y5y6 homo sapien	955	8	2.2	95	2	Q6IKF9	Q6ikf9 drosophila
883	9	2.5	855	1	ST14_MOUSE	P56677 mus musculus	956	8	2.2	96	2	Q9VKS2	Q9vks2 drosophila
884	9	2.5	855	2	Q9QUJ7	Q9qji7 rattus norv	957	8	2.2	96	2	Q8W327	Q8w327 oryza sativ
885	9	2.5	860	2	Q944E2	Q944e2 oryza sativ	958	8	2.2	96	2	Q6DT49	Q6dt49 arabidopsis
886	9	2.5	860	2	Q6ZF89	Q6zf89 oryza sativ	959	8	2.2	97	2	Q6YZN4	Q6yzn4 oryza sativ
887	9	2.5	868	2	Q9YIV3	Q9yiv3 polyandroca	960	8	2.2	98	2	Q8DHT1	Q8dht1 synecococc
888	9	2.5	875	1	NETR_HUMAN	P56730 homo sapien	961	8	2.2	100	2	Q7PFS0	Q7pfs0 anopheles g
889	9	2.5	889	1	HCN2_HUMAN	Q9ul51 homo sapien	962	8	2.2	100	2	Q9SMS7	Q9sm57 arabidopsis
890	9	2.5	907	2	Q9C946	Q9c946 arabidopsis	963	8	2.2	100	2	Q99N26	Q99n26 mus musculus
891	9	2.5	965	2	Q6K4N9	Q6k4n9 oryza sativ	964	8	2.2	101	1	RLI2_METTH	P05394 methanobact
892	9	2.5	985	2	Q8RUA3	Q8rua3 oryza sativ	965	8	2.2	101	2	Q8W0I4	Q8w0i4 oryza sativ

c 966	8	2.2	101	2	Q7MI58	Q7ni58 gloeobacter	1039	8	2.2	128	2	Q8MV32	Q8mv32 plasmodium
c 967	8	2.2	102	2	Q9YA21	Q9ya21 aeropyrum p	c1040	8	2.2	128	2	Q9N2V3	Q9n2v3 caenorhabdi
c 968	8	2.2	103	2	Q84JC7	Q84jc7 oryza sativ	c1041	8	2.2	128	2	Q69QF1	Q69qf1 oryza sativ
c 969	8	2.2	103	2	Q9M045	Q9m045 arabidopsis	c1042	8	2.2	128	2	Q82HG1	Q82hg1 streptomyce
c 970	8	2.2	103	2	Q7I2H9	Q7i2h9 xenopus lae	1043	8	2.2	129	2	Q8MV17	Q8mv17 plasmodium
c 971	8	2.2	104	2	Q8PY50	Q8py50 methanosarc	1044	8	2.2	129	2	Q8MV28	Q8mv28 plasmodium
c 972	8	2.2	104	2	Q8TI79	Q8ti79 methanosarc	1045	8	2.2	129	2	Q9XVD8	Q9xvd8 caenorhabdi
c 973	8	2.2	104	2	Q8L565	Q8l565 oryza sativ	c1046	8	2.2	129	2	P7I958	P7i958 mycobacteri
c 974	8	2.2	106	1	YNL6 CAEEL	P45898 caenorhabdi	c1047	8	2.2	129	2	Q7TY62	Q7ty62 mycobacteri
c 975	8	2.2	107	2	Q75MS7	P45898 caenorhabdi	1048	8	2.2	129	2	Q7TY62	Q7ty62 mus musculu
c 976	8	2.2	107	2	Q53321	Q53321 synechococc	1049	8	2.2	130	2	Q8CV19	Q8cv19 plasmodium
c 977	8	2.2	107	2	Q55345	Q55345 synechococc	1050	8	2.2	130	2	Q8MV24	Q8mv24 plasmodium
c 978	8	2.2	107	2	Q79F26	Q79f26 synechococc	c1051	8	2.2	130	2	Q6ZAX7	Q6zax7 oryza sativ
c 979	8	2.2	108	2	Q6H7A9	Q6h7a9 oryza sativ	1052	8	2.2	130	2	Q8VUP9	Q8vup9 pseudomonas
c 980	8	2.2	109	2	Q70T17	Q70t17 homo sapien	1053	8	2.2	131	2	Q6KE13	Q6ke13 plasmodium
c 981	8	2.2	110	2	Q7SGE3	Q7sge3 neurospora	c1054	8	2.2	131	2	Q8LHK9	Q8lhk9 oryza sativ
c 982	8	2.2	110	2	Q6Q1W4	Q6qiw4 plasmodium	1055	8	2.2	131	2	Q6Z4T2	Q6z4t2 oryza sativ
c 983	8	2.2	110	2	Q6Q1X9	Q6qix9 caenorhabdi	c1056	8	2.2	131	2	Q74DN0	Q74dn0 geobacter s
c 984	8	2.2	110	2	Q6YSX4	Q6yex4 oryza sativ	1057	8	2.2	132	2	Q8MV22	Q8mv22 plasmodium
c 985	8	2.2	110	2	Q79F40	Q79f40 anabaena va	c1058	8	2.2	133	2	Q9HRQ0	Q9hrq0 halobacteri
c 986	8	2.2	110	2	Q44555	Q44555 anabaena sp	1059	8	2.2	133	2	Q7SEW5	Q7sew5 neurospora
c 987	8	2.2	111	2	Q945U9	Q945u9 caenorhabdi	1060	8	2.2	133	2	Q8MV29	Q8mv29 plasmodium
c 988	8	2.2	111	2	Q6F446	Q6f446 plutella xy	1061	8	2.2	134	1	H3_EUPEU	P32103 eulotes eu
c 989	8	2.2	111	2	Q9LHL1	Q9lhl1 arabidopsis	c1062	8	2.2	134	2	Q6NE0	Q6neo0 homo sapien
c 990	8	2.2	111	2	Q7V6R5	Q7v6r5 prochloroco	1063	8	2.2	134	2	Q6KE19	Q6ke19 plasmodium
c 991	8	2.2	112	2	Q6S5E4	Q6s5e4 plasmodium	1064	8	2.2	134	2	Q6KE21	Q6ke21 plasmodium
c 992	8	2.2	112	2	Q7KTD2	Q7ktd2 drosophila	1065	8	2.2	134	2	Q6KE22	Q6ke22 plasmodium
c 993	8	2.2	112	2	Q7PP05	Q7pp05 anopheles g	c1066	8	2.2	134	2	Q658A5	Q658a5 oryza sativ
c 994	8	2.2	112	2	Q6Z9K7	Q6z9k7 oryza sativ	1067	8	2.2	134	2	Q97679	Q97679 human immun
c 995	8	2.2	113	2	Q6TXJ2	Q6txj2 rattus norv	1068	8	2.2	135	2	Q6K8H6	Q6k8h6 oryza sativ
c 996	8	2.2	114	2	Q6S5E5	Q6s5e5 plasmodium	1069	8	2.2	135	2	Q9CAH6	Q9cah6 arabidopsis
c 997	8	2.2	114	2	Q9F6W7	Q9f6w7 chloroflexu	c1070	8	2.2	135	2	P95012	P95012 mycobacteri
c 998	8	2.2	115	2	Q69S24	Q69s24 oryza sativ	c1071	8	2.2	135	2	Q92PI0	Q92pi0 rhizobium m
c 999	8	2.2	115	2	Q9CUK2	Q9cuk2 mus musculu	c1072	8	2.2	135	2	Q7TYC5	Q7tyc5 mycobacteri
1000	8	2.2	115	2	Q90YW9	Q90yw9 ictalurus p	c1073	8	2.2	136	2	Q84444	Q84444 caenorhabdi
c1001	8	2.2	116	2	Q6MN64	Q6mn64 dellovibri	1074	8	2.2	136	2	Q8MV21	Q8mv21 plasmodium
1002	8	2.2	117	2	Q9PUF3	Q9puf3 bothrops ja	1075	8	2.2	136	2	Q6KE18	Q6ke18 plasmodium
1003	8	2.2	118	2	Q6S5C9	Q6s5c9 plasmodium	1076	8	2.2	136	2	Q6KE20	Q6ke20 plasmodium
1004	8	2.2	118	2	Q6YU92	Q6yu92 oryza sativ	c1077	8	2.2	136	2	Q6RY61	Q6ry61 nicotiana s
1005	8	2.2	119	2	Q6S5D3	Q6s5d3 plasmodium	1078	8	2.2	136	2	Q67QC7	Q67qc7 symbiobacte
1006	8	2.2	119	2	Q6S5D5	Q6s5d5 plasmodium	c1079	8	2.2	137	2	Q7QFA5	Q7qfa5 anopheles g
1007	8	2.2	119	2	Q6S5E9	Q6s5e9 plasmodium	c1080	8	2.2	137	2	Q67V41	Q67v41 oryza sativ
1008	8	2.2	120	2	Q6JIA6	Q6jia6 homo sapien	1081	8	2.2	138	2	Q8MV26	Q8mv26 plasmodium
1009	8	2.2	120	2	Q6S5D6	Q6s5d6 plasmodium	1082	8	2.2	138	2	Q8MV31	Q8mv31 plasmodium
1010	8	2.2	120	2	Q6S5D7	Q6s5d7 plasmodium	1083	8	2.2	138	2	Q8H5N8	Q8h5n8 oryza sativ
1011	8	2.2	120	2	Q6S5E2	Q6s5e2 plasmodium	1084	8	2.2	139	2	Q6KE15	Q6ke15 plasmodium
1012	8	2.2	120	2	Q6S5F6	Q6s5f6 plasmodium	1085	8	2.2	140	2	Q6MUW0	Q6muw0 neurospora
1013	8	2.2	120	2	Q9J0I8	Q9j0i8 human immun	1086	8	2.2	140	2	Q6KE12	Q6ke12 plasmodium
1014	8	2.2	120	2	Q9J0I9	Q9j0i9 human immun	c1087	8	2.2	140	2	Q67VX0	Q67vx0 oryza sativ
1015	8	2.2	121	2	Q6ZQN3	Q6zqn3 homo sapien	1088	8	2.2	141	2	Q6ZR98	Q6zr98 homo sapien
1016	8	2.2	121	2	Q6S5F0	Q6s5f0 plasmodium	c1089	8	2.2	142	1	GRP1_SORBI	Q99069 sorghum bic
1017	8	2.2	121	2	Q9GQP2	Q9gqp2 plasmodium	1090	8	2.2	142	2	Q00917	Q00917 plasmodium
1018	8	2.2	122	2	Q6S5D4	Q6s5d4 plasmodium	1091	8	2.2	142	2	Q00921	Q00921 plasmodium
1019	8	2.2	122	2	Q9DBH5	Q9dbh5 mus musculu	1092	8	2.2	142	2	Q8HYM3	Q8hym3 felis silve
1020	8	2.2	123	2	Q6QIW3	Q6qiw3 plasmodium	1093	8	2.2	143	2	Q6DUN8	Q6dun8 plasmodium
1021	8	2.2	123	2	Q6S5C8	Q6s5c8 plasmodium	c1094	8	2.2	143	2	Q7PJB3	Q7pjb3 anopheles g
c1022	8	2.2	124	2	Q86SJO	Q86sj0 homo sapien	c1095	8	2.2	143	2	Q9FRF4	Q9frf4 oryza sativ
1023	8	2.2	124	2	Q6S5E3	Q6s5e3 plasmodium	c1096	8	2.2	144	2	Q6KXX9	Q6kxx9 picophilus
c1024	8	2.2	124	2	Q7SG67	Q7sg67 oryza sativ	1097	8	2.2	144	2	Q6DUQ8	Q6duq8 plasmodium
c1025	8	2.2	125	2	Q9LWC8	Q9lwc8 oryza sativ	1098	8	2.2	144	2	Q6DUR7	Q6dur7 plasmodium
1026	8	2.2	125	2	Q804G0	Q804g0 spherooides	1099	8	2.2	144	2	Q6DUR8	Q6dur8 plasmodium
1027	8	2.2	126	2	Q11299	Q11299 molluscum c	1100	8	2.2	144	2	Q6DUT3	Q6dut3 plasmodium
1028	8	2.2	127	2	Q8N0F0	Q8n0f0 plasmodium	1101	8	2.2	144	2	Q6DUU0	Q6duu0 plasmodium
1029	8	2.2	127	2	Q9U4R9	Q9u4r9 plasmodium	1102	8	2.2	144	2	Q6KE14	Q6ke14 plasmodium
1030	8	2.2	127	2	Q9U4S0	Q9u4s0 plasmodium	c1103	8	2.2	144	2	Q7PJA8	Q7pja8 anopheles g
1031	8	2.2	127	2	Q9U4S2	Q9u4s2 plasmodium	c1104	8	2.2	144	2	Q6K839	Q6k839 oryza sativ
1032	8	2.2	127	2	Q9U4S3	Q9u4s3 plasmodium	1105	8	2.2	144	2	Q6LCS2	Q6lcs2 human papil
1033	8	2.2	127	2	Q9U4S4	Q9u4s4 plasmodium	1106	8	2.2	144	2	Q76TT6	Q76tt6 human papil
1034	8	2.2	127	2	Q9U4S5	Q9u4s5 plasmodium	1107	8	2.2	145	2	Q6DUQ1	Q6duq1 plasmodium
1035	8	2.2	127	2	Q9U4S6	Q9u4s6 plasmodium	1108	8	2.2	145	2	Q6DUT4	Q6dut4 plasmodium
1036	8	2.2	127	2	Q9U4T1	Q9u4t1 plasmodium	1109	8	2.2	145	2	Q6DXW1	Q6dxw1 plasmodium
c1037	8	2.2	127	2	Q84R67	Q84r67 oryza sativ	1110	8	2.2	145	2	Q9U4S8	Q9u4s8 plasmodium
1038	8	2.2	128	2	Q8MV23	Q8mv23 plasmodium	1111	8	2.2	145	2	Q9U4S9	Q9u4s9 plasmodium

1112	8	2.2	145	2	Q9U4T0	Q9U4T0 plasmodium	1185	8	2.2	152	2	Q86PN9	Q86pn9 plasmodium
1113	8	2.2	145	2	Q9U4T2	Q9U4T2 plasmodium	1186	8	2.2	152	2	Q86PP0	Q86pp0 plasmodium
1114	8	2.2	145	2	Q9U4T4	Q9U4T4 plasmodium	1187	8	2.2	152	2	Q86PP2	Q86pp2 plasmodium
1115	8	2.2	145	2	Q9U4T6	Q9U4T6 plasmodium	1188	8	2.2	152	2	Q86PP3	Q86pp3 plasmodium
1116	8	2.2	145	2	Q9U4T8	Q9U4T8 plasmodium	1189	8	2.2	152	2	Q9XZC4	Q9xzc4 helicoverpa
1117	8	2.2	145	2	Q9B8Z0	Q9B8Z0 plasmodium	ci190	8	2.2	152	2	Q6Z4G2	Q6z4g2 oryza sativ
1118	8	2.2	146	2	P93486	P93486 pisum sativ	ci191	8	2.2	152	2	Q92T22	Q92tz2 rhizobium m
1119	8	2.2	146	2	Q71KW7	Q71KW7 rattus norv	1192	8	2.2	153	2	Q6DUN3	Q6dun3 plasmodium
1120	8	2.2	147	2	Q81837	Q81837 plasmodium	1193	8	2.2	153	2	Q6DUN7	Q6dun7 plasmodium
1121	8	2.2	147	2	Q81I19	Q81I19 drosophila	1194	8	2.2	153	2	Q6DUP5	Q6dup5 plasmodium
1122	8	2.2	147	2	Q86PM9	Q86pm9 plasmodium	1195	8	2.2	153	2	Q6DUQ4	Q6duq4 plasmodium
1123	8	2.2	147	2	Q8HZD0	Q8hzd0 saquinus oe	1196	8	2.2	153	2	Q6DUQ7	Q6duq7 plasmodium
1124	8	2.2	147	2	Q9D2F0	Q9D2F0 mus musculu	1197	8	2.2	153	2	Q6DUQ9	Q6duq9 plasmodium
1125	8	2.2	148	2	Q6DUM9	Q6dum9 plasmodium	1198	8	2.2	153	2	Q6DUS2	Q6dus2 plasmodium
1126	8	2.2	148	2	Q6DUN5	Q6dun5 plasmodium	1199	8	2.2	153	2	Q6DUS7	Q6dus7 plasmodium
1127	8	2.2	148	2	Q6DUQ2	Q6duq2 plasmodium	1200	8	2.2	153	2	Q6DUS8	Q6dus8 plasmodium
1128	8	2.2	148	2	Q6DUT5	Q6dut5 plasmodium	1201	8	2.2	153	2	Q6DUS9	Q6dus9 plasmodium
1129	8	2.2	148	2	Q6DXU3	Q6dxu3 plasmodium	1202	8	2.2	153	2	Q6DUU7	Q6duu7 plasmodium
1130	8	2.2	148	2	Q6DXU4	Q6dxu4 plasmodium	1203	8	2.2	153	2	Q6H339	Q6h339 plasmodium
1131	8	2.2	148	2	Q6DXU5	Q6dxu5 plasmodium	1204	8	2.2	153	2	Q6H341	Q6h341 plasmodium
1132	8	2.2	148	2	Q6DXU6	Q6dxu6 plasmodium	1205	8	2.2	153	2	Q86PP1	Q86pp1 plasmodium
1133	8	2.2	148	2	Q6DXU7	Q6dxu7 plasmodium	1206	8	2.2	153	2	Q8X064	Q8x064 mus musculu
1134	8	2.2	148	2	Q6DXU8	Q6dxu8 plasmodium	ci207	8	2.2	153	2	Q7SSW5	Q7ssw5 chimpanzee
1135	8	2.2	148	2	Q6DXU9	Q6dxu9 plasmodium	1208	8	2.2	154	1	YQSB CAEEL	Q09254 caenorhabdi
1136	8	2.2	148	2	Q6DXV0	Q6dxv0 plasmodium	ci209	8	2.2	154	2	Q9C7J5	Q9c7j5 arabidopsis
1137	8	2.2	148	2	Q6DXV1	Q6dxv1 plasmodium	ci210	8	2.2	154	2	Q9CAL7	Q9cal7 arabidopsis
1138	8	2.2	148	2	Q6DXV2	Q6dxv2 plasmodium	1211	8	2.2	155	2	Q9HSE3	Q9hse3 halobacteri
1139	8	2.2	148	2	Q6DXV3	Q6dxv3 plasmodium	ci212	8	2.2	155	2	Q9GND8	Q9gnd8 drosophila
1140	8	2.2	148	2	Q6DXV4	Q6dxv4 plasmodium	ci213	8	2.2	155	2	Q9GP74	Q9gp74 drosophila
1141	8	2.2	148	2	Q6DXV5	Q6dxv5 plasmodium	ci214	8	2.2	155	2	Q9LD76	Q9ld76 oryza sativ
1142	8	2.2	148	2	Q6DXV6	Q6dxv6 plasmodium	ci215	8	2.2	155	2	Q9XEL4	Q9xel4 picea glauc
1143	8	2.2	148	2	Q6DXV7	Q6dxv7 plasmodium	ci216	8	2.2	155	2	Q64876	Q64876 simian aden
1144	8	2.2	148	2	Q6DXV9	Q6dxv9 plasmodium	ci217	8	2.2	156	2	Q9GNB7	Q9gnb7 drosophila
1145	8	2.2	148	2	Q6DXW0	Q6dxw0 plasmodium	ci218	8	2.2	156	2	Q9GP73	Q9gp73 drosophila
1146	8	2.2	148	2	Q6DXW5	Q6dxw5 plasmodium	1219	8	2.2	156	2	Q6K9N7	Q6k9n7 oryza sativ
1147	8	2.2	148	2	Q86PM7	Q86pm7 plasmodium	ci220	8	2.2	156	2	Q8GYL1	Q8gyll arabidopsis
1148	8	2.2	148	2	Q86PN0	Q86pn0 plasmodium	ci221	8	2.2	157	1	GRPA_MAIZE	P10979 zea mays (m
1149	8	2.2	148	2	Q86PN2	Q86pn2 plasmodium	1222	8	2.2	157	2	Q8ZU13	Q8zul3 pyrobaculum
ci1150	8	2.2	148	2	Q6V5D5	Q6v5d5 olimarabido	1223	8	2.2	157	2	Q8I826	Q8i826 plasmodium
1151	8	2.2	149	2	Q6DUS0	Q6dus0 plasmodium	1224	8	2.2	157	2	Q8I829	Q8i829 plasmodium
1152	8	2.2	149	2	Q6DUT7	Q6dut7 plasmodium	1225	8	2.2	157	2	Q8I832	Q8i832 plasmodium
1153	8	2.2	149	2	Q6H342	Q6h342 plasmodium	1226	8	2.2	157	2	Q8I834	Q8i834 plasmodium
1154	8	2.2	149	2	Q86PN5	Q86pn5 plasmodium	1227	8	2.2	157	2	Q8I836	Q8i836 plasmodium
1155	8	2.2	149	2	Q7VUS8	Q7vus8 bordetella	1228	8	2.2	157	2	Q8I839	Q8i839 plasmodium
1156	8	2.2	149	2	Q7W3W0	Q7w3w0 bordetella	1229	8	2.2	157	2	Q6DUR4	Q6dur4 plasmodium
1157	8	2.2	149	2	Q7WFP90	Q7wfp90 bordetella	1230	8	2.2	157	2	Q6DUR6	Q6dur6 plasmodium
1158	8	2.2	149	2	Q35327	Q35327 mus musculu	ci231	8	2.2	157	2	Q9GP77	Q9gp77 drosophila
1159	8	2.2	149	2	Q6DUT8	Q6dut8 hypophthalm	1232	8	2.2	157	2	Q6B338	Q6b338 symphysodon
1160	8	2.2	150	2	Q7Q8X3	Q7q8x3 anopheles g	ci233	8	2.2	157	2	Q6IRD1	Q6ird1 xenopus lae
1161	8	2.2	151	2	Q26170	Q26170 plasmodium	ci234	8	2.2	158	2	Q95UW4	Q95uw4 drosophila
ci1162	8	2.2	151	2	Q96617	Q96617 caenorhabdi	ci235	8	2.2	158	2	Q9VYD8	Q9vyd8 drosophila
1163	8	2.2	151	2	Q7YUC6	Q7yuc6 caenorhabdi	ci236	8	2.2	159	2	Q95UW1	Q95uw1 drosophila
1164	8	2.2	151	2	Q86PN4	Q86pn4 plasmodium	ci237	8	2.2	159	2	Q95UW5	Q95uw5 drosophila
1165	8	2.2	151	2	Q9GSN3	Q9gsn3 chrysomya b	1238	8	2.2	159	2	Q77669	Q77669 canis fami
1166	8	2.2	151	2	Q9TVL1	Q9tvll plasmodium	1239	8	2.2	159	2	Q8HZD1	Q8hzd1 macaca sp.
1167	8	2.2	152	2	Q8I842	Q8i842 plasmodium	1240	8	2.2	159	2	Q8HZD2	Q8hzd2 pongo pygma
1168	8	2.2	152	2	Q8I843	Q8i843 plasmodium	1241	8	2.2	159	2	Q8HZD3	Q8hzd3 gorilla gor
1169	8	2.2	152	2	Q8I845	Q8i845 plasmodium	1242	8	2.2	159	2	Q8HZD4	Q8hzd4 pan troglod
1170	8	2.2	152	2	Q8I846	Q8i846 plasmodium	1243	8	2.2	159	2	Q80YV0	Q80yv0 mus musculu
1171	8	2.2	152	2	Q8I847	Q8i847 plasmodium	1244	8	2.2	160	2	Q9UB96	Q9ub96 aedes aegyp
1172	8	2.2	152	2	Q8I848	Q8i848 plasmodium	ci245	8	2.2	160	2	Q9SWA8	Q9swa8 glycine max
1173	8	2.2	152	2	Q8I849	Q8i849 plasmodium	ci246	8	2.2	160	2	Q98ML5	Q98ml5 rhizobium l
1174	8	2.2	152	2	Q8I850	Q8i850 plasmodium	ci247	8	2.2	161	2	Q95UW6	Q95uw6 drosophila
1175	8	2.2	152	2	Q8I851	Q8i851 plasmodium	ci248	8	2.2	161	2	Q95UX3	Q95ux3 drosophila
1176	8	2.2	152	2	Q8I852	Q8i852 plasmodium	ci249	8	2.2	161	2	Q7XT20	Q7xt20 oryza sativ
1177	8	2.2	152	2	Q8I853	Q8i853 plasmodium	1250	8	2.2	161	2	Q9M0N0	Q9m0n0 arabidopsis
1178	8	2.2	152	2	Q95XT6	Q95xt6 caenorhabdi	1251	8	2.2	162	2	Q95PD1	Q95pd1 anopheles d
1179	8	2.2	152	2	Q7YUC3	Q7yuc3 plasmodium	ci252	8	2.2	162	2	Q95UX5	Q95ux5 drosophila
1180	8	2.2	152	2	Q7YUC4	Q7yuc4 plasmodium	ci253	8	2.2	162	2	Q8LPB2	Q8lpb2 physcomitre
1181	8	2.2	152	2	Q86PM5	Q86pm5 plasmodium	ci254	8	2.2	163	2	Q95NU6	Q95nu6 drosophila
1182	8	2.2	152	2	Q86PN1	Q86pn1 plasmodium	ci255	8	2.2	163	2	Q95UW7	Q95uw7 drosophila
1183	8	2.2	152	2	Q86PN7	Q86pn7 plasmodium	ci256	8	2.2	163	2	Q95UW9	Q95uw9 drosophila
1184	8	2.2	152	2	Q86PN8	Q86pn8 plasmodium	ci257	8	2.2	163	2	Q95UX4	Q95ux4 drosophila

c1258	8	2.2	163	2	Q61JR6	Q61jr6 drosophila	1331	8	2.2	182	2	Q86KAI	Q86kal dictyosteli
c1259	8	2.2	163	2	Q7XKC7	Q7xkc7 oryza sativ	1332	8	2.2	182	2	Q9GSL7	Q9gsl7 chrysomya b
c1260	8	2.2	163	2	O52169	O52169 salmoneilla	1333	8	2.2	182	2	Q9U560	Q9u560 plasmodium
c1261	8	2.2	164	2	Q95NP2	Q95np2 drosophila	1334	8	2.2	182	2	Q98324	Q98324 molluscum c
c1262	8	2.2	164	2	Q95UW3	Q95uw3 drosophila	c1335	8	2.2	183	1	GRP2_ORYSA	P29834 oryza sativ
c1263	8	2.2	164	2	Q9AXJ1	Q9axj1 oryza sativ	c1336	8	2.2	183	2	Q9UQL5	Q9uql5 homo sapien
c1264	8	2.2	165	1	GRP1_ORYSA	P25074 oryza sativ	c1337	8	2.2	183	2	Q9GV53	Q9gv53 drosophila
c1265	8	2.2	165	2	Q86Y58	Q86y58 homo sapien	c1338	8	2.2	183	2	Q9GV54	Q9gv54 drosophila
c1266	8	2.2	165	2	Q81TU9	Q81tu9 plasmodium	c1339	8	2.2	183	2	Q9GV55	Q9gv55 drosophila
c1267	8	2.2	165	2	Q95NR6	Q95nr6 drosophila	c1340	8	2.2	183	2	Q9VRI3	Q9vri3 drosophila
c1268	8	2.2	165	2	Q95QI9	Q95qi9 caenorhabdi	c1341	8	2.2	183	2	Q8K392	Q8k392 mus musculu
c1269	8	2.2	165	2	Q95UW2	Q95uw2 drosophila	c1342	8	2.2	184	2	Q6AVE8	Q6ave8 oryza sativ
c1270	8	2.2	165	2	Q95UX1	Q95ux1 drosophila	1343	8	2.2	185	1	NO20_SOYBN	P09860 glycine max
c1271	8	2.2	165	2	Q95UX2	Q95ux2 drosophila	1344	8	2.2	185	2	Q6X139	Q6x139 drosophila
c1272	8	2.2	165	2	Q9GP44	Q9gp44 drosophila	c1345	8	2.2	185	2	Q7XDV1	Q7xdv1 oryza sativ
c1273	8	2.2	165	2	Q8VX74	Q8vx74 ricinus com	c1346	8	2.2	186	2	Q6YV98	Q6yv98 oryza sativ
c1274	8	2.2	166	1	YK3_CABEL	P46553 caenorhabdi	c1347	8	2.2	186	2	Q6Z7V0	Q6z7v0 oryza sativ
c1275	8	2.2	166	2	Q95UX0	Q95ux0 drosophila	1348	8	2.2	187	2	Q9NB78	Q9nb78 heliothis z
c1276	8	2.2	167	2	Q71RF1	Q71rf1 homo sapien	1349	8	2.2	187	2	Q6Z9Z2	Q6z9z2 oryza sativ
c1277	8	2.2	167	2	Q7Z7F0	Q7z7f0 homo sapien	c1350	8	2.2	188	2	Q23709	Q23709 drosophila
c1278	8	2.2	167	2	Q6URK9	Q6urk9 bothrops ja	1351	8	2.2	188	2	Q6X144	Q6x144 drosophila
c1279	8	2.2	168	1	GRP2_SORBI	Q99070 sorghum bic	c1352	8	2.2	188	2	Q9V9U0	Q9v9u0 drosophila
c1280	8	2.2	168	2	Q6ZP5	Q6zpa5 homo sapien	1353	8	2.2	188	2	Q654Y5	Q654y5 oryza sativ
c1281	8	2.2	168	2	Q95UW8	Q95uw8 drosophila	c1354	8	2.2	188	2	Q6PH14	Q6ph14 brachydanio
c1282	8	2.2	169	1	GR10_BRANA	Q05966 brassica na	c1355	8	2.2	189	2	Q6IGP7	Q6igp7 drosophila
c1283	8	2.2	169	2	Q35315	Q35315 mus musculu	c1356	8	2.2	189	2	Q6XIT4	Q6xit4 drosophila
c1284	8	2.2	170	2	Q8L4U3	Q8l4u3 oryza sativ	c1357	8	2.2	189	2	Q7XDS8	Q7xds8 oryza sativ
c1285	8	2.2	170	2	Q9FUD5	Q9fud5 sorghum bic	c1358	8	2.2	190	2	Q8W5C7	Q8w5c7 oryza sativ
c1286	8	2.2	171	2	Q7SCS1	Q7scs1 neurospora	1359	8	2.2	190	2	Q91792	Q91792 xenopus lae
c1287	8	2.2	171	2	Q6X140	Q6x140 drosophila	1360	8	2.2	190	2	Q7ZYN3	Q7zyn3 xenopus lae
c1288	8	2.2	171	2	O04339	O04339 arabidopsis	1361	8	2.2	191	1	MLE1_CHICK	P02604 gallus gall
c1289	8	2.2	171	2	Q6Z2V7	Q6z2v7 oryza sativ	1362	8	2.2	191	1	MLE1_RABIT	P02602 cryctolagus
c1290	8	2.2	172	2	Q6T776	Q6t776 homo sapien	1363	8	2.2	192	2	Q9NB88	Q9nb88 agrotis ips
c1291	8	2.2	172	2	Q6DUP0	Q6dup0 plasmodium	1364	8	2.2	192	2	Q8S248	Q8s248 oryza sativ
c1292	8	2.2	173	2	Q7SGU3	Q7sgu3 neurospora	1365	8	2.2	192	2	Q6V5B6	Q6v5b6 arabidopsis
c1293	8	2.2	173	2	Q6X130	Q6x130 drosophila	c1366	8	2.2	192	2	Q7XDS2	Q7xds2 oryza sativ
c1294	8	2.2	174	2	Q6H6P9	Q6h6p9 oryza sativ	c1367	8	2.2	192	2	Q60399	Q60399 cricetus cr
c1295	8	2.2	174	2	Q6LCS0	Q6lcs0 human papil	1368	8	2.2	192	2	Q6W5H1	Q6w5h1 meleagris g
c1296	8	2.2	176	2	Q15098	Q15098 homo sapien	c1369	8	2.2	193	2	Q7YWQ8	Q7ywq8 caenorhabdi
c1297	8	2.2	176	2	Q7XM25	Q7xm25 oryza sativ	1370	8	2.2	193	2	Q7FLJ4	Q7flj4 oryza sativ
c1298	8	2.2	177	2	Q9GN47	Q9gn47 drosophila	1371	8	2.2	193	2	Q91Z58	Q91z58 mus musculu
c1299	8	2.2	177	2	Q9GN45	Q9gna5 drosophila	c1372	8	2.2	194	2	Q6T9T7	Q6t9t7 oryza sativ
c1300	8	2.2	177	2	Q9GV56	Q9gv56 drosophila	1373	8	2.2	195	1	MLR_LUMTE	P80164 lumbricus t
c1301	8	2.2	177	2	Q9GV57	Q9gv57 drosophila	1374	8	2.2	195	1	N20A_SOYBN	Q43460 glycine max
c1302	8	2.2	177	2	Q9GV60	Q9gv60 drosophila	1375	8	2.2	195	2	Q07277	Q07277 homo sapien
c1303	8	2.2	177	2	Q9GV61	Q9gv61 drosophila	c1376	8	2.2	195	2	Q9V3T8	Q9v3t8 drosophila
c1304	8	2.2	177	2	Q9GV63	Q9gv63 drosophila	1377	8	2.2	195	2	Q6N0B5	Q6n0b5 magnetospir
c1305	8	2.2	177	2	Q9GV64	Q9gv64 drosophila	1378	8	2.2	196	2	Q45044	Q45044 helicoverpa
c1306	8	2.2	177	2	Q9GV66	Q9gv66 drosophila	c1379	8	2.2	196	2	Q8LQD5	Q8lqd5 oryza sativ
c1307	8	2.2	177	2	Q9GV67	Q9gv67 drosophila	c1380	8	2.2	196	2	Q6Z2H5	Q6z2h5 oryza sativ
c1308	8	2.2	177	2	Q9GV68	Q9gv68 drosophila	c1381	8	2.2	197	1	PTL2_HUMAN	Q9h106 homo sapien
c1309	8	2.2	177	2	Q8GVR5	Q8gvr5 oryza sativ	c1382	8	2.2	197	2	Q6ZC83	Q6zc83 oryza sativ
c1310	8	2.2	178	2	Q9UR55	Q9ur55 klyveromyc	c1383	8	2.2	197	2	Q700C4	Q700c4 arabidopsis
c1311	8	2.2	178	2	Q61606	Q61606 drosophila	c1384	8	2.2	197	2	Q84UR8	Q84ur8 oryza sativ
c1312	8	2.2	178	2	Q948J2	Q948j2 oryza sativ	1385	8	2.2	197	2	Q7WNB1	Q7wnb1 bordetella
c1313	8	2.2	178	2	Q7XEV5	Q7xev5 oryza sativ	1386	8	2.2	198	2	Q83ZC4	Q83zc4 borrelia tu
c1314	8	2.2	178	2	Q93594	Q93594 dicentrarch	1387	8	2.2	198	2	Q83ZC5	Q83zc5 borrelia tu
c1315	8	2.2	180	2	Q96A30	Q96a30 homo sapien	1388	8	2.2	198	2	Q7UWG2	Q7uwg2 rhodopirell
c1316	8	2.2	180	2	Q6T775	Q6t775 homo sapien	c1389	8	2.2	199	2	Q6L4P7	Q6l4p7 oryza sativ
c1317	8	2.2	180	2	Q7QG97	Q7qg97 anopheles g	1390	8	2.2	199	2	Q84NQ7	Q84nq7 oryza sativ
c1318	8	2.2	180	2	Q7QKU0	Q7qku0 anopheles g	c1391	8	2.2	200	2	Q8RZ55	Q8rz55 oryza sativ
c1319	8	2.2	181	2	Q8P518	Q8ps18 methanosarc	c1392	8	2.2	201	2	Q7PHE9	Q7phe9 anopheles g
c1320	8	2.2	181	2	Q9GND5	Q9gnd5 drosophila	c1393	8	2.2	201	2	P93539	P93539 silene prat
c1321	8	2.2	181	2	Q9GSM5	Q9gsm5 chrysomya b	1394	8	2.2	201	2	Q6YWL5	Q6ywl5 oryza sativ
c1322	8	2.2	181	2	Q9GSM1	Q9gsm1 chrysomya b	c1395	8	2.2	201	2	Q8BJV3	Q8bjv3 mus musculu
c1323	8	2.2	181	2	Q9GV58	Q9gv58 drosophila	c1396	8	2.2	202	2	Q7XUX3	Q7xux3 oryza sativ
c1324	8	2.2	181	2	Q9GV59	Q9gv59 drosophila	c1397	8	2.2	202	2	Q9AXB4	Q9axb4 oryza sativ
c1325	8	2.2	181	2	Q9GV62	Q9gv62 drosophila	1398	8	2.2	203	2	Q96BZ3	Q96bz3 homo sapien
c1326	8	2.2	181	2	Q9GV65	Q9gv65 drosophila	1399	8	2.2	203	2	Q7YYP5	Q7yyp5 cryptospori
c1327	8	2.2	181	2	Q6H494	Q6h494 oryza sativ	c1400	8	2.2	203	2	Q41188	Q41188 arabidopsis
c1328	8	2.2	181	2	Q84NL1	Q84nl1 oryza sativ	c1401	8	2.2	205	2	Q9VY29	Q9vy29 drosophila
c1329	8	2.2	182	1	YN03_CABEL	Q03607 caenorhabdi	c1402	8	2.2	205	2	Q8SBA2	Q8sba2 oryza sativ
1330	8	2.2	182	2	Q6PLJ5	Q6plj5 neocairidina	1403	8	2.2	205	2	Q6ZB66	Q6zb66 oryza sativ

c1404	8	2.2	205	2	Q75QN9	Q75qn9 tritium ae	1477	8	2.2	227	2	Q6XI22	Q6xi22 drosophila
c1405	8	2.2	205	2	Q7XC68	Q7xc68 oryza sativ	c1478	8	2.2	227	2	Q84ZC1	Q84zcl oryza sativ
1406	8	2.2	205	2	Q7XSA7	Q7xsa7 oryza sativ	1479	8	2.2	227	2	O06556	O06556 mycobacteri
1407	8	2.2	206	2	Q6GIW8	Q6giw8 drosophila	1480	8	2.2	227	2	O7U0I4	O7u0i4 mycobacteri
c1408	8	2.2	207	1	EGG2 SCHJA	P19469 schistosoma	1481	8	2.2	228	2	O9XY49	O9xy49 ctenocephal
1409	8	2.2	207	1	SCX MOUSE	Q64124 mus musculus	1482	8	2.2	229	1	TRYP_SQUAC	P00764 squalus aca
c1410	8	2.2	207	2	Q03797	Q03797 schistosoma	1483	8	2.2	229	2	O7PKJ8	O7pkj8 anopheles g
c1411	8	2.2	207	2	Q8S765	Q8s765 oryza sativ	c1484	8	2.2	229	2	O7QFX3	O7qfx3 anopheles g
c1412	8	2.2	207	2	Q6YW94	Q6yw94 oryza sativ	c1485	8	2.2	229	2	O8LPA7	O8lpa7 tritium ae
c1413	8	2.2	207	2	Q92220	Q92220 rhizobium m	c1486	8	2.2	229	2	O6AUN6	O6aun6 oryza sativ
1414	8	2.2	207	2	Q6P6L3	Q6p6l3 mus musculus	1487	8	2.2	229	2	O6AVV7	O6avv7 oryza sativ
1415	8	2.2	208	2	Q9H7I8	Q9h7i8 homo sapien	c1488	8	2.2	229	2	O64IWO	O64iwo xenopus lae
c1416	8	2.2	208	2	Q6F3C6	Q6f3c6 oryza sativ	c1489	8	2.2	230	2	Q9FLS1	Q9fls1 arabidopsis
1417	8	2.2	208	2	Q6Z1Y5	Q6z1y5 oryza sativ	1490	8	2.2	230	2	O6XND4	O6xnd4 rhodococcus
1418	8	2.2	209	2	Q8N1J9	Q8n1j9 homo sapien	1491	8	2.2	230	2	O6N1P8	O6n1p8 rhodopseudo
1419	8	2.2	209	2	Q7VVU4	Q7vvu4 bordetella	c1492	8	2.2	231	1	NOA1 MOUSE	O9cy66 mus musculu
1420	8	2.2	209	2	Q7W9D4	Q7w9d4 bordetella	1493	8	2.2	231	1	TRY2_SALSA	P35032 salmo salar
1421	8	2.2	209	2	Q7W9C9	Q7whc9 bordetella	1494	8	2.2	231	1	TRYP_PIG	P00761 sus scrofa
1422	8	2.2	210	2	Q9NHC9	Q9nxc9 homo sapien	c1495	8	2.2	231	2	Q7SQN8	O7sgn8 tritium ae
1423	8	2.2	211	2	Q6HO16	Q6ho16 fremyella d	c1496	8	2.2	231	2	O8H555	O8h555 oryza sativ
c1424	8	2.2	212	1	EGG1 SCHJA	P19470 schistosoma	1497	8	2.2	232	1	VSP1_BOTJA	P81824 bothriops ja
c1425	8	2.2	212	2	Q7F5N7	Q7f5n7 oryza sativ	1498	8	2.2	232	1	VSPA_BOTJA	P81661 bothriops ja
1426	8	2.2	212	2	O6MJR4	O6mjr4 bdellovibri	1499	8	2.2	232	2	O94508	O94508 dermatophag
c1427	8	2.2	213	2	O8FNV1	O8fnv1 corynebacte	1500	8	2.2	232	2	O9XY45	O9xy45 ctenocephal
c1428	8	2.2	214	1	GRF2_NICSY	P27484 nicotiana s							
c1429	8	2.2	214	2	O49280	O49280 arabidopsis							
1430	8	2.2	214	2	Q73GW8	Q73gw8 wolbachia p							
1431	8	2.2	215	2	O8MPJ2	O8mpj2 plasmodium							
c1432	8	2.2	215	2	O67UN2	O67un2 oryza sativ							
1433	8	2.2	215	2	O89UY6	O89uy6 bradyrhizob							
1434	8	2.2	216	1	CTR2_VESOR	P00768 vespa orien							
1435	8	2.2	216	1	VSPB_LACMU	P84036 lachesis mu							
1436	8	2.2	216	2	O8MPJ3	O8mpj3 plasmodium							
1437	8	2.2	216	2	O8MPJ4	O8mpj4 plasmodium							
1438	8	2.2	216	2	O8MPJ6	O8mpj6 plasmodium							
1439	8	2.2	216	2	O8MPJ7	O8mpj7 plasmodium							
c1440	8	2.2	216	2	O8L524	O8l524 oryza sativ							
1441	8	2.2	216	2	O94DVO	O94dvo oryza sativ							
c1442	8	2.2	216	2	O75KH8	O75kh8 oryza sativ							
c1443	8	2.2	216	2	O7XU81	O7xu81 oryza sativ							
1444	8	2.2	216	2	O7O6M4	O7o6m4 pseudomonas							
c1445	8	2.2	217	1	NOA1 HUMAN	O9ny12 homo sapien							
1446	8	2.2	218	1	CTR2_VESCR	P00769 vespa crabr							
c1447	8	2.2	218	2	O6ZS46	O6zs46 homo sapien							
1448	8	2.2	218	2	O8MPI7	O8mpi7 plasmodium							
c1449	8	2.2	218	2	O6Z1I4	O6z1i4 oryza sativ							
1450	8	2.2	219	2	O8MPJ8	O8mpj8 plasmodium							
1451	8	2.2	219	2	O7FJ75	O7fj75 anopheles g							
c1452	8	2.2	219	2	O75LD8	O75ld8 oryza sativ							
1453	8	2.2	219	2	O9M3G8	O9m3g8 arabidopsis							
c1454	8	2.2	219	2	Q66A81	Q66a81 yersinia ps							
c1455	8	2.2	219	2	O8ZE52	O8ze52 yersinia pe							
1456	8	2.2	219	2	O9I036	O9i036 gadus morhu							
c1457	8	2.2	220	2	O7FJ13	O7fj13 anopheles g							
1458	8	2.2	220	2	O8RZV1	O8rzv1 oryza sativ							
1459	8	2.2	220	2	O43631	O43631 phaseolus v							
1460	8	2.2	220	2	O75LR6	O75lr6 oryza sativ							
c1461	8	2.2	221	2	O65514	O65514 arabidopsis							
c1462	8	2.2	222	1	OS28_PLAGA	O05439 plasmodium							
1463	8	2.2	222	2	O7S1G2	O7s1g2 solenopsis							
1464	8	2.2	222	2	O8AV11	O8av11 oncorhynch							
c1465	8	2.2	223	2	O7BY56	O7ey56 oryza sativ							
c1466	8	2.2	224	2	O8W0N9	O8w0n9 oryza sativ							
c1467	8	2.2	224	2	O9ZS09	O9zs09 arabidopsis							
1468	8	2.2	225	2	O8L7T1	O8l7t1 arabidopsis							
1469	8	2.2	225	2	O6DL00	O6dl00 oryza sativ							
c1470	8	2.2	225	2	O75HQ2	O75hq2 oryza sativ							
1471	8	2.2	225	2	O9LTJ1	O9ltj1 arabidopsis							
c1472	8	2.2	226	2	O948H7	O948h7 oryza sativ							
c1473	8	2.2	226	2	O7XEU0	O7xeu0 oryza sativ							
c1474	8	2.2	226	2	O6AYAI	O6ayal rattus norv							
1475	8	2.2	227	1	TRYP_SACER	P24664 saccharopol							
1476	8	2.2	227	2	O81XI4	O81xi4 homo sapien							

## ALIGNMENTS

## RESULT 1

## KLKC\_HUMAN

ID KLKC\_HUMAN STANDARD; PRT; 248 AA.

AC Q9UKR0; Q9UKR1;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)  
 DE (KLK-L5) (UNQ669/PRO1303).  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=20118156; PubMed=10652563;  
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
 RT "Identification of novel human kallikrein-like genes on chromosome  
 RT 19q13.3-q13.4.";  
 RL Anticancer Res. 19:2843-2852(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;  
 RT "Cloning of new alternatively spliced forms of the kallikrein-like  
 RT gene 5 (KLK-L5).";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepker B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,







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DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Alignment Scores:
Pred. No.: 1,49e-20 Length: 234
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q9CV76 (1-234)

QY 700 GATGCTGCGAGGTGATTCTGGGGCCCCCTGGTGTGGGGAGTCTTCAAGTCTG 759
Db 180 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeu 199
QY 760 GTGTCTCTGGGGGTGTGTGGGGCCCTGTGGACAA 792
Db 200 ValSerTyrGlySerValGlyProCysGlyGln 210

RESULT 4
Q7ZT70
ID Q7ZT70 PRELIMINARY; PRT; 681 AA.
AC Q7ZT70;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannose-binding lectin associated serine protease-1.
GN Name=MASP-1;
OS Lampetia japonica (Japanese lamprey) (Entosphenus japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=94989;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
RA Matsushita M., Fujita T.;
RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1
RT and MASP-3 involved in the lectin complement pathway traced back to
RT the invertebrate, amphioxus."
RL J. Immunol. 170:4701-4707(2003).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB08265; BAC75884.1; -.
DR HSSP; Q9JJS8; INT0.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006956; P:complement activation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Peptidase_S1.
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DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR011361; Pept_S1_Comp_Act.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001155; C1r_C1s_MASP; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00034; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.
SQ SEQUENCE 681 AA; 75277 MW; 27386FA117C1D437 CRC64;

Alignment Scores:
Pred. No.: 0.000434 Length: 681
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.92% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q7ZT70 (1-681)

QY 694 GGGCAGGATGCTGCCAGGTGATTCTGGGGCCCCCTGGTG 735
Db 622 GlyGlnAspAlaCysGlnGlyAspSerGlyGlyProLeuVal 635

RESULT 5
Q924U6
ID Q924U6 PRELIMINARY; PRT; 200 AA.
AC Q924U6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine protease-like 1.
GN Name=1700036D21rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsui H., Takahashi T.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB047758; BAB63919.1; -.
DR HSSP; P00750; 1RTF.
DR MEROPS; S01.106; -.
DR MGI; MGI:1920586; 1700036D21rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
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Alignment Scores:  
Pred. No.: 0.00463 Length: 200  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q924U6 (1-200)

QY 700 GATGCTGCACGGGTGATTCTGGGGCCCCCTGGTGTGT 738  
Db 128 AspaAcySGInGlyAspSerGlyGlyProLeuValCys 140

RESULT 6  
QFHW3 ID Q6FWH3 PRELIMINARY; PRT; 228 AA.  
AC Q6FWH3;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE DF protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., Labaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; CR536575; CAG38812.1; -  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Protease; Serine protease.  
SQ SEQUENCE 228 AA; 24423 MW; B1B9EA3B73E802C5 CRC64;

Alignment Scores:  
Pred. No.: 0.00457 Length: 228  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q6FWH3 (1-228)

QY 712 GGTGATTCGGGGCCCCCTGGTGTGGGGAGTCCTT 750  
Db 181 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 193

RESULT 7  
Q8N4E0 ID Q8N4E0 PRELIMINARY; PRT; 235 AA.  
AC Q8N4E0;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE DF protein (Fragment).  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; BC034529; AAH34529.1; -  
DR HSP; P00746; 1BIO.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Protease; Serine protease.  
FT NON TER 1  
SQ SEQUENCE 235 AA; 25110 MW; 9DEF67A48D5913F6 CRC64;

Alignment Scores:  
Pred. No.: 0.00455 Length: 235  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q8N4E0 (1-235)

QY 712 GGTGATTCGGGGCCCCCTGGTGTGGGGAGTCCTT 750  
Db 188 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 200

RESULT 8  
Q80VS4 ID Q80VS4 PRELIMINARY; PRT; 242 AA.  
AC Q80VS4;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Kkl14 protein (Fragment).  
GN Name=Kkl14;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
CC !- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; BC044756; AAH44756.1; --  
DR HSSP; P00760; 1EZX.  
DR MEROPS; S01.029; --  
DR MGD; MG1:2447564; Kkl14.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:001254; Peptidase S1.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR009003; Peptidase S1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS0240; TRYPsin DOM; 1.  
DR PROSITE; PS00134; TRYPsin HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPsin\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
FT NON\_TER 1  
SQ SEQUENCE 242 AA; 26059 MW; A3F8AC24D5481D36 CRC64;

Alignment Scores:  
Pred. No.: 0.00454 Length: 242  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q80VS4 (1-242)

QY 706 TCCAGGAGTGATTCGGGGCCCCCTGTGTGTGGGGA 744  
Db 191 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 203  
RESULT 9  
Q86VJ5

ID Q86VJ5 PRELIMINARY; PRT; 243 AA.  
AC Q86VJ5;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE DF protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC !- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; BC051001; AAH51001.1; --  
DR HSSP; P00746; 1BIO.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1.  
DR InterPro; IPR009003; Peptidase S1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS0240; TRYPsin DOM; 1.  
DR PROSITE; PS00134; TRYPsin HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPsin\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
FT NON\_TER 1  
SQ SEQUENCE 243 AA; 25809 MW; 67F02995119490BC CRC64;

Alignment Scores:  
Pred. No.: 0.00454 Length: 243  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q86VJ5 (1-243)

QY 712 GGTGATTCGGGGCCCCCTGTGTGTGGGAGTCCTT 750  
Db 196 GlyaspSerGlyGlyProLeuValCysGlyGlyValLeu 208

```
RESULT 10
OB8301 ID OB8301 PRELIMINARY; PRT; 246 AA.
AC O88301;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Brain serine protease (BSP) (BSSP).
GN Name=Prs18; Synonym=BSP, mbSP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Brain;
RX MEDLINE=20219148; PubMed=103753908; DOI=10.1074/jbc.275.15.11050;
RA Matsui H., Kimura A., Yamashiki N., Moriyama A., Kaya M., Yoshida I.,
RA Takagi N., Takahashi T.;
RT "Molecular and biochemical characterization of a serine proteinase
RT predominantly expressed in the medulla oblongata and cerebellar white
RT matter of mouse brain.";
RL J. Biol. Chem. 275:11050-11057(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Skin;
RX MEDLINE=99262106; PubMed=10329394; DOI=10.1006/bbr.1999.0600;
RA Meier N., Dear T.N., Boehm T.;
RT "A novel serine protease overexpressed in the hair follicles of nude
RT mice.";
RL Biochem. Biophys. Res. Commun. 258:374-378(1999).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB015206; BAA28895.1; -.
DR EMBL; Y18723; CAA7269.1; -.
DR EMBL; AB032402; BAA84544.1; -.
DR HSSP; P00746; 1FDP.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prs18.
DR GO; GO:0005737; C:cytoplasm; ISS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0042982; P:amyloid precursor protein metabolism; ISS.
DR GO; GO:0007417; P:central nervous system development; ISS.
DR GO; GO:0030574; P:collagen catabolism; ISS.
DR GO; GO:0042445; P:hormone metabolism; ISS.
DR GO; GO:0042552; P:myelination; ISS.
DR GO; GO:0016540; P:protein autophosphorylation; ISS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CRC64;

Alignment Scores:
Pred. No.: 0.00453 Length: 246
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x OB8301 (1-246)

QY 706 TCCTGGGGTGGTCTGGGGGCCCTGGTGTGGGGGA 744
DB 193 CysGinglyAspSerGlyGlyProLeuValCysGlygly 205

RESULT 11
Q66PG9 ID Q66PG9 PRELIMINARY; PRT; 247 AA.
AC Q66PG9;
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Trypsinogen.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC Roach J.C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AY661445; AAU06120.1; -.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 247 AA; 27244 MW; EB6EFD0C9060F4552 CRC64;

Alignment Scores:
Pred. No.: 0.00453 Length: 247
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q66PG9 (1-247)

QY 700 GATGCTGCGAGGTGANTCTGGGGGCCCTGGTGTGTGT 738
DB 194 AspAlaCysGinglyAspSerGlyGlyProLeuValCys 206

RESULT 12
Q9W7Q5 ID Q9W7Q5 PRELIMINARY; PRT; 247 AA.
AC Q9W7Q5;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Trypsinogen 3.
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Paralicthidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=21607773; PubMed=11742759; DOI=10.1016/S1096-4959(01)00487-0;
RA Suzuki T., Srivastava A.S., Kurokawa T.;
RT "cDNA cloning and phylogenetic analysis of pancreatic serine proteases
RT from Japanese flounder, Paralicthys olivaceus.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 131:63-70(2002).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB029752; BAA82364.2; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.124; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
```

DR GO: GO:0008233; F:peptidase activity; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR Pfam: PF00089; Trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 247 AA; 26948 MW; DC4B647179DD972 CRC64;

Alignment Scores:  
Pred. No.: 0.00453 Length: 247  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q9W7Q5 (1-247)

QY 700 GATGCTGCAGGGTGAATTCGGGGCCCCCTGGTGTGT 738  
|||  
DB 194 AspAlaCysGlnGlyAspSerGlyProLeuValCys 206  
|||

RESULT 13  
Q6QX59  
ID Q6QX59 PRELIMINARY; PRT; 249 AA.  
AC Q6QX59;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DE Intestinal trypsin 5 precursor (EC 3.4.21.4).  
OS Leuophtheirus salmonis (salmon louse).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Copepoda;  
OC Siphonostomatoida; Caligidae; Leuophtheirus.  
OX NCBI\_TaxID=72036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kvaume B.O., Skern R., Frost P., Nilsen F.;  
RT "Molecular characterization of five trypsin-like peptidase transcripts  
from the salmon louse (Leuophtheirus salmonis) intestine.";  
RL Int. J. Parasitol. 0.0-0(2004).  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL: AY522441; AAS91796.1; -.  
DR HSSP: P00761; 1AKS.  
DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
DR GO: GO:0008233; F:peptidase activity; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0008508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR Pfam: PF00089; Trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease; Signal.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 23 activation peptide.  
SQ SEQUENCE 249 AA; 26915 MW; 58C604D819043096 CRC64;

Alignment Scores:  
Pred. No.: 0.00452 Length: 249  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q6QX59 (1-249)

QY 700 GATGCTGCAGGGTGAATTCGGGGCCCCCTGGTGTGT 738  
|||  
DB 199 AspAlaCysGlnGlyAspSerGlyProLeuValCys 211  
|||

RESULT 14  
Q8CGR5  
ID Q8CGR5 PRELIMINARY; PRT; 250 AA.  
AC Q8CGR5;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Glandular kallikrein KUK14.  
GN Name=Klk14;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;  
RA Olsson A.Y., Lundwall A.;  
RT "Organization and evolution of the glandular kallikrein locus in Mus  
musculus";  
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Adams M., Mural R.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL: AY152433; AAN78421.1; -.  
DR HSSP: P00760; IEZX.  
DR MEROPS: S01.029; -.  
DR MGD: MGI:2447564; Klk14.  
DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
DR GO: GO:0008233; F:peptidase activity; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR Pfam: PF00089; Trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;

Alignment Scores:  
Pred. No.: 0.00452 Length: 250  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.64% Indels: 0  
DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x Q8CGR5 (1-250)

QY 706 TCCAGGGTGAATTCGGGGCCCCCTGGTGTGTGGGGA 744  
|||  
DB 199 CysGlnGlyAspSerGlyProLeuValCysGlyGly 211  
|||

RESULT 15  
O54854  
ID O54854 PRELIMINARY; PRT; 251 AA.  
AC O54854;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)

01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Myelencephalon specific protease.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 OX [1]

SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RC MEDLINE=97477435; PubMed=9334391;  
 RA Scarisbrick I.A.; Towner M.D.; Isackson P.J.;  
 RT "Nervous system-specific expression of a novel serine protease:  
 regulation in the adult rat spinal cord by excitotoxic injury.";  
 RL J. Neurosci. 17:8156-8168(1997).  
 CC -!- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AF016269; AAC02300.1; -;  
 DR HSSP; P00760; IEZX.  
 DR MEROPS; S01.236; -;  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 251 AA; 28014 MW; E21967BF06CEBBF9 CRC64;

Alignment Scores:  
 Pred. No.: 0.00452 Length: 251  
 Score: 13.00 Matches: 13  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.64% Indels: 0  
 DB: 2 Gaps: 0

US-10-015-385A-193 (1-1091) x O54854 (1-251)  
 QY 706 TGCAGGGTGATTCTGGGGGCCCTGTGTGGGGGA 744  
 Db 200 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 212

Search completed: March 5, 2005, 23:56:35  
 Job time : 240.5 secs





OM protein - protein search, using sw model  
Run on: March 5, 2005, 20:42:45 ; Search time 167 Seconds  
(without alignments)  
574.351 Million cell updates/sec

Title: US-10-015-385A-194  
Perfect score: 1374  
Sequence: 1 MGSLFLLCVGLGSLQATP.....GVYVICKYVDWIRIMRNN 248  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%

Database :  
Listing first 1500 summaries  
A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB21304	standard; protein; 248 AA.				
DE	Human KIK-L5 protein #4.					
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN ) MOUNT SINAI HOSPITAL.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 2						
ID	AAB24428	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:203.					
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 3						
ID	AAB24032	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:33.					
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 4						
ID	AAY93933	standard; protein; 248 AA.				
DE	Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.					
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 5						
ID	AAW23994	standard; protein; 248 AA.				
DE	Human EST encoded protein SEQ ID NO: 1519.					
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 6						
ID	AAB66142	standard; protein; 248 AA.				

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DE Protein of the invention #54.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 7  
ID ABO33635 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US20030731130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 6; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 8  
ID ABO44488 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 9  
ID ABO33512 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US20030731129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 10  
ID ADC18063 standard; protein; 248 AA.  
DE Human PRO polypeptide #54.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 11  
ID ADD70709 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 12  
ID ADD39786 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 13  
ID ADD70232 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 14  
ID ADD38353 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 15  
ID ADD39309 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.

PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 16  
ID ADD38832 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 17  
ID ADD40263 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 18  
ID ADE50484 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 19  
ID ADE20096 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 20  
ID ADE50007 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 21  
ID ADE21565 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 22  
ID ADF29990 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 23  
ID ADF55883 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 24  
ID ADH99387 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003065142-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 25  
ID ADE96567 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 26  
ID ADF25878 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 27  
ID ADF24777 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 28  
ID ADF29513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 29  
ID ADE97044 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 30  
ID ADH03082 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 31  
ID ADH04036 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 32  
ID ADH03559 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 33  
ID ADH04513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004005626-A1.  
PD 08-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 34  
ID ADH61514 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 35  
ID ADN10927 standard; protein; 248 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 36  
ID ADL94713 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 37  
ID ADT94373 standard; protein; 248 AA.  
DE Human PRO1303 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 38  
ID AAO29516 standard; protein; 248 AA.  
DE Human kallikrein-like protein 5 (19817).  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.5%; Score 1367; DB 6; Length 248;  
Best Local Similarity 99.6%; Pred. No. 1.7e-97;  
RESULT 39  
ID AAB21303 standard; protein; 254 AA.  
DE Human KLK-L5 protein #3.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 3; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 40  
ID ABG66676 standard; protein; 254 AA.  
DE Human novel polypeptide #11.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 94.7%; Score 1301; DB 5; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 41  
ID ADN10926 standard; protein; 254 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 42  
ID ADP56174 standard; protein; 254 AA.  
DE Human PRO protein sequence SEQ ID NO:2150.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.

Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 43  
ID AAB21301 standard; protein; 184 AA.  
DE Human KLK-L5 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 74.2%; Score 1019; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.5e-71;  
RESULT 44  
ID AAY28642 standard; protein; 162 AA.  
DE Human secreted protein from cDNA clone HKAFV61.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.0%; Score 811; DB 2; Length 162;  
Best Local Similarity 64.1%; Pred. No. 8.1e-55;  
RESULT 45  
ID AAY32852 standard; protein; 260 AA.  
DE Human serine protease protein sequence.  
PN JP11225765-A.  
PD 24-AUG-1999.  
PA (SUNR ) SUNTORY LTD.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 46  
ID AAY41744 standard; protein; 260 AA.  
DE Human PRO322 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 47  
ID AAY03220 standard; protein; 260 AA.  
DE Amino acid sequence of human tumour antigen derived gene-14 protein.  
PN WO9909138-A1.  
PD 25-FEB-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 48  
ID AAB21322 standard; protein; 260 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 49  
ID AAB44300 standard; protein; 260 AA.  
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 50  
ID AAY51131 standard; protein; 260 AA.  
DE Human neuropsin protein.  
PN JP11318461-A.  
PD 24-NOV-1999.  
PA (SHIO/) SHIOZAKA S.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 51  
ID AAU12369 standard; protein; 260 AA.  
DE Human PRO322 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 52  
ID AAB53087 standard; protein; 260 AA.  
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 53  
ID ABG23373 standard; protein; 260 AA.  
DE Novel human diagnostic protein #23364.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 54  
ID ABB84852 standard; protein; 260 AA.  
DE Human PRO322 protein sequence SEQ ID NO:72.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 55  
ID AAU61959 standard; protein; 260 AA.  
DE Human PRO322.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 56  
ID ABB95438 standard; protein; 260 AA.  
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 57  
ID ADI17076 standard; protein; 260 AA.  
DE Human NOVX protein homologue SeqID 612.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 58  
ID ABO17813 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 59  
ID ABO25246 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 60  
ID ABU81067 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 61  
ID ABU72252 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 62  
ID ADA05702 standard; protein; 260 AA.  
DE Human NOV11h protein SEQ ID NO:62.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 63  
ID ABU66767 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 64  
ID ABU84932 standard; protein; 260 AA.  
DE Human secreted and transmembrane PRO polypeptide #8.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 65  
ID ABU59848 standard; protein; 260 AA.  
DE Novel secreted and transmembrane protein PRO322.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 66  
ID ABU61130 standard; protein; 260 AA.  
DE Human PRO322 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 67  
ID ABO25038 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein (PRO) #198.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 68

ID ABU80399 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein PRO322.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 69  
ID ABU67043 standard; protein; 260 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 70  
ID ADA45915 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003023238-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 71  
ID ADA76346 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 72  
ID ADA18996 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 73  
ID ADA61619 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 74  
ID ADB19404 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 75  
ID ADB27945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 76  
ID ADA96424 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 77  
ID ADB15988 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 78  
ID ADA47774 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 79  
ID ADA67569 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 80  
ID ADB30576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 81  
ID ADA85872 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 82  
ID ADA97084 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 83  
ID ADA79388 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 84  
ID ADA87527 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 85  
ID ADB16729 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 86  
ID ADA91821 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.

PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 87  
ID ADB14884 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 88  
ID ADA24934 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 89  
ID ADB18845 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 90  
ID ADA94060 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200307722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 91  
ID ADB19956 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 92  
ID ADB13268 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 93  
ID ABO43346 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 94  
ID ABO19701 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 95  
ID ADA12595 standard; protein; 260 AA.  
DE Human secreted/transmembrane polypeptide PRO322.  
PN US2003055216-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 96  
ID ADA74522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 97  
ID ADB24755 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 98  
ID ADA82279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 99  
ID ADA75242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 100  
ID ADA85320 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 101  
ID ADA84768 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 102  
ID ADB30024 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 103  
ID ADA80552 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 104  
ID ADA75794 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082703-A1.  
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 105  
ID ADA47019 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 106  
ID ADB25315 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 107  
ID ADA93491 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 108  
ID ADB26841 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 109  
ID ADB31128 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200309386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 110  
ID ADA61056 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 111  
ID ADB24203 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 112  
ID ADA96532 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 113  
ID ADA81104 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 114  
ID ADA95980 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 115  
ID ADB26289 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 116  
ID ADB21774 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 117  
ID ABO19592 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane polypeptide #60.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 118  
ID ADA77553 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 119  
ID ADB18293 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077110-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 120  
ID ADA86976 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 121  
ID ADA88079 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 122  
ID ADA46467 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 123  
ID ADB28497 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 124  
ID ADB29049 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 125  
ID ADA77001 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 126  
ID ADA88631 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 127  
ID ADA97636 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 128  
ID ADB27393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 129  
ID ADB22326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 130  
ID ADA67017 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 131  
ID ADB22878 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 132  
ID ADB3651 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003082764-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 133  
ID ADA92373 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 134  
ID ADB15436 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 135  
ID ADB38688 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 136  
ID ADB38136 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 137  
ID ADB66608 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 138  
ID ADB89688 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 139  
ID ADB90420 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 140  
ID ADB80561 standard; protein; 260 AA.  
DE Ovarian cancer-associated protein #63.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (ECSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 141  
ID ADB39521 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082764-A1.



PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 142  
ID ADB73901 standard; protein; 260 AA.  
DE Human PRO polypeptide #60.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 143  
ID ADB47144 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 144  
ID ADB86751 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 145  
ID ADB76617 standard; protein; 260 AA.  
DE Human PRO polypeptide #60.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 146  
ID ADB77356 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 147  
ID ADB34513 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 148  
ID ADB35617 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 149  
ID ADB33961 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 150  
ID ADB35065 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077718-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 151  
ID ADB36169 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 152  
ID ADB46564 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 153  
ID ADC44043 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 154  
ID ADC61803 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 155  
ID ADC63767 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 156  
ID ADC66867 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 157  
ID ADC88991 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 158  
ID ADC63051 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 159  
ID ADC68116 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 169

ID ADCS0515 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.

PEN US2003087367-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 170

ID ADCS0990 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.

PEN US2003087361-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 171

ID ADC65517 standard; protein; 260 AA.

DE Human PRO polypeptide #198.

PEN US2003087362-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 172

ID ADC54615 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein Seq ID396.

PEN US2003087363-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 173

ID ADC3576 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein Seq ID396.

PEN US2003087359-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 174

ID ADC59099 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein Seq ID396.

PEN US2003087359-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 175

ID ADC55977 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein Seq ID396.

PEN US2003087360-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 176

ID ADC58547 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein Seq ID396.

PEN US2003087346-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 177

ID ADDO3221 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.

PEN US2003092104-A1.

PD 15-MAY-2003.

PA (GETH ) GENENTECH INC.

Query Match             45.9%;    Score 630.5; DB 7; Length 260;

Best Local Similarity    50.2%;    Pred. No. 1.1e-40;

RESULT 178  
ID ADC90213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 179  
ID ADC69632 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 180  
ID ADC48521 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 181  
ID ADD10050 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 182  
ID ADD04625 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 183  
ID ADC80581 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 184  
ID ADD09100 standard; protein; 260 AA.  
DE Human kalikrein 8 protein SEQ ID NO:2.  
PN WO2003085404-A1.  
PD 16-OCT-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 185  
ID ADD11088 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 186  
ID ADD10361 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 187  
ID ABW00074 standard; protein; 260 AA.

ID ADC47969 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 188  
ID ADC80029 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 189  
ID ADD11321 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 190  
ID ADD09498 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 191  
ID ADD41211 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 192  
ID ADD52350 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 193  
ID ADD53090 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 194  
ID ADD53642 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 195  
ID ADD37114 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 196  
ID ABW00074 standard; protein; 260 AA.

DE Human tumour antigen derived gene-14 (TADG-14) protein.  
PN US2002037591-A1.  
PD 28-MAR-2002.  
PA (UABR-) UAB RES FOUND.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 197  
ID ADD51798 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 198  
ID ADD02597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 199  
ID ADD02031 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 200  
ID ADD54213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 201  
ID ADE49429 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 202  
ID ADD92530 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 203  
ID ADD91426 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 204  
ID ADE04040 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 205  
ID ADE32337 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.

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PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 206  
ID ADE22269 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 207  
ID ADD79493 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 208  
ID ADE35483 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 209  
ID ADE16597 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 210  
ID ADD73212 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 211  
ID ADE42029 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 212  
ID ADE17846 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 213  
ID ADD91978 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 214  
ID ADE33441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194767-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 215  
ID ADE33993 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 216  
ID ADD80045 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 217  
ID ADD93082 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 218  
ID ADD72570 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 219  
ID ADE19502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 220  
ID ADE18950 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 221  
ID ADE43146 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 222  
ID ADD95935 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 223  
ID ADE22821 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199064-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 224  
ID ADD78939 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 225  
ID ADE32889 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 226  
ID ADE42581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 227  
ID ADE17221 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 228  
ID ADD80597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 229  
ID ADD89625 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 230  
ID ADE40909 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 231  
ID ADE04708 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 232  
ID ADE92837 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 233  
ID ADP47235 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 234  
ID ADG21546 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 235  
ID ADG23187 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 236  
ID ADF97522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 237  
ID ADG80586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 238  
ID ADG52992 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 239  
ID ADG60312 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 240  
ID ADG80034 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 241  
ID ADH55326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 242  
ID ADH55878 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 243  
ID ADI61072 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 244  
ID ADI64097 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 245  
ID ADH81959 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 246  
ID ADH81407 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 247  
ID ADM82576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 248  
ID ADNI5975 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 249  
ID ADNI6604 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 250  
ID ADN39182 standard; protein; 260 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 251  
ID ADN15423 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 252  
ID ADN14871 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 253  
ID ADI65046 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 254  
ID ADI63545 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 255  
ID ADC81133 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 256  
ID ADD76581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 257  
ID ADD87945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 258  
ID ADD86349 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 259  
ID ADE75797 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 260  
ID ADE89830 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 261  
ID ADE41322 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 262  
ID ADE23373 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 263  
ID ADE23925 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 264  
ID ADE24568 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 265  
ID ADD87393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 266  
ID ADE89259 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 267  
ID ADE18398 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 268  
ID ADE88707 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 269  
ID ADE89830 standard; protein; 260 AA.

DE Human secreted/transmembrane protein, PRO322.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERE/) GERBER H.  
PA (GERG/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 270  
ID ADF61470 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 271  
ID ADF40162 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 272  
ID ADF45958 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 273  
ID ADE94727 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 274  
ID ADE91138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 275  
ID ADE92285 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 276  
ID ADE91389 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 277  
ID ADF24354 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 278  
ID ADF40786 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 279  
ID ADF23730 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 280  
ID ADF33713 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 281  
ID ADF34970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 282  
ID ADF27180 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 283  
ID ADF27816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 284  
ID ADE92285 standard; protein; 260 AA.



DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 285  
ID ADE90586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 286  
ID ADF41410 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 287  
ID ADF33089 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 288  
ID ADF25455 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 289  
ID ADF26556 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 290  
ID ADF34345 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 291  
ID ADF46582 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 292  
ID ADE91733 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 293  
ID ADG03312 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 294  
ID ADG22098 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 295  
ID ADG20168 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 296  
ID ADF98074 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 297  
ID ADG24291 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 298  
ID ADF98645 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 299  
ID ADG03476 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 300  
ID ADF99197 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 301  
ID ADG16782 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 302  
ID ADG05241 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207375-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 303
ID ADG19508 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 304
ID ADG13345 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 305
ID ADG08402 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 306
ID ADG15572 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 307
ID ADF96970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 308
ID ADG06155 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 309
ID ADG23739 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 310
ID ADG04028 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 311
ID ADG24929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 312
ID ADG07226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 313
ID ADG07778 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 314
ID ADG55273 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 315
ID ADG60937 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 316
ID ADG62041 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 317
ID ADG82242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 318
ID ADG57481 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 319
ID ADG56929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 8; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 320
ID ADG5825 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 321  
ID ADG58585 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 322  
ID ADG70951 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 323  
ID ADG58033 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 324  
ID ADG53617 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 325  
ID ADG71503 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 326  
ID ADG50568 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 327  
ID ADG81690 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 328  
ID ADH10652 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200307723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 329  
ID ADH12019 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 330  
ID ADG49944 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 331  
ID ADG51816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 332  
ID ADG52441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 333  
ID ADG54169 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 334  
ID ADG49320 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 335  
ID ADG81138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 336  
ID ADG56377 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 337  
ID ADH12643 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 338  
ID ADG48696 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 339  
ID ADG48696 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

ID ADG61489 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 340  
ID ADH28576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 341  
ID ADG54721 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 342  
ID ADG59761 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 343  
ID ADG51192 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 344  
ID ADH43505 standard; protein; 260 AA.  
DE Human PRO polypeptide #36.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 345  
ID ADG59136 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 346  
ID ADG62592 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 347  
ID ADI81185 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 348  
ID ADI39730 standard; protein; 260 AA.

DE Human TADG-14 protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 349  
ID ADH25617 standard; protein; 260 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 350  
ID ADG09928 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 351  
ID ADI15399 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 352  
ID ADG09276 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 353  
ID ADI14731 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 354  
ID ADI18326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 355  
ID ADI37154 standard; protein; 260 AA.  
DE Human TADG-14 protein.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 356  
ID ADJ63607 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 357  
ID ADJ77502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.

PN US2004038336-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 358  
 ID ADK82850 standard; protein; 260 AA.  
 DE Human PRO polypeptide #36.  
 PN US2004043927-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 359  
 ID ADJ65624 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004038335-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 360  
 ID ADM27760 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004048333-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 361  
 ID ADM17394 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 362  
 ID ADL07228 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 363  
 ID ADM42484 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004058424-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 364  
 ID ADN62866 standard; protein; 260 AA.  
 DE Human NOV11h.  
 PN US2004038223-A1.  
 PD 26-FEB-2004.  
 PA (SMIT ) SMITHSON G.  
 PA (MILL ) MILLET I.  
 PA (PEYM ) PEYMAN J A.  
 PA (KEK ) KEKUDA R.  
 PA (JULJ ) JU J.  
 PA (LILL ) LI L.  
 PA (GUOK ) GUO X.  
 PA (PATT ) PATTURAJAN M.  
 PA (SPYT ) SPYTEK K A.  
 PA (EDIN ) EDINGER S R.  
 PA (ELLE ) ELLERMAN K.  
 PA (MALY ) MALYANKAR U M.  
 PA (ORTT ) ORT T.  
 PA (GORM ) GORMAN L.  
 PA (ZERH ) ZERHUSEN B D.

PA (ANDE ) ANDERSON D W.  
 PA (ZHON ) ZHONG M.  
 PA (CATT ) CATTERTON E.  
 PA (JIWW ) JI W.  
 PA (MILL ) MILLER C E.  
 PA (RAST ) RASTELLI L.  
 PA (STON ) STONE D J.  
 PA (PENA ) PENA C E A.  
 PA (SHEN ) SHENOY S G.  
 PA (SHIM ) SHIMKETS R A.  
 PA (ROTH ) ROTHENBERG M E.  
 PA (LEAC ) LEACH M D.  
 PA (AGEE ) AGE M L.  
 PA (BERG ) BERGHS C.  
 PA (DIFI ) DIPIPO V A.  
 PA (EISE ) EISEN A.  
 PA (GANG ) GANGOLLI E A.  
 PA (RIEG ) RIEGER D K.  
 PA (SPAD ) SPADERNA S K.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 365  
 ID ADN04214 standard; protein; 260 AA.  
 DE Antipsoziatic protein sequence #302.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 366  
 ID ADM28346 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004077064-A1.  
 PD 22-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 367  
 ID ADI95828 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003077659-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 368  
 ID ADI96380 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 369  
 ID ADR72883 standard; protein; 260 AA.  
 DE Human ovarian cancer-related tumour marker kallikrein 8 (HK8) protein.  
 PN WO2004075713-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 370  
 ID AAY32853 standard; protein; 305 AA.  
 DE Human serine protease protein sequence.  
 PN JP11225765-A.  
 PD 24-AUG-1999.  
 PA (SUNR ) SUNTORY LTD.  
 Query Match 45.6%; Score 627; DB 2; Length 305;  
 Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
 RESULT 371  
 ID AAB37985 standard; protein; 306 AA.  
 DE Human secreted protein encoded by gene 2 clone HWJAE49.  
 PN WO200055371-A1.

PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.6%; Score 627; DB 3; Length 306;  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 372  
ID ABP41332 standard; protein; 315 AA.  
DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.6%; Score 627; DB 5; Length 315;  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 373  
ID AAW87703 standard; protein; 260 AA.  
DE A human serine protease designated HGBAB90.  
PN EP887414-A2.  
PD 30-DEC-1998.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 45.6%; Score 626.5; DB 2; Length 260;  
Best Local Similarity 50.4%; Pred. No. 2.2e-40;  
RESULT 374  
ID AAB21311 standard; protein; 275 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.6%; Score 626.5; DB 3; Length 275;  
Best Local Similarity 50.4%; Pred. No. 2.3e-40;  
RESULT 375  
ID AAW10694 standard; protein; 260 AA.  
DE Human recombinant neuropsin, used for antibody production.  
PN JP09245700-A.  
PD 24-SEP-1996.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 376  
ID AAW12393 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN JP08311099-A.  
PD 26-NOV-1996.  
PA (SHIO/) SHIOZAKA S.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 377  
ID AAY06438 standard; protein; 260 AA.  
DE Human protease HUPW-7.  
PN WO9936550-A2.  
PD 22-JUL-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.8%; Pred. No. 4.5e-40;  
RESULT 378  
ID ABB57219 standard; protein; 260 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 45.3%; Score 622.5; DB 5; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 379  
ID ADI17073 standard; protein; 260 AA.  
DE Murine NOVX protein homologue SeqID 609.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.3%; Score 622.5; DB 5; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 380  
ID ADI39731 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN US6642013-B1.  
PD 04-NOV-2003.

PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 45.3%; Score 622.5; DB 8; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 381  
ID ADI37155 standard; protein; 260 AA.  
DE Mouse neuropsin.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.3%; Score 622.5; DB 8; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 382  
ID ADI17074 standard; protein; 260 AA.  
DE Rat NOVX protein homologue SeqID 610.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.2%; Score 621.5; DB 5; Length 260;  
Best Local Similarity 48.6%; Pred. No. 5.3e-40;  
RESULT 383  
ID AAB21325 standard; protein; 250 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 3; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 384  
ID AAY99390 standard; protein; 250 AA.  
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 3; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 385  
ID AAB66139 standard; protein; 250 AA.  
DE Protein of the invention #51.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 386  
ID AAUI2424 standard; protein; 250 AA.  
DE Human PRO1279 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 387  
ID ABB50479 standard; protein; 250 AA.  
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 388  
ID AAU83684 standard; protein; 250 AA.  
DE Human PRO protein, Seq ID No 186.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 389  
ID ABG61816 standard; protein; 250 AA.  
DE Prostate cancer-associated protein #17.  
PN WO200230268-A2.  
PD 18-APR-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 390  
ID ABB84920 standard; protein; 250 AA.  
DE Human PRO1279 protein sequence SEQ ID NO:208.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 391  
ID ABB95526 standard; protein; 250 AA.  
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 392  
ID ABO17868 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 393  
ID ABUS0831 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 394  
ID ABO33797 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 395  
ID ABUS1122 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 396  
ID ABUS6739 standard; protein; 250 AA.  
DE Lung cancer-associated polypeptide #332.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 397  
ID ABUS6822 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 398  
ID ABUS9903 standard; protein; 250 AA.  
DE Novel secreted and transmembrane protein PRO1279.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 399  
ID ABO25093 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein (PRO) #253.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 400  
ID ABUS2140 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 401  
ID ABUS67098 standard; protein; 250 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.  
PN US20030322155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 402  
ID ADA6025 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 403  
ID ADA76456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 404  
ID ABJ72320 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 405  
ID ADA19106 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 406  
ID ADA19106 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADA61729 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 407  
ID ADB19514 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 408  
ID ADB28055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 409  
ID ADA86534 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 410  
ID ADB16098 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 411  
ID ADA47884 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 412  
ID ABO44736 standard; protein; 250 AA.  
DE Novel human secreted protein #179.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 413  
ID ABO33632 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 414  
ID ADA67679 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 415  
ID ADB30686 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 416  
ID ADA85982 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 417  
ID ADA97194 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 418  
ID ADA79498 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 419  
ID ADA87637 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 420  
ID ADB16839 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 421  
ID ADA1931 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 422  
ID ADB14994 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 423  
ID ADB18955 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 424  
ID ADA94170 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.



PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 425  
ID ADB20066 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 426  
ID ADB13378 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 427  
ID ABO43401 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 428  
ID ADA74632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 429  
ID ADB24865 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 430  
ID ADA82389 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 431  
ID ADA75352 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 432  
ID ADA85430 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 433  
ID ADA84878 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082708-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 434  
ID ADB30134 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 435  
ID ADA80662 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 436  
ID ADA75904 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 437  
ID ADA47129 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 438  
ID ADB25425 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 439  
ID ADA93601 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 440  
ID ADB26951 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 441  
ID ADB31238 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 442  
ID ABJ72448 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 443  
ID ADA61166 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 444  
ID ADB24313 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077114-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 445  
ID ADA81214 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 446  
ID ADA96642 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 447  
ID ADA96090 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 448  
ID ADB26399 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 449  
ID ADB21884 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 450  
ID ABO34343 standard; protein; 250 AA.  
DE Human secreted/transmembrane polypeptide PRO 1279.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 451  
ID ADA77663 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 452  
ID ADB18403 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077110-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 453  
ID ADA87086 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 454  
ID ABO44485 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 455  
ID ADA88189 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 456  
ID ADA46577 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 457  
ID ADB28607 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 458  
ID ADB29159 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 459  
ID ABO26216 standard; protein; 250 AA.  
DE Human protein from novel secreted protein gene 179.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 460  
ID ADA77111 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 461  
ID ABO33509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 462  
ID ADA88741 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 463  
ID ADA97746 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 464  
ID ADB27503 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 465  
ID ADB22436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 466  
ID ABU72150 standard; protein; 250 AA.  
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 467  
ID ADA67127 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 468  
ID ADB22988 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 469  
ID ADB23761 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 470  
ID ADA92483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 471  
ID ADB15546 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 472  
ID ADB83676 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 473  
ID ADB80782 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 474  
ID ADB73323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 475  
ID ADB38798 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 476  
ID ADB78405 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 477  
ID ADB38246 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 478  
ID ADB66718 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 479  
ID ADB85053 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.

PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 480  
ID ADB89798 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 481  
ID ADB90530 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 482  
ID ADB90596 standard; protein; 250 AA.  
DE Ovarian cancer-associated protein #81.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 483  
ID ADB39631 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 484  
ID ADB78159 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 485  
ID ADB87225 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 486  
ID ADB84807 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 487  
ID ADB47254 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 488  
ID ADB33922 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003069397-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 489  
ID ADB86861 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 490  
ID ADB73077 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 491  
ID ADB77466 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 492  
ID ADB75388 standard; protein; 250 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 493  
ID ADB34623 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 494  
ID ADB35727 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 495  
ID ADB34071 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 496  
ID ADB35175 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 497  
ID ADB36279 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077720-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 498  
ID ADB46674 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 499  
ID ADC18039 standard; protein; 250 AA.  
DE Human PRO polypeptide #51.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 500  
ID ADC36915 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003088055-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 501  
ID ADC21905 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 502  
ID ADC50547 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 503  
ID ADC72094 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 504  
ID ADC60073 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 505  
ID ADC49936 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 506  
ID ADC49135 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 507  
ID ADC49652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 508  
ID ADC47513 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 509  
ID ADC53080 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 510  
ID ADC57434 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 511  
ID ADC60625 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 512  
ID ADC51100 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 513  
ID ADC65627 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 514  
ID ADC54725 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 515  
ID ADC53686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 516  
ID ADC49135 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 516  
ID ADC59209 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 517  
ID ADC56087 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 518  
ID ADC58657 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 519  
ID ADC47258 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 520  
ID ADD03331 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 521  
ID ADC90323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 522  
ID ADC69742 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 523  
ID ADC48631 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 524  
ID ADD10160 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 525  
ID ADC78133 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 526  
ID ADD04735 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 527  
ID ADD06368 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 528  
ID ADC80691 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 529  
ID ADD11198 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 530  
ID ADD10497 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 531  
ID ADC48079 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 532  
ID ADC77887 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 533  
ID ADC80139 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 534  
ID ADD10160 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADD11457 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PD US2003105013-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 535  
ID ADD09608 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 536  
ID ADD50850 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PD US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 537  
ID ADD41321 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PD US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 538  
ID ADD52460 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 539  
ID ADD51096 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PD US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 540  
ID ADD70685 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PD US200309625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 541  
ID ADD39762 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PD US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 542  
ID ADD53200 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 543  
ID ADD53752 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PD US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 544  
ID ADD70208 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PD US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 545  
ID ADD37250 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PD US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 546  
ID ADD38329 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PD US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 547  
ID ADD39285 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PD US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 548  
ID ADD51908 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 549  
ID ADD02707 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 550  
ID ADD50577 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PD US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 551  
ID ADD02141 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PD US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 552  
ID ADD54323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 553  
ID ADD50331 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 554  
ID ADD38808 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 555  
ID ADD40239 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 556  
ID ADD51342 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 557  
ID ADE50460 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 558  
ID ADD92640 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 559  
ID ADD91536 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 560  
ID ADE04150 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 561  
ID ADE20072 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003092883-A1.

PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 562  
ID ADE32447 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 563  
ID ADE22379 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 564  
ID ADD79603 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 565  
ID ADE42139 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 566  
ID ADE17956 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 567  
ID ADD92088 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 568  
ID ADE33551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 569  
ID ADE34103 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 570  
ID ADD80155 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207417-A1.  
PD 06-NOV-2003.



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PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 571
ID ADE49983 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 572
ID ADD93192 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 573
ID ADE19612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 574
ID ADE21541 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 575
ID ADE19060 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 576
ID ADE43256 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 577
ID ADD96045 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 578
ID ADE22931 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 579
ID ADD79049 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 580
ID ADE32999 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 581
ID ADE42691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 582
ID ADD80707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 583
ID ADD89735 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 584
ID ADE41019 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 585
ID ADE04818 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 587
ID ADF29966 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 588
ID ADF55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 589  
ID ADG21656 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 590  
ID ADG23297 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 591  
ID ADF97632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 592  
ID ADG80696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 593  
ID ADG80144 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 594  
ID ADH55436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 595  
ID ADH55988 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 596  
ID ADH99363 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 597  
ID ADI64207 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 598  
ID ADI65156 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 599  
ID ADH82069 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 600  
ID ADH81517 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 601  
ID ADM82686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 602  
ID ADNI6085 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 603  
ID ADNI6714 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 604  
ID ADN39242 standard; protein; 250 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 605  
ID ADNI5533 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 606  
ID ADNI4981 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 607

ID ADI63655 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 608  
ID ADC48889 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 609  
ID ADC81243 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 610  
ID ADE21060 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 611  
ID ADE05904 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 612  
ID ADD76691 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 613  
ID ADD75133 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 614  
ID ADD75879 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 615  
ID ADD85111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 616  
ID ADD86937 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 617  
ID ADE20814 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 618  
ID ADE39111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 619  
ID AD088055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 620  
ID ADD86459 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 621  
ID ADE05658 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 622  
ID ADD73643 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 623  
ID ADE75907 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 624  
ID ADD78483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 625  
ID ADE41458 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.

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PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 626
ID ADE23493 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 627
ID ADE21306 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 628
ID ADD77421 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 629
ID ADE20568 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 630
ID ADD75633 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 631
ID ADD74149 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 632
ID ADD74395 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 633
ID ADD76125 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 634
ID ADD85617 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100721-A1.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 635
ID ADE24035 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 636
ID ADE24678 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 637
ID ADD87503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 638
ID ADE05166 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 639
ID ADD75379 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 640
ID ADD76923 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 641
ID ADD86691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 642
ID ADE89369 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 643
ID ADD78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100731-A1.
PD 29-MAY-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 644  
ID ADE18508 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 645  
ID ADE88817 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 646  
ID ADD77667 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 647  
ID ADD77913 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 648  
ID ADD85371 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 649  
ID ADD73903 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 650  
ID ADD74641 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 651  
ID ADD77169 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 652  
ID ADD85863 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 653  
ID ADE05412 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 654  
ID ADD74887 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 655  
ID ADE96543 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 656  
ID ADE94837 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 657  
ID ADE91248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 658  
ID ADF25854 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 659  
ID ADE95389 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 660  
ID ADE93499 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 661  
ID ADF24753 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 662  
ID ADF29489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 663  
ID ADF35080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 664  
ID ADE97020 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 665  
ID ADE92395 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 666  
ID ADE90696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 667  
ID ADE91843 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 668  
ID ADG05699 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 669  
ID ADG27253 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 670  
ID ADG02422 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 671  
ID ADG22208 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 672  
ID ADG20278 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 673  
ID ADF98184 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 674  
ID ADG24401 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 675  
ID ADF98755 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 676  
ID ADG03586 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 677  
ID ADF99307 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 678  
ID ADG16892 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 679  
ID ADG05351 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 680

ID ADG19618 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 681  
ID ADG11316 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 682  
ID ADG13455 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 683  
ID ADG08512 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 684  
ID ADG15682 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 685  
ID ADG12095 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 686  
ID ADF97080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 687  
ID ADG06265 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 688  
ID ADG23849 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 689  
ID ADG04138 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 690  
ID ADG25039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 691  
ID ADF94652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 692  
ID ADG07336 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 693  
ID ADG07888 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 694  
ID ADG06748 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 695  
ID ADG55383 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 696  
ID ADG61047 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 697  
ID ADG62151 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 698  
ID ADH03058 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.

PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 699  
ID ADG82352 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 700  
ID ADG57591 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 701  
ID ADG57039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 702  
ID ADG55935 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 703  
ID ADG58695 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 704  
ID ADG71061 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 705  
ID ADH04012 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 706  
ID ADH03535 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 707  
ID ADH39092 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096965-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 708  
ID ADG58143 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 709  
ID ADG53727 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 710  
ID ADG71613 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 711  
ID ADG81800 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 712  
ID ADH30762 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 713  
ID ADH12129 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 714  
ID ADG52551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 715  
ID ADG54279 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 716  
ID ADG81248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.



Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 717  
ID ADG56487 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 718  
ID ADH12753 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 719  
ID ADG61599 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 720  
ID ADH28686 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 721  
ID ADG54831 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 722  
ID ADG59871 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 723  
ID ADH43641 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 724  
ID ADG34182 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 725  
ID ADH04489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 726  
ID ADI81295 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 727  
ID ADI33652 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 728  
ID ADH69746 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 729  
ID ADH61490 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 730  
ID ADG10038 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 731  
ID ADI15509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 732  
ID ADG09386 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 733  
ID ADI14841 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 734  
ID ADI29907 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 735  
ID ADI18436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 736  
ID ADM27304 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 737  
ID ADJ63717 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 738  
ID ADJ77612 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 739  
ID ADK32986 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 740  
ID ADK6662 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 741  
ID ADJ65734 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 742  
ID ADM27870 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 743  
ID ADM42594 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 744  
ID AAY43636 standard; protein; 282 AA.

ID ADL94689 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 745  
ID ADM28456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 746  
ID ADI95938 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 747  
ID ADI96490 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 748  
ID ADR72632 standard; protein; 250 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 749  
ID ADR72890 standard; protein; 250 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 750  
ID ADS34892 standard; protein; 250 AA.  
DE Human autoimmune disease-related protein - SEQ ID 106.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 751  
ID AAY42439 standard; protein; 282 AA.  
DE CASB12 amino acid sequence.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 45.0%; Score 618.5; DB 2; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 752  
ID AAB11712 standard; protein; 282 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 753  
ID AAY43636 standard; protein; 282 AA.

DE A human prostate-associated serum protease (PRASP).  
PN WO941387-A2.  
PD 19-AUG-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 754  
ID ADN11325 standard; protein; 282 AA.  
DE Human kallikrein-11, marker for prostate cancer.  
PN WO2004029616-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 755  
ID ADQ17587 standard; protein; 282 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 756  
ID ADR72631 standard; protein; 282 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 757  
ID ADR72889 standard; protein; 282 AA.  
DE Human ovarian cancer-related tumour-marker kallikrein 11 (hK11) protein1.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 758  
ID ADS34893 standard; protein; 282 AA.  
DE Human autoimmune disease-related protein - SEQ ID 107.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 759  
ID AAY42440 standard; protein; 281 AA.  
DE CASB12 polypeptide derived from Expressed Sequence Tag products.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMUK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 44.6%; Score 612.5; DB 2; Length 281;  
Best Local Similarity 48.0%; Pred. No. 2.8e-39;  
RESULT 760  
ID AAB36482 standard; protein; 288 AA.  
DE Fusion gene with human serine protease catalytic domain protein #13.  
PN WO200065709-A2.  
PD 09-NOV-2000.  
PA (ORTH ) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.9%; Score 602.5; DB 3; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 761  
ID AAB67542 standard; protein; 288 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 43.9%; Score 602.5; DB 4; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 762  
ID AAY36093 standard; protein; 250 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 478.

PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 43.8%; Score 601.5; DB 2; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 763  
ID ADP19401 standard; protein; 250 AA.  
DE Human secreted polypeptide #252.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST ) GENSET SA.  
Query Match 43.8%; Score 601.5; DB 8; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 764  
ID AAB11714 standard; protein; 275 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 43.7%; Score 601; DB 3; Length 275;  
Best Local Similarity 44.2%; Pred. No. 2.1e-38;  
RESULT 765  
ID AAU82732 standard; protein; 320 AA.  
DE Amino acid sequence of novel human protease #31.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 766  
ID AAE19166 standard; protein; 320 AA.  
DE Human protease, PRTS-3 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 767  
ID ADI17075 standard; protein; 225 AA.  
DE Murine NOVX protein homologue SeqID 611.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 43.6%; Score 599; DB 5; Length 225;  
Best Local Similarity 49.8%; Pred. No. 2.5e-38;  
RESULT 768  
ID AAU93930 standard; protein; 256 AA.  
DE Novel human kallikrein KUK15.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 5; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 769  
ID ADN10932 standard; protein; 256 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 8; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 770  
ID AAB36483 standard; protein; 289 AA.  
DE Fusion gene with human serine protease catalytic domain protein #14.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH ) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.6%; Score 598.5; DB 3; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-38;  
RESULT 771  
ID AAB67543 standard; protein; 289 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.

PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 43.6%; Score 598.5; DB 4; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-38;  
RESULT 772  
ID AAE08017 standard; protein; 248 AA.  
DE Human FSL33 consensus protein sequence.  
PN US6232456-B1.  
PD 15-MAY-2001.  
PA (ABSO ) ABBOTT LAB.  
Query Match 43.5%; Score 597.5; DB 4; Length 248;  
Best Local Similarity 47.8%; Pred. No. 3.6e-38;  
RESULT 773  
ID AAB11713 standard; protein; 276 AA.  
DE Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.  
PN WO20031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 43.5%; Score 597.5; DB 3; Length 276;  
Best Local Similarity 47.0%; Pred. No. 4e-38;  
RESULT 774  
ID ADC31389 standard; protein; 298 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1471.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSEQ ) HYSEQ INC.  
Query Match 43.3%; Score 595; DB 7; Length 298;  
Best Local Similarity 48.1%; Pred. No. 6.8e-38;  
RESULT 775  
ID ADI17077 standard; protein; 260 AA.  
DE Human NOVX protein homologue SeqID 613.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA ) CURAGEN CORP.  
Query Match 43.2%; Score 593.5; DB 5; Length 260;  
Best Local Similarity 48.6%; Pred. No. 7.7e-38;  
RESULT 776  
ID AAB21312 standard; protein; 228 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 43.1%; Score 592; DB 3; Length 228;  
Best Local Similarity 49.3%; Pred. No. 8.7e-38;  
RESULT 777  
ID AAW08475 standard; protein; 247 AA.  
DE Porcine trypsinogen.  
PN WO9700316-A1.  
PD 03-JAN-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 41.7%; Score 573; DB 2; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 778  
ID ABB98258 standard; protein; 247 AA.  
DE Pig trypsinogen SEQ ID NO 1.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 41.7%; Score 573; DB 5; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 779  
ID ADJ92132 standard; protein; 247 AA.  
DE Pig pro-trypsin.  
PN US2004043455-A1.  
PD 04-MAR-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
Query Match 41.7%; Score 573; DB 8; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 780  
ID AAB21306 standard; protein; 251 AA.  
DE Human KLK-L6 protein #2.  
PN WO200053776-A2.

PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 3; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 781  
ID ADN10930 standard; protein; 251 AA.  
DE Human kallikrein 14, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 8; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 782  
ID ABJ26666 standard; protein; 267 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.  
PN WO200300844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 41.4%; Score 569.5; DB 6; Length 267;  
Best Local Similarity 46.9%; Pred. No. 5.6e-36;  
RESULT 783  
ID AAB21298 standard; protein; 250 AA.  
DE Human KLK-L3 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 3; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 784  
ID ABP64969 standard; protein; 250 AA.  
DE Human protein SEQ ID 629.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSEQ-) HYSEQ INC.  
Query Match 41.4%; Score 568.5; DB 5; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 785  
ID ABR55400 standard; protein; 250 AA.  
DE Amino acid sequence of human kallikrein 9 (hk9).  
PN WO200303731-A2.  
PD 24-APR-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 6; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 786  
ID ADN05516 standard; protein; 250 AA.  
DE Antipsoriatic protein sequence #924.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.4%; Score 568.5; DB 8; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 787  
ID AAB21300 standard; protein; 277 AA.  
DE Human KLK-L4 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.3%; Score 567; DB 3; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 788  
ID ABO00554 standard; protein; 277 AA.  
DE Novel human polypeptide #141.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSEQ-) HYSEQ INC.  
Query Match 41.3%; Score 567; DB 6; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 789  
ID ADL71094 standard; protein; 277 AA.  
DE Human kallikrein 13 protein SEQ ID NO:1.  
PN WO2004021009-A2.  
PD 11-MAR-2004.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 790  
ID ADN04184 standard; protein; 277 AA.  
DE Antipsoriatic protein sequence #287.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.3%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 791  
ID ADR14575 standard; protein; 277 AA.  
DE Human NF-kappaB pathway-associated protein SeqID576.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 41.3%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 792  
ID AAU16971 standard; protein; 251 AA.  
DE Human novel secreted protein, SEQ ID 212.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.2%; Score 566.5; DB 4; Length 251;  
Best Local Similarity 46.9%; Pred. No. 8.9e-36;  
RESULT 793  
ID AAU23217 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #303.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 247;  
Best Local Similarity 46.9%; Pred. No. 1.3e-35;  
RESULT 794  
ID AAY16777 standard; protein; 293 AA.  
DE Human keratinocyte derived protease (KDP).  
PN WO9918219-A1.  
PD 15-APR-1999.  
PA (PROCT ) PROCTER & GAMBLE CO.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 795  
ID AAY30524 standard; protein; 293 AA.  
DE Human PDSP-1 protein.  
PN WO9946391-A2.  
PD 16-SEP-1999.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 796  
ID AAY38412 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 797  
ID AAY38426 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 798  
ID AAY66726 standard; protein; 293 AA.  
DE Membrane-bound protein PRO1132.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 800  
ID AAB65249 standard; protein; 293 AA.  
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 801  
ID AAU12399 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 802  
ID AAU81966 standard; protein; 293 AA.  
DE Human PRO1132.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 5; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 803  
ID ABUS8064 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 804  
ID ABUS9142 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1132.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 805  
ID ABUS2654 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 806  
ID ABO17843 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 807  
ID ADA57425 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 808

ID ADA56974 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 809  
ID ADA57427 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 810  
ID ADA57428 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 811  
ID ABU60573 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 812  
ID ABU13955 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 813  
ID ABU81097 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 814  
ID ABU72540 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 815  
ID ABU66797 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 816  
ID ADA41303 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
ID ADA41305 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1346.  
PN US2003027985-A1.  
PD 06-FEB-2003.

DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 818  
ID ADA40825 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 819  
ID ADA41306 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 820  
ID ABU59878 standard; protein; 293 AA.  
DE Novel secreted and transmembrane protein PRO1132.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 821  
ID ABU59289 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 822  
ID ABO25986 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 823  
ID ABO25068 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein (PRO) #228.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 824  
ID ABU58995 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 825  
ID ABU92373 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 826  
ID ABU59438 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1346.  
PN US2003027985-A1.  
PD 06-FEB-2003.

Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 827  
ID ABUG7073 standard; protein; 293 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 456.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 828  
ID ABUG2204 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 829  
ID ABU10910 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 830  
ID ABU81662 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 831  
ID ABU88601 standard; protein; 293 AA.  
DE Human secreted and transmembrane polypeptide PRO1132.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 832  
ID ABO34115 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 833  
ID ADA45975 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US200302328-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 834  
ID ADA76406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 835  
ID ADA19056 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 836

ID ADA61679 standard; protein; 293 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 837  
ID ADB19464 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 838  
ID ADB28005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 839  
ID ADA86484 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 840  
ID ADB16048 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 841  
ID ADA37820 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003082937-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 842  
ID ADA47834 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 843  
ID ADA21506 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 844  
ID ADA10293 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, PRO1132.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 845  
ID ADA67629 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068795-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 846  
ID ADB30636 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 847  
ID ADA85932 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 848  
ID ADA17837 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 849  
ID ADA97144 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 850  
ID ADA79448 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 851  
ID ADA87587 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 852  
ID ADB16789 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 853  
ID ADA27945 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 854  
ID ADA91881 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 855  
ID ADB14944 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 856  
ID ADB18905 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 857  
ID ADA94120 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 858  
ID ADB20016 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 859  
ID ADB13328 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 860  
ID ABO43376 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 861  
ID ADA94525 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 862  
ID ADA74582 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 863  
ID ADB24815 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 864  
ID ADB24815 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;



PN	US2003077715-A1.				
PD	24-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 874					
ID	ADA93551 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003077721-A1.				
PD	24-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 875					
ID	ADB26901 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003092147-A1.				
PD	15-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 876					
ID	ADB31188 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003096386-A1.				
PD	22-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 877					
ID	ADA92871 standard; protein; 293 AA.				
DE	Human secreted/transmembrane protein PRO1132.				
PN	US2003060407-A1.				
PD	27-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 878					
ID	ADA61116 standard; protein; 293 AA.				
DE	Homo sapiens.				
PN	US2003049817-A1.				
PD	13-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 879					
ID	ADB24263 standard; protein; 293 AA.				
DE	Human PRO polypeptide SEQ ID NO 456.				
PN	US2003077714-A1.				
PD	24-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 880					
ID	ADA96592 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003082690-A1.				
PD	01-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 881					
ID	ADA81164 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003082702-A1.				
PD	01-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	41.1%;	Score 564.5;	DB 6;	Length 293;	
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;			
RESULT 882					
ID	ADA96040 standard; protein; 293 AA.				
DE	Human PRO polypeptide #228.				
PN	US2003082759-A1.				
PD	01-MAY-2003.				

PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 883  
ID ADB26349 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 884  
ID ADB21834 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 885  
ID ADA77613 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 886  
ID ADB18353 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077110-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 887  
ID ADA87036 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 888  
ID ADA98139 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 889  
ID ADA46527 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 890  
ID ADB28557 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082659-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 891  
ID ADB29109 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 892  
ID ABO53201 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 893  
ID ADA77061 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 894  
ID ADA22432 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 895  
ID ADA88691 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 896  
ID ADA97696 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 897  
ID ADB27453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 898  
ID ADB22386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 899  
ID ABO22571 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 900  
ID ADA06598 standard; protein; 293 AA.  
DE Human secreted/transmembrane PRO polypeptide #96.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 901  
ID ADA39291 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059782-A1.  
PD 27-MAR-2003.

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Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 902
ID ADA67077 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 903
ID ADB22938 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 904
ID ADB23711 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 905
ID ADA92433 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 906
ID ADB15496 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 907
ID ADB38748 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 908
ID ADB96317 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 909
ID ADB38196 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 910
ID ADB66668 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 911
ID ADB89748 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 912
ID ADB30480 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 913
ID ADB80490 standard; protein; 293 AA.
DE Ovarian cancer-associated protein #27.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EO5B-) EOS BIOTECHNOLOGY INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 914
ID ADB39581 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 915
ID ADB47204 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 916
ID ADB86811 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 917
ID ADB77416 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 918
ID ADB34573 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 919
ID ADB35677 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 920
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ID ADB34021 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 921  
ID ADB35125 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 922  
ID ADB36229 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 923  
ID ADB46624 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 924  
ID ADC57789 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 925  
ID ADC55153 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 926  
ID ADC12020 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 927  
ID ADC56442 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 928  
ID ADC07497 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 929  
ID ADC11487 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 930  
ID ADC50497 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 931  
ID ADC72044 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 932  
ID ADC60023 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 933  
ID ADC53030 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 934  
ID ADC57384 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 935  
ID ADC60575 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 936  
ID ADC51050 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 937  
ID ADC65577 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 938  
ID ADC54675 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 939

ID ADC53636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PD US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 940  
ID ADC59159 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PD US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 941  
ID ADC56037 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PD US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 942  
ID ADC5607 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PD US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 943  
ID ADC14609 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 944  
ID ADD08141 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003068623-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 945  
ID ADD03281 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 946  
ID ADC90273 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 947  
ID ADC81966 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PD US2003083461-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 948  
ID ADC69692 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PD US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 949  
ID ADC48581 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PD US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 950  
ID ADD10110 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PD US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 951  
ID ADD07608 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 952  
ID ADD04685 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 953  
ID ADC82499 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PD US2003059833-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 954  
ID ADC80641 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 955  
ID ADD11148 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PD US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 956  
ID ADC48029 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PD US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 957  
ID ADD08679 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PD US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 958  
ID ADC80089 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 959  
ID ADD06928 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 960  
ID ADD09558 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 961  
ID ADC81175 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 962  
ID ADD41271 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 963  
ID ADD52410 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 964  
ID ADD53150 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 965  
ID ADD53702 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 966  
ID ADD55282 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 967  
ID ADD56240 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003087304-A1.  
PD 08-MAY-2003.

PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 968  
ID ADD51858 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 969  
ID ADD02657 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 970  
ID ADD02091 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 971  
ID ADD54273 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 972  
ID ADD54678 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 973  
ID ADD92590 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 974  
ID ADD91486 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 975  
ID ADE04100 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 976  
ID ADE26832 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087304-A1.  
PD 08-MAY-2003.

Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 977  
ID ADE32397 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 978  
ID ADE22329 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 979  
ID ADD79553 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 980  
ID ADE42089 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 981  
ID ADE17906 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 982  
ID ADD92038 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 983  
ID ADE33501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 984  
ID ADE34053 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 985  
ID ADD80105 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 986  
ID ADD93142 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 987  
ID ADE19562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 988  
ID ADE19010 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 989  
ID ADE43206 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 990  
ID ADD95995 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 991  
ID ADE22881 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 992  
ID ADD78999 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 993  
ID ADE26299 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 994  
ID ADE32949 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 995

ID ADE42641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 996  
ID AD80657 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 997  
ID AD89685 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 998  
ID ADE4069 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 999  
ID ADE04768 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1000  
ID ADE2897 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1001  
ID ADF67236 standard; protein; 293 AA.  
DE Human PRO1132 amino acid sequence SEQ ID NO:309.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1002  
ID ADG21606 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1003  
ID ADG23247 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1004  
ID ADF97582 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207388-A1.

DE Human PRO polypeptide #228.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1005  
ID ADG80646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1006  
ID ADG80094 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1007  
ID ADH55386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1008  
ID ADH55938 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1009  
ID ADI35490 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1010  
ID ADI64157 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1011  
ID ADI65106 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1012  
ID ADI63605 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1013  
ID ADH82019 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207388-A1.



PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1014  
ID ADH99982 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1015  
ID ADH81467 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1016  
ID ADM82636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1017  
ID ADN16035 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1018  
ID ADN16664 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1019  
ID ADN39198 standard; protein; 293 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOBB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1020  
ID ADN15483 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1021  
ID ADN14931 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1022  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1023  
ID ADD76641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1024  
ID ADD88005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1025  
ID ADD86409 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1026  
ID ADE75857 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1027  
ID ADE23433 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1028  
ID ADE23985 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1029  
ID ADE24628 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1030  
ID ADD87453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1031  
ID ADE89319 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1032  
ID ADE18458 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1033  
ID ADE88767 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1034  
ID ADE94787 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1035  
ID ADE91198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1036  
ID ADF35435 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1037  
ID ADE95339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1038  
ID ADE93449 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199050-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1039  
ID ADF35030 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1040  
ID ADE92345 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1041

ID ADE90646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1042  
ID ADE91793 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1043  
ID ADG11685 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1044  
ID ADG02372 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1045  
ID ADG22158 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1046  
ID ADG20228 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1047  
ID ADF98134 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1048  
ID ADG24351 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1049  
ID ADF98705 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1050  
ID ADG03536 standard; protein; 293 AA.

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DE Human PRO polypeptide #228.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1051
ID ADF99257 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1052
ID ADG16842 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1053
ID ADG05301 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1054
ID ADG19568 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1055
ID ADG13405 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1056
ID ADG08462 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1057
ID ADG15632 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1058
ID ADF97030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1059
ID ADG06215 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1060
ID ADG23799 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1061
ID ADG04088 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1062
ID ADG24989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1063
ID ADG07286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1064
ID ADG07838 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1065
ID ADG55333 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1066
ID ADG60997 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1067
ID ADG62101 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1068
ID ADG82302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
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PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1078  
ID ADH19555 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1079  
ID ADH30712 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1080  
ID ADH12079 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1081  
ID ADG52501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1082  
ID ADG54229 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1083  
ID ADG81198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1084  
ID ADG56437 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1085  
ID ADH12703 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1086  
ID ADH21048 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1076  
ID ADG71563 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1075  
ID ADG53677 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1074  
ID ADG58093 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1073  
ID ADG71011 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1072  
ID ADG58645 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1071  
ID ADG55885 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1070  
ID ADG56989 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1069  
ID ADG57541 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1068  
ID ADH19555 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1067  
ID ADG81750 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207805-A1.  
PD 06-NOV-2003.

RESULT 1087  
ID ADG61549 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1088  
ID ADH20088 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1089  
ID ADH28636 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1090  
ID ADG54781 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1091  
ID ADG59821 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1092  
ID ADI81245 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1093  
ID ADG09988 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1094  
ID ADI15459 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1095  
ID ADG09336 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1096  
ID ADI14791 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1097  
ID ADI18386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1098  
ID ADJ63667 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1099  
ID ADJ77562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1100  
ID ADJ65684 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1101  
ID ADM27820 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1102  
ID ADK52481 standard; protein; 293 AA.  
DE Human kallikrein 5 protein.  
PN WO2004021008-A2.  
PD 11-MAR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
PA (YOUS/) YOUSEF G.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1103  
ID ADM42544 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1104  
ID ADM28406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1105

ID ADI95888 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1106  
ID ADI96440 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US200307354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1107  
ID ADR72621 standard; protein; 293 AA.  
DE Human renal cell carcinoma-related kallikrein 5 (hk5) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1108  
ID ADR72873 standard; protein; 293 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 5 (hk5) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1109  
ID AAY14072 standard; protein; 322 AA.  
DE Human BS247 specific epitope.  
PN WO9922027-A1.  
PD 06-MAY-1999.  
PA (ABBOTT ) ABBOTT LAB.  
Query Match 41.1%; Score 564.5; DB 2; Length 322;  
Best Local Similarity 45.3%; Pred. No. 1.6e-35;  
RESULT 1110  
ID AAW07620 standard; protein; 276 AA.  
DE Human NES1 polypeptide.  
PN WO9639175-A1.  
PD 12-DEC-1996.  
PA (NEVE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
Query Match 41.0%; Score 564; DB 2; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1111  
ID AAB21327 standard; protein; 276 AA.  
DE Human NES1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 3; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1112  
ID ABG96356 standard; protein; 276 AA.  
DE Human ovarian cancer marker OV32.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 5; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1113  
ID AAU82729 standard; protein; 276 AA.  
DE Amino acid sequence of novel human protease #28.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGR-) SUGEN INC.  
Query Match 41.0%; Score 564; DB 5; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1114  
ID ADB80527 standard; protein; 276 AA.

DE Ovarian cancer-associated protein #46.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1115  
ID ADE40473 standard; protein; 276 AA.  
DE Human kallikrein 10 (gene ID 2045) protein.  
PN WO2003070883-A2.  
PD 28-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1116  
ID ADN39880 standard; protein; 276 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1117  
ID ADN04446 standard; protein; 276 AA.  
DE Antipsoriatic protein sequence #416.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1118  
ID ADQ89070 standard; protein; 276 AA.  
DE Human urological disorder related protein 2045 SEQ:22.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1119  
ID ADR72628 standard; protein; 276 AA.  
DE Human renal cell carcinoma-related kallikrein 10 (hk10) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1120  
ID ADR72886 standard; protein; 276 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 10 (hk10) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1121  
ID AAB21305 standard; protein; 237 AA.  
DE Human KLK-L6 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 562; DB 3; Length 237;  
Best Local Similarity 48.1%; Pred. No. 1.9e-35;  
RESULT 1122  
ID AAB21299 standard; protein; 256 AA.  
DE Human KLK-L4 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 561.5; DB 3; Length 256;  
Best Local Similarity 49.1%; Pred. No. 2.2e-35;  
RESULT 1123  
ID AAB21309 standard; protein; 287 AA.  
DE Human KLK-L2.

PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 561.5; DB 3; Length 287;  
Best Local Similarity 46.1%; Pred. No. 2.5e-35;  
RESULT 1124  
ID ABB98259 standard; protein; 228 AA.  
DE Synthetic shortened trypsinogen SEQ ID NO 23.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 40.8%; Score 561; DB 5; Length 228;  
Best Local Similarity 46.7%; Pred. No. 2.1e-35;  
RESULT 1125  
ID AAB21310 standard; protein; 239 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 239;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1126  
ID AAR44532 standard; protein; 244 AA.  
DE Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1127  
ID AAW22985 standard; protein; 244 AA.  
DE Human serine protease 59 (SP59).  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR ) SUNTORY LTD.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1128  
ID AAW51006 standard; protein; 244 AA.  
DE Protease M, a novel serine protease.  
PN WO9811238-A2.  
PD 19-MAR-1998.  
PA (DAND ) DANA FARRER CANCER INST INC.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1129  
ID AAB21323 standard; protein; 244 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1130  
ID AAE37572 standard; protein; 244 AA.  
DE Human 2047 protein.  
PN WO2003037258-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 6; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1131  
ID ADB80567 standard; protein; 244 AA.  
DE Ovarian cancer-associated protein #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1132  
ID ADN39212 standard; protein; 244 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.

PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1133  
ID ADN04074 standard; protein; 244 AA.  
DE Antipsoriatic protein sequence #232.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1134  
ID ADN29289 standard; protein; 244 AA.  
DE Human kallikrein 6 associated protein.  
PN US2004097452-A1.  
PD 20-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1135  
ID ADQ89076 standard; protein; 244 AA.  
DE Human urological disorder related protein 2047 SEQ:28.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1136  
ID ADR72624 standard; protein; 244 AA.  
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1137  
ID ADR72876 standard; protein; 244 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1138  
ID ABG96357 standard; protein; 244 AA.  
DE Human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 560; DB 5; Length 244;  
Best Local Similarity 46.9%; Pred. No. 2.7e-35;  
RESULT 1139  
ID AAB21297 standard; protein; 296 AA.  
DE Human KIK-L3 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.5%; Score 557; DB 3; Length 296;  
Best Local Similarity 46.1%; Pred. No. 5.7e-35;  
RESULT 1140  
ID AAR67888 standard; protein; 253 AA.  
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).  
PN WO9500851-A1.  
PD 05-JAN-1995.  
PA (SYMB-) SYMBICOM AB.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1141  
ID AAW05383 standard; protein; 253 AA.  
DE Human amyloid precursor protein protease.  
PN WO9631122-A1.

PD 10-OCT-1996.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1142  
ID ABB84421 standard; peptide; 253 AA.  
DE Human SCCE protein N-terminal fragment SEQ ID 48.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1143  
ID ABB84406 standard; protein; 253 AA.  
DE Human SCCE protein.  
PD WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1144  
ID AAU82740 standard; protein; 253 AA.  
DE Amino acid sequence of novel human protease #39.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1145  
ID ABU07440 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #43.  
PD WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1146  
ID ABU07471 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #74.  
PD WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1147  
ID ABR58471 standard; protein; 253 AA.  
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.  
PD WO2003029468-A1.  
PD 10-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1148  
ID ADB80484 standard; protein; 253 AA.  
DE Ovarian cancer-associated protein #24.  
PD WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1149  
ID ADJ68833 standard; protein; 253 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID639.  
PD WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1150  
ID ADN39180 standard; protein; 253 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.  
PD WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1151  
ID ADI06515 standard; protein; 253 AA.  
DE Human tumour-associated antigenic target (TAT) polypeptide #14.  
PD WO2004016225-A2.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1152  
ID ADN04182 standard; protein; 253 AA.  
DE Antipsoriatic protein sequence #286.  
PD WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1153  
ID ADR72880 standard; protein; 253 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.  
PD WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1154  
ID ADA05734 standard; protein; 252 AA.  
DE Human NOV18b protein SEQ ID NO:94.  
PD WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.3%; Score 553.5; DB 6; Length 252;  
Best Local Similarity 46.6%; Pred. No. 9e-35;  
RESULT 1155  
ID ADN62898 standard; protein; 252 AA.  
DE Human NOV18b.  
PD US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIFI/) DIPIPO V A.



PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 40.3%; Score 553.5; DB 8; Length 252;  
Best Local Similarity 46.8%; Pred. No. 9e-35;  
RESULT 1156  
ID AAY08025 standard; protein; 253 AA.  
DE Mouse protease-related protein (PVP).  
PN DE19736198-Cl.  
PD 24-DEC-1998.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
Query Match 40.3%; Score 553.5; DB 2; Length 253;  
Best Local Similarity 43.5%; Pred. No. 9e-35;  
RESULT 1157  
ID ADN62896 standard; protein; 250 AA.  
DE Human NOV18a.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUUG/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHIM/) SHIMOKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPPIO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 40.2%; Score 553; DB 8; Length 250;  
Best Local Similarity 44.8%; Pred. No. 9.8e-35;  
RESULT 1158  
ID AAY77494 standard; protein; 229 AA.  
DE Bovine trypsinogen.  
PN WO200005384-A1.  
PD 03-FEB-2000.  
PA (PROD-) PRODIGENE INC.  
Query Match 40.2%; Score 552; DB 3; Length 229;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1159  
ID AAR53638 standard; protein; 230 AA.  
DE Bovine trypsinogen.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (EILJ) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 2; Length 230;  
Best Local Similarity 47.5%; Pred. No. 1.1e-34;  
RESULT 1160  
ID AAY91926 standard; protein; 231 AA.  
DE Recombinant trypsin.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (EILJ) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 3; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1161  
ID AAB80953 standard; protein; 231 AA.  
DE Bovine met-phe-trypsinogen.  
PN WO200119970-A2.  
PD 22-MAR-2001.  
PA (EILJ) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 4; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1162  
ID ADA05732 standard; protein; 250 AA.  
DE Human NOV18a protein SEQ ID NO:92.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.2%; Score 552; DB 6; Length 250;  
Best Local Similarity 44.8%; Pred. No. 1.2e-34;  
RESULT 1163  
ID ABB84420 standard; peptide; 249 AA.  
DE Porcine SCCE protein N-terminal fragment SEQ ID 47.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.1%; Score 550.5; DB 5; Length 249;  
Best Local Similarity 46.7%; Pred. No. 1.5e-34;  
RESULT 1164  
ID AAB35701 standard; protein; 247 AA.  
DE Human trypsin hL amino acid sequence.  
PN JP2000253887-A.  
PD 19-SEP-2000.  
PA (TTPH-) TT PHARMA KK.  
Query Match 40.0%; Score 549.5; DB 3; Length 247;  
Best Local Similarity 44.0%; Pred. No. 1.8e-34;  
RESULT 1165  
ID AAU86677 standard; protein; 247 AA.  
DE Novel human connective tissue related polypeptide #243.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1166  
ID AAU23752 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #838.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1167  
ID AAU17043 standard; protein; 247 AA.  
DE Human novel secreted protein, SEQ ID 284.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1168  
ID ADB60011 standard; protein; 247 AA.  
DE Connective tissue antigen (CTA) #243.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 7; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1169  
ID AAW81767 standard; peptide; 223 AA.

DE Bovine TRYP peptide fragment.  
PN JP10287696-A.  
PD 27-OCT-1998.  
PA (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.  
Query Match 39.8%; Score 547; DB 2; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1170  
ID AAY69973 standard; protein; 223 AA.  
DE TRYP protein.  
PN WO9962004-A1.  
PD 02-DEC-1999.  
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.  
Query Match 39.8%; Score 547; DB 3; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1171  
ID ABG31841 standard; protein; 223 AA.  
DE Example protein #3 used in three-dimensional structure analysis method.  
PN WO200257954-A1.  
PD 25-JUL-2002.  
PA (MITU) MITSUBISHI CHEM CORP.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 5; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1172  
ID ADC73287 standard; protein; 223 AA.  
DE Bovine 2PTC E protein - SEQ ID 13.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1173  
ID ADD35545 standard; protein; 223 AA.  
DE Cationic bovine trypsinogen TRY1.  
PN WO2003040093-A2.  
PD 15-MAY-2003.  
PA (FARB) BAYER AG.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1174  
ID AAR53637 standard; protein; 224 AA.  
DE Bovine trypsin.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (LELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 2; Length 224;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1175  
ID AAY91925 standard; protein; 233 AA.  
DE Trypsinogen analogue.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (LELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 3; Length 233;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1176  
ID AD139734 standard; protein; 244 AA.  
DE Human protease M (proM) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1177  
ID AD137158 standard; protein; 244 AA.  
DE Human protease m (Protm).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1178

ID AAY78974 standard; protein; 247 AA.  
DE Canine cationic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJY YAKUHIIN KOGYO KK.  
Query Match 39.7%; Score 546; DB 3; Length 247;  
Best Local Similarity 45.6%; Pred. No. 3.3e-34;  
RESULT 1179  
ID ADA05742 standard; protein; 247 AA.  
DE Human NOV18f protein SEQ ID NO:102.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.7%; Score 546; DB 6; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1180  
ID ADN62906 standard; protein; 247 AA.  
DE Human NOV18f.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJY/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 39.7%; Score 546; DB 8; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1181  
ID AAB98502 standard; protein; 225 AA.  
DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 39.7%; Score 545; DB 4; Length 225;  
Best Local Similarity 46.5%; Pred. No. 3.6e-34;  
RESULT 1182  
ID AAY78975 standard; protein; 246 AA.  
DE Canine anionic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJY YAKUHIIN KOGYO KK.  
Query Match 39.7%; Score 545; DB 3; Length 246;  
Best Local Similarity 44.2%; Pred. No. 4e-34;  
RESULT 1183

ID AAB21326 standard; protein; 257 AA.  
DE Human HSCBE.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 39.6%; Score 544; DB 3; Length 257;  
Best Local Similarity 44.1%; Pred. No. 5e-34;  
RESULT 1184  
ID AAW64260 standard; protein; 246 AA.  
DE Human amyloid beta-protein precursor inhibitor.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 39.5%; Score 543; DB 2; Length 246;  
Best Local Similarity 44.5%; Pred. No. 5.7e-34;  
RESULT 1185  
ID ADC73299 standard; protein; 220 AA.  
DE Stereostereorelated 2PTC\_E protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 220;  
Best Local Similarity 46.8%; Pred. No. 7.2e-34;  
RESULT 1186  
ID ADC73301 standard; protein; 279 AA.  
DE Stereostereorelated 2PTC protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 279;  
Best Local Similarity 46.8%; Pred. No. 9.2e-34;  
RESULT 1187  
ID ADI16686 standard; protein; 259 AA.  
DE Human NOVX protein to treat human pathological conditions SeqID222.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.3%; Score 539.5; DB 5; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1188  
ID ADN42340 standard; protein; 259 AA.  
DE Human novel protein NOV 62.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LILL/) LI L.  
PA (GANG/) GANGOLLI E A.  
PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELLI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TAUF/) TAUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (WOLE/) WOLENC A R.  
PA (PENA/) PENA C E A.  
PA (FURT/) FURTAK K.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
Query Match 39.3%; Score 539.5; DB 8; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1189  
ID ABB78122 standard; peptide; 223 AA.

DE Amino acid sequence of trypsin.  
PN US2002072863-A1.  
PD 13-JUN-2002.  
PA (FUITSU ) FUITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1190  
ID ABB83322 standard; protein; 223 AA.  
DE Partial trypsin sequence.  
PN US2002035434-A1.  
PD 21-MAR-2002.  
PA (FUITSU ) FUITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1191  
ID ABB84419 standard; peptide; 243 AA.  
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.7%; Score 531.5; DB 5; Length 243;  
Best Local Similarity 43.8%; Pred. No. 4.3e-33;  
RESULT 1192  
ID ABB04644 standard; protein; 240 AA.  
DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISE ) JAPAN TOBACCO INC.  
Query Match 38.2%; Score 525; DB 5; Length 240;  
Best Local Similarity 45.7%; Pred. No. 1.3e-32;  
RESULT 1193  
ID AAW64261 standard; protein; 232 AA.  
DE Kallikrein substrate binding site.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 38.1%; Score 524; DB 2; Length 232;  
Best Local Similarity 43.6%; Pred. No. 1.6e-32;  
RESULT 1194  
ID ABB84423 standard; peptide; 249 AA.  
DE Murine SCCE protein N-terminal fragment SEQ ID 50.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.0%; Score 521.5; DB 5; Length 249;  
Best Local Similarity 43.0%; Pred. No. 2.6e-32;  
RESULT 1195  
ID ABR96164 standard; protein; 261 AA.  
DE Human NOV13a protein SEQ ID NO:70.  
PN WO200290568-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.8%; Score 519.5; DB 6; Length 261;  
Best Local Similarity 40.0%; Pred. No. 3.9e-32;  
RESULT 1196  
ID ADL15205 standard; protein; 232 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 37.8%; Score 519; DB 7; Length 232;  
Best Local Similarity 44.5%; Pred. No. 3.8e-32;  
RESULT 1197  
ID ABG70276 standard; protein; 247 AA.  
DE Human Serine Protease TLSP-like protein.  
PN WO200255702-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.6%; Score 516; DB 5; Length 247;  
Best Local Similarity 42.5%; Pred. No. 6.9e-32;  
RESULT 1198

ID AAW94493 standard; protein; 268 AA.  
DE Human Kallikrein.  
PN WO9842849-A1.  
PD 01-OCT-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 37.4%; Score 514; DB 2; Length 268;  
Best Local Similarity 46.4%; Pred. No. 1.1e-31;  
RESULT 1199  
ID ABB04645 standard; protein; 241 AA.  
DE Engraulis japonicus trypsinogen (aTry II) SEQ ID NO:2.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISB) JAPAN TOBACCO INC.  
Query Match 36.7%; Score 504; DB 5; Length 241;  
Best Local Similarity 45.9%; Pred. No. 5.6e-31;  
RESULT 1200  
ID AAU87693 standard; protein; 247 AA.  
DE Human pancreatic tumour protein #5.  
PN WO200212331-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.5%; Score 501; DB 5; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1201  
ID ADN04140 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #265.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1202  
ID ADN99594 standard; protein; 247 AA.  
DE Novel human protein sequence #410.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1203  
ID ADQ30589 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin II precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1204  
ID ABR41530 standard; protein; 261 AA.  
DE Human DITP protein modification/maintenance protein.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 36.5%; Score 501; DB 6; Length 261;  
Best Local Similarity 43.3%; Pred. No. 1e-30;  
RESULT 1205  
ID AAB03862 standard; protein; 223 AA.  
DE Human neurosin amino acid sequence.  
PN WO200031284-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Query Match 36.4%; Score 500; DB 3; Length 223;  
Best Local Similarity 43.5%; Pred. No. 1.1e-30;  
RESULT 1206  
ID AAB21294 standard; protein; 254 AA.  
DE Human KIK-L1 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 498; DB 3; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1207  
ID AAM01174 standard; protein; 254 AA.  
DE Human prostate-specific amino acid sequence P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1208  
ID AAU69819 standard; protein; 254 AA.  
DE Human prostate cDNA encoded protein #27.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1209  
ID AAG99059 standard; protein; 254 AA.  
DE Human prostate-specific amino acid of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1210  
ID ABU71710 standard; protein; 254 AA.  
DE Prostate cancer specific antigen P703P #7.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1211  
ID ABB95279 standard; protein; 254 AA.  
DE Human P703P putative full length protein SEQ ID NO 525.  
PN US200202248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A. 36.2%; Score 498; DB 5; Length 254;  
Query Match  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1212  
ID ABP54360 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:13.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 6; Length 254;  
RESULT 1213  
ID ABP54357 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:6.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 6; Length 254;  
RESULT 1214  
ID ABR54391 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 525.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 6; Length 254;  
RESULT 1215  
ID ADB13975 standard; protein; 254 AA.  
DE Human prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 7; Length 254;  
RESULT 1216  
ID ADG26391 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #60.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 7; Length 254;  
RESULT 1217  
ID AAB74830 standard; protein; 1079 AA.  
DE Prostate tumour antigen amino acid sequence for a fusion protein.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 4; Length 1079;  
RESULT 1218  
ID ABU71860 standard; protein; 1079 AA.  
DE Prostate specific antigen fusion protein #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISK/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match  
Best Local Similarity 43.1%; Score 498; DB 4; Length 1079;  
RESULT 1219  
ID ADI17268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 47.4%; Score 497.5; DB 5; Length 230;  
RESULT 1220  
ID ADI17276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 47.4%; Score 497.5; DB 5; Length 230;  
RESULT 1221  
ID ADJ33075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match  
Best Local Similarity 47.4%; Score 497.5; DB 7; Length 230;  
RESULT 1222  
ID ADL27345 standard; peptide; 280 AA.  
DE Amino acid sequence of trypsinogen.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match  
Best Local Similarity 42.7%; Score 497.5; DB 8; Length 280;  
RESULT 1223  
ID ADL27346 standard; peptide; 461 AA.  
DE Amino acid sequence of trypsinogen-0aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match  
Best Local Similarity 42.7%; Score 497.5; DB 8; Length 461;

Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1224  
ID ADL27347 standard; peptide; 464 AA.  
DE Amino acid sequence of trypsinogen-3aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFXY/) APEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 464;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1225  
ID ADL27348 standard; peptide; 485 AA.  
DE Amino acid sequence of trypsinogen-20aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFXY/) APEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 485;  
Best Local Similarity 42.7%; Pred. No. 3.6e-30;  
RESULT 1226  
ID AAB21307 standard; protein; 249 AA.  
DE Human prostatic.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 497; DB 3; Length 249;  
Best Local Similarity 43.1%; Pred. No. 2e-30;  
RESULT 1227  
ID AAB21320 standard; protein; 254 AA.  
DE Human prostate.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 497; DB 3; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1228  
ID AAY72525 standard; protein; 254 AA.  
DE Human prostate antigen #3.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 497; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1229  
ID AAU74901 standard; protein; 254 AA.  
DE Protein sequence of prostate homologue #3.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.2%; Score 497; DB 5; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1230  
ID AAU74932 standard; protein; 254 AA.  
DE Amino acid sequence of prostate protein fragment #3.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.2%; Score 497; DB 5; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1231  
ID AAW60592 standard; protein; 248 AA.  
DE Human prostate-specific kallikrein (HPSK) protein.  
PN WO9820117-A1.  
PD 14-MAY-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 36.1%; Score 496.5; DB 2; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1232  
ID AAY72524 standard; protein; 248 AA.  
DE Human prostate antigen #2.  
PN WO200104143-A2.  
PD 18-JAN-2001.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 36.1%; Score 496.5; DB 4; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1233  
ID AAU74770 standard; protein; 248 AA.  
DE Protein sequence of prostate homologue #2.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.1%; Score 496.5; DB 5; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1234  
ID AAU74931 standard; protein; 248 AA.  
DE Amino acid sequence of prostate protein fragment #2.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.1%; Score 496.5; DB 5; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1235  
ID ABG76997 standard; protein; 262 AA.  
DE Human kallikrein protein variant #1.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 36.0%; Score 495; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3e-30;  
RESULT 1236  
ID ADR90673 standard; protein; 246 AA.  
DE Human trypsinogen partial protein.  
PN WO200407877-A2.  
PD 16-SEP-2004.  
PA (BIOR-) BIOREXIS PHARM CORP.  
Query Match 36.0%; Score 494.5; DB 8; Length 246;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1237  
ID AAB21321 standard; protein; 247 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.0%; Score 494.5; DB 3; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1238  
ID ABR54239 standard; protein; 247 AA.  
DE Human NOV35a protein SEQ ID NO:146.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.0%; Score 494.5; DB 6; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1239  
ID ABR54241 standard; protein; 247 AA.  
DE Human NOV35c protein SEQ ID NO:150.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.0%; Score 494.5; DB 6; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1240  
ID ADQ30588 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin I precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 36.0%; Score 494.5; DB 8; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1241  
ID AAM01173 standard; protein; 254 AA.

DE Human prostate-specific amino acid mature form of P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1242  
ID AAU69818 standard; protein; 254 AA.  
DE Human prostate cDNA encoded protein #26.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1243  
ID AAG99058 standard; protein; 254 AA.  
DE Human prostate-specific mature protein of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1244  
ID ABU71709 standard; protein; 254 AA.  
DE Prostate cancer associated protein #12.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUGJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DRAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1245  
ID ABB95278 standard; protein; 254 AA.  
DE Human P703P mature protein SEQ ID NO 523.  
PN US200202248-A1.  
PD 21-FEB-2002.  
PA (XUGJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.

Query Match 36.0%; Score 494; DB 5; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1246  
ID ABR54390 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 523.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 6; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1247  
ID ADB13973 standard; protein; 254 AA.  
DE Human mature prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1248  
ID ADG26389 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #59.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1249  
ID AAB21319 standard; protein; 262 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.0%; Score 494; DB 3; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1250  
ID ABG76996 standard; protein; 262 AA.  
DE Human kallikrein protein.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 36.0%; Score 494; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1251  
ID ADL15197 standard; protein; 262 AA.  
DE Human pancreatic kallikrein.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 36.0%; Score 494; DB 7; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1252  
ID ADL4969 standard; protein; 262 AA.  
DE Human kallikrein protein (KLK1).  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUIL/) HUI L.  
PA (PERR/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERR/) ZERBA K.  
Query Match 36.0%; Score 494; DB 8; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1253  
ID ADQ39654 standard; protein; 262 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Query Match 36.0%; Score 494; DB 8; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1254  
ID ADS34891 standard; protein; 262 AA.  
DE Human autoimmune disease-related protein - SEQ ID 105.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 36.0%; Score 494; DB 8; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1255  
ID ABR54277 standard; protein; 240 AA.  
DE Human trypsinogen protein SEQ ID NO:341.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 35.9%; Score 493.5; DB 6; Length 240;  
Best Local Similarity 42.6%; Pred. No. 3.6e-30;  
RESULT 1256  
ID AAB21316 standard; protein; 241 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 35.9%; Score 493.5; DB 3; Length 241;  
Best Local Similarity 42.6%; Pred. No. 3.6e-30;  
RESULT 1257  
ID ADN04297 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #343.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GENTH) GENENTECH INC.  
Query Match 35.9%; Score 493; DB 8; Length 247;  
Best Local Similarity 42.1%; Pred. No. 4.1e-30;  
RESULT 1258  
ID AAB21308 standard; protein; 253 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 35.9%; Score 493; DB 3; Length 253;  
Best Local Similarity 42.8%; Pred. No. 4.2e-30;  
RESULT 1259  
ID AAB21324 standard; protein; 258 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 35.9%; Score 493; DB 3; Length 259;  
Best Local Similarity 42.8%; Pred. No. 4.2e-30;  
RESULT 1260  
ID AAW71005 standard; protein; 262 AA.  
DE Human prostate-associated kallikrein designated HPAK.  
PN WO9832865-A1.  
PD 30-JUL-1998.  
PA (INGY-) INCYTE PHARM INC.  
Query Match 35.9%; Score 493; DB 2; Length 262;  
Best Local Similarity 40.4%; Pred. No. 4.3e-30;  
RESULT 1261  
ID ABP74711 standard; protein; 262 AA.  
DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.  
PN WO200281646-A2.  
PD 17-OCT-2002.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match 35.9%; Score 493; DB 6; Length 262;  
Best Local Similarity 40.4%; Pred. No. 4.3e-30;  
RESULT 1262  
ID ADL15204 standard; protein; 262 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.9%; Score 493; DB 7; Length 262;

Best Local Similarity 40.4%; Pred. No. 4.3e-30;  
RESULT 1263  
ID ADM72846 standard; protein; 263 AA.  
DE Human glandular kallikrein 1 protein SEQ ID NO:105.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Query Match 35.9%; Score 493; DB 8; Length 263;  
Best Local Similarity 40.4%; Pred. No. 4.3e-30;  
RESULT 1264  
ID AAB98503 standard; protein; 225 AA.  
DE Human trypsin serine protease catalytic domain.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 35.8%; Score 492; DB 4; Length 225;  
Best Local Similarity 43.7%; Pred. No. 4.4e-30;  
RESULT 1265  
ID AAW93488 standard; protein; 230 AA.  
DE Human TRYI trypsinogen variant protein.  
PN WO9910503-A1.  
PD 04-MAR-1999.  
PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
Query Match 35.8%; Score 492; DB 2; Length 230;  
Best Local Similarity 43.7%; Pred. No. 4.5e-30;  
RESULT 1266  
ID AAB21315 standard; protein; 256 AA.  
DE Human KIK1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 35.8%; Score 492; DB 3; Length 256;  
Best Local Similarity 41.1%; Pred. No. 5e-30;  
RESULT 1267  
ID AAP95121 standard; protein; 262 AA.  
DE Kallikrein encoded by clone lambda HK65a.  
PN EP297913-A.  
PD 04-JAN-1989.  
PA (AMGE-) AMGEN.  
Query Match 35.8%; Score 492; DB 1; Length 262;  
Best Local Similarity 40.4%; Pred. No. 5.2e-30;  
RESULT 1268  
ID ABG76998 standard; protein; 262 AA.  
DE Human kallikrein protein variant #2.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 35.8%; Score 492; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 5.2e-30;  
RESULT 1269  
ID AAB54293 standard; protein; 267 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.  
PN WO200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 35.8%; Score 492; DB 3; Length 267;  
Best Local Similarity 40.4%; Pred. No. 5.3e-30;  
RESULT 1270  
ID ABG77002 standard; protein; 262 AA.  
DE Human kallikrein 1 polymorphic sequence.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 35.7%; Score 491; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 6.2e-30;  
RESULT 1271  
ID ADA05744 standard; protein; 224 AA.  
DE Human NOV18g protein SEQ ID NO:104.  
PN WO2003029424-A2.



PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP. 35.7%; Score 490; DB 6; Length 224;  
Query Match 35.7%; Score 488; DB 8; Length 247;  
Best Local Similarity 45.3%; Pred. No. 6.3e-30;  
RESULT 1272  
ID ADN62908 standard; protein; 224 AA.  
DE Human NOV189.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KERODA R.  
PA (JUUJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JINW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RASI/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 35.7%; Score 490; DB 8; Length 224;  
Best Local Similarity 45.3%; Pred. No. 6.3e-30;  
RESULT 1273  
ID AAE00397 standard; protein; 234 AA.  
DE Human serine protease, PROST 07.  
PD 12-APR-2001.  
PA (SCHD/) SCHERING AG. 35.6%; Score 489.5; DB 4; Length 234;  
Query Match 35.6%; Score 488.5; DB 2; Length 231;  
Best Local Similarity 43.0%; Pred. No. 7.2e-30;  
RESULT 1274  
ID AAY25510 standard; protein; 231 AA.  
DE Human prostate serine protease protein.  
PN RP936270-A2.  
PD 18-AUG-1999.  
PA (BADI/) BASF AG. 35.6%; Score 488.5; DB 2; Length 231;  
Query Match 35.6%; Score 488; DB 8; Length 247;  
Best Local Similarity 43.9%; Pred. No. 8.4e-30;  
RESULT 1275  
ID ADN04726 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #544.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH/) GENENTECH INC. 35.5%; Score 488; DB 8; Length 247;  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 35.5%; Score 488; DB 8; Length 247;  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 42.3%; Pred. No. 9.9e-30;  
RESULT 1277  
ID AAM01227 standard; protein; 449 AA.  
DE P703P and PSA fusion amino acid sequence.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1278  
ID AAU69872 standard; protein; 449 AA.  
DE Human prostate serum antigen/P703P fusion protein.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1279  
ID ABU71763 standard; protein; 449 AA.  
DE Prostate cancer specific antigen fusion protein #1.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISK/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1280  
ID ABB95332 standard; protein; 449 AA.  
DE Human P703P/PSA fusion protein SEQ ID NO 617.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISK/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Query Match 35.5%; Score 487.5; DB 5; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;

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RESULT 1281
ID ABR54444 standard; protein; 449 AA.
DE Prostate tumour specific protein sequence SEQ ID 617.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 6; Length 449;
  Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1282
ID ADB14067 standard; protein; 449 AA.
DE Human prostate specific protein P703P/PSA fusion protein.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 7; Length 449;
  Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1283
ID ADG26483 standard; protein; 449 AA.
DE Human prostate-specific polypeptide #113.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 7; Length 449;
  Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1284
ID ABU71889 standard; protein; 585 AA.
DE Prostate cancer specific antigen fusion protein #3.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 4; Length 585;
  Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1285
ID ABU71888 standard; protein; 585 AA.
DE Prostate cancer associated protein #72.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 4; Length 585;
  Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1286
ID ABU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 7; Length 585;
  Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1287
ID ADB14470 standard; protein; 585 AA.
DE POPF/hPAP fusion protein, POPF3.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 7; Length 585;
  Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1288
ID ADG26993 standard; protein; 585 AA.
DE Human prostate-specific polypeptide #249.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 7; Length 585;
  Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1289
ID ABU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
  Best Local Similarity 35.5%; Score 487.5; DB 4; Length 801;
  Best Local Similarity 44.1%; Pred. No. 3.6e-29;
RESULT 1290
ID AAV31160 standard; protein; 224 AA.
DE Human trypsin serine protease protein domain.
PN US5948892-A.
PD 07-SEP-1999.
PA (AMGE-) AMGEN INC.
Query Match
  Best Local Similarity 35.4%; Score 487; DB 2; Length 224;
  Best Local Similarity 43.4%; Pred. No. 1.1e-29;
RESULT 1291
ID ADL15207 standard; protein; 261 AA.
DE Pancreatic kallikrein #3.
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PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.3%; Score 484.5; DB 7; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.9e-29;  
RESULT 1292  
ID ABM83249 standard; protein; 261 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 261;  
Best Local Similarity 43.5%; Pred. No. 2.1e-29;  
RESULT 1293  
ID ABM83250 standard; protein; 333 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 333;  
Best Local Similarity 43.5%; Pred. No. 2.7e-29;  
RESULT 1294  
ID AAW57740 standard; protein; 240 AA.  
DE Trypsinogen-like protein.  
PN JP10099080-A.  
PD 21-APR-1998.  
PA (SHIS-) SHISEIDO CO LTD.  
Query Match 35.2%; Score 483.5; DB 2; Length 240;  
Best Local Similarity 42.5%; Pred. No. 2.1e-29;  
RESULT 1295  
ID ADL15206 standard; protein; 260 AA.  
DE Pancreatic kallikrein #2.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.2%; Score 483; DB 7; Length 260;  
Best Local Similarity 39.8%; Pred. No. 2.5e-29;  
RESULT 1296  
ID AAB21293 standard; protein; 237 AA.  
DE Human KLK-L1 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN-) MOUNT SINAI HOSPITAL.  
Query Match 35.1%; Score 482.5; DB 3; Length 237;  
Best Local Similarity 42.2%; Pred. No. 2.5e-29;  
RESULT 1297  
ID AAP70568 standard; protein; 262 AA.  
DE Human kallikrein-like substance has hypotensive activity.  
PN JP62126980-A.  
PD 09-JUN-1987.  
PA (NAKA-) NAKANISHI S.  
Query Match 35.0%; Score 481; DB 1; Length 262;  
Best Local Similarity 40.0%; Pred. No. 3.6e-29;  
RESULT 1298  
ID AAU01290 standard; protein; 216 AA.  
DE Human serine protease HETAA37p.  
PN WO200123587-A2.  
PD 05-APR-2001.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 34.8%; Score 477.5; DB 4; Length 216;  
Best Local Similarity 44.3%; Pred. No. 5.5e-29;  
RESULT 1299  
ID AAY72526 standard; protein; 226 AA.  
DE Human prostatic antigen P703PDE5 sequence.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
DE Protein sequence of prostate homologue #4.

PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1301  
ID AAU74933 standard; protein; 226 AA.  
DE Amino acid sequence of prostate protein fragment #4.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1302  
ID AAY72522 standard; protein; 312 AA.  
DE NS1-P703P-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1303  
ID AAU74768 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NS1-p703-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1304  
ID AAU74929 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NS1-p703P-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1305  
ID ABU71886 standard; protein; 344 AA.  
DE Human prostate specific antigen (PSA) epitope #26.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ-) XU J.  
PA (DILL-) DILLON D C.  
PA (MITC-) MITCHAM J L.  
PA (HARL-) HARLOCKER S L.  
PA (JIAN-) JIANG Y.  
PA (KALO-) KALOS M D.  
PA (FANG-) FANGER G R.  
PA (RETT-) RETTER M W.  
PA (STOL-) STOLK J A.  
PA (DAYC-) DAY C H.  
PA (VEDV-) VEDVICK T S.  
PA (CART-) CARTER D.  
PA (LISK-) LI S X.  
PA (WANG-) WANG A.  
PA (SKEI-) SKEIKY Y A W.  
PA (HEEL-) HEPLER W T.  
PA (HEND-) HENDERSON R A.  
PA (HURA-) HURAL J.  
PA (MCNE-) MCNEILL P D.  
PA (HOUG-) HOUGHTON R L.  
PA (DEAS-) Y DE BASSOLS C V.  
PA (FOYT-) FOY T M.  
Query Match 34.8%; Score 477.5; DB 4; Length 344;  
Best Local Similarity 43.8%; Pred. No. 8.9e-29;  
RESULT 1306  
ID ABM82601 standard; protein; 239 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

Query Match  
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;  
RESULT 1307  
ID ABM82602 standard; protein; 239 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2851.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;  
RESULT 1308  
ID ABM82603 standard; protein; 239 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2852.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;  
RESULT 1309  
ID ADN99649 standard; protein; 280 AA.  
DE Novel human protein sequence #465.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 34.4%; Score 473; DB 8; Length 280;  
RESULT 1310  
ID AAY82008 standard; protein; 220 AA.  
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.  
PN WO20000419-A2.  
PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 3; Length 220;  
RESULT 1311  
ID AAM01123 standard; protein; 220 AA.  
DE Human prostate-specific amino acid sequence P703PDE5.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;  
RESULT 1312  
ID AAU69768 standard; protein; 220 AA.  
DE Human prostate cDNA encoded protein #8.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;  
RESULT 1313  
ID AAB74806 standard; protein; 220 AA.  
DE Prostate tumour antigen predicted amino acid sequence for P703PDE5.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;  
RESULT 1314  
ID AAG99008 standard; protein; 220 AA.  
DE Human prostate-specific amino acid sequence P703PDE5.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;  
RESULT 1315  
ID AAG62147 standard; protein; 220 AA.  
DE Human P703P inventive antigen SEQ ID NO: 330.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;

Best Local Similarity 43.8%; Pred. No. 1.4e-28;  
RESULT 1316  
ID ABU71659 standard; protein; 220 AA.  
DE Prostate cancer specific antigen P703P #4.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ-) XU J.  
PA (DILL-) DILLON D C.  
PA (MITC-) MITCHAM J L.  
PA (HARL-) HARLOCKER S L.  
PA (JIAN-) JIANG Y.  
PA (KALO-) KALOS M D.  
PA (FANG-) FANGER G R.  
PA (RETT-) RETTER M W.  
PA (STOL-) STOLK J A.  
PA (DAYC-) DAY C H.  
PA (VEDV-) VEDVICK T S.  
PA (CART-) CARTER D.  
PA (LISX-) LI S X.  
PA (WANG-) WANG A.  
PA (SKEI-) SKEIKY Y A W.  
PA (HEPL-) HEPLER W T.  
PA (HEND-) HENDERSON R A.  
PA (HURA-) HURAL J.  
PA (MCNE-) MCNEILL P D.  
PA (HOUG-) HOUGHTON R L.  
PA (DBAS-) Y DE BASSOLS C V.  
PA (FOYT-) FOY T M.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;  
RESULT 1317  
ID ABB95228 standard; protein; 220 AA.  
DE Human P703PDES protein SEQ ID NO 327.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ-) XU J.  
PA (DILL-) DILLON D C.  
PA (MITC-) MITCHAM J L.  
PA (HARL-) HARLOCKER S L.  
PA (JIAN-) JIANG Y.  
PA (KALO-) KALOS M D.  
PA (FANG-) FANGER G R.  
PA (RETT-) RETTER M W.  
PA (STOL-) STOLK J A.  
PA (DAYC-) DAY C H.  
PA (VEDV-) VEDVICK T S.  
PA (CART-) CARTER D.  
PA (LISX-) LI S X.  
PA (WANG-) WANG A.  
PA (SKEI-) SKEIKY Y A W.  
PA (HEPL-) HEPLER W T.  
PA (HEND-) HENDERSON R A.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 5; Length 220;  
RESULT 1318  
ID ABR54340 standard; protein; 220 AA.  
DE Prostate tumour specific protein sequence SEQ ID 327.  
PN WO200269747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 6; Length 220;  
RESULT 1319  
ID ADB13777 standard; protein; 220 AA.  
DE Human prostate specific protein P703PDE5.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 34.4%; Score 472.5; DB 7; Length 220;  
RESULT 1320  
ID ADG26193 standard; protein; 220 AA.  
DE Human prostate-specific polypeptide #9.

PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 34.4%; Score 472.5; DB 7; Length 220;  
Best Local Similarity 43.8%; Pred. No. 1.4e-28;  
RESULT 1321  
ID ADI39732 standard; protein; 262 AA.  
DE Human glandular kallikrein (HK2) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 34.4%; Score 472.5; DB 8; Length 262;  
Best Local Similarity 38.9%; Pred. No. 1.6e-28;  
RESULT 1322  
ID ADI37156 standard; protein; 262 AA.  
DE Human glandular kallikrein (hHK2) protein.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 34.4%; Score 472.5; DB 8; Length 262;  
Best Local Similarity 38.9%; Pred. No. 1.6e-28;  
RESULT 1323  
ID ABR96163 standard; protein; 274 AA.  
DE Human NOV12a protein SEQ ID NO:68.  
PN WO200290568-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 34.4%; Score 472.5; DB 6; Length 274;  
Best Local Similarity 40.7%; Pred. No. 1.7e-28;  
RESULT 1324  
ID AAP92314 standard; protein; 245 AA.  
DE Human recombinant kallikrein gene.  
PN EP297913-A.  
PD 04-JAN-1989.  
PA (AMGE-) AMGEN.  
Query Match 34.3%; Score 471; DB 1; Length 245;  
Best Local Similarity 40.2%; Pred. No. 2e-28;  
RESULT 1325  
ID AAB21313 standard; protein; 255 AA.  
DE Human PSA.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 34.2%; Score 470.5; DB 3; Length 255;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1326  
ID AAU06276 standard; protein; 257 AA.  
DE Prostate specific Antigen (PSA) polypeptide.  
PN WO200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMUNE INC.  
Query Match 34.2%; Score 470.5; DB 4; Length 257;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1327  
ID AAW13649 standard; protein; 261 AA.  
DE Human prostatic specific antigen.  
PN WO9711172-A1.  
PD 27-MAR-1997.  
PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.  
Query Match 34.2%; Score 470.5; DB 2; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1328  
ID AAY56048 standard; protein; 261 AA.  
DE Human prostate-specific antigen.  
PN WO9961068-A1.  
PD 02-DEC-1999.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1329  
ID AAY77842 standard; protein; 261 AA.  
DE Human prostate-specific antigen (PSA) sequence.  
PN WO9960984-A2.

PD 02-DEC-1999.  
PA (ENTR-) ENTREMED INC.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1330  
ID AAB21317 standard; protein; 261 AA.  
DE Human PSA.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1331  
ID AAB74821 standard; protein; 261 AA.  
DE Prostate tumour antigen amino acid sequence for PSA.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1332  
ID AAG62144 standard; protein; 261 AA.  
DE Human prostate specific membrane antigen SEQ ID NO: 327.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1333  
ID AAG62146 standard; protein; 261 AA.  
DE Human prostate specific antigen SEQ ID NO: 329.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1334  
ID ABU71859 standard; protein; 261 AA.  
DE Human prostatic specific membrane antigen (PSMA).  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ) XU J.  
PA (DILL) DILLON D C.  
PA (MITC) MITCHAM J L.  
PA (HARL) HARLOCKER S L.  
PA (JIAN) JIANG Y.  
PA (KALO) KALOS M D.  
PA (FANG) FANGER G R.  
PA (RETT) RETTER M W.  
PA (STOL) STOLK J A.  
PA (DAYC) DAY C H.  
PA (VEDV) VEDVICK T S.  
PA (CAST) CARTER D.  
PA (LISX) LI S X.  
PA (WANG) WANG A.  
PA (SKEI) SKEIKY Y A W.  
PA (HEPL) HEPLER W T.  
PA (HEND) HENDERSON R A.  
PA (HURA) HURAL J.  
PA (MCNE) MCNEILL P D.  
PA (HOUG) HOUGHTON R L.  
PA (DBAS) Y DE BASSOLS C V.  
PA (FOYT) FOY T M.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1335  
ID ABP74202 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO200281645-A2.  
PD 17-OCT-2002.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match 34.2%; Score 470.5; DB 6; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1336  
ID ADB82777 standard; protein; 261 AA.  
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1337  
ID ADC09580 standard; protein; 261 AA.  
DE PSA protein #SEQ ID 78.  
PN WO2003008537-A2.  
PD 30-JAN-2003.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1338  
ID ADJ59022 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1339  
ID ADI39733 standard; protein; 261 AA.  
DE Human prostate specific antigen (PSA) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1340  
ID ADI37157 standard; protein; 261 AA.  
DE Human prostate specific antigen (hPSA).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1341  
ID ADM72819 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1342  
ID ABM82166 standard; protein; 261 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1343  
ID AAB08449 standard; protein; 375 AA.  
DE A human prostate specific antigen variant polypeptide.  
PN WO2000049158-A2.  
PD 24-AUG-2000.  
PA (COMP-) COMPUGEN LTD.  
Query Match 34.2%; Score 470.5; DB 3; Length 375;  
Best Local Similarity 40.4%; Pred. No. 3.4e-28;  
RESULT 1344  
ID AAG62154 standard; protein; 692 AA.  
DE Human wt1/PSA fusion protein SEQ ID NO: 357.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 692;  
Best Local Similarity 40.4%; Pred. No. 6.3e-28;

RESULT 1345  
ID AAB67545 standard; protein; 284 AA.  
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Query Match 34.1%; Score 469; DB 4; Length 284;  
Best Local Similarity 43.8%; Pred. No. 3.3e-28;  
RESULT 1346  
ID ADJ59024 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.1%; Score 468.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 3.3e-28;  
RESULT 1347  
ID AAU74903 standard; protein; 231 AA.  
DE Amino acid sequence of p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1348  
ID AAU74934 standard; protein; 231 AA.  
DE Amino acid sequence of P703p mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1349  
ID AAU72521 standard; protein; 312 AA.  
DE NS1-P703p mutated-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.0%; Score 467.5; DB 4; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1350  
ID AAU74767 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1351  
ID AAU74928 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-P703p mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1352  
ID AAP81243 standard; protein; 247 AA.  
DE Human spleen trypsin III (trypsinogen III).  
PN JP63160582-A.  
PD 04-JUL-1988.  
PA (SANY) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 1; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;  
RESULT 1353  
ID AAR82703 standard; protein; 247 AA.  
DE Human pancreatic trypsin III.  
PN JP07184655-A.  
PD 25-JUL-1995.  
PA (SANY) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 2; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;

RESULT 1354  
ID ADJ59026 standard; protein; 261 AA.  
DE Human PSA analogue (Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.0%; Score 466.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 4.7e-28;  
RESULT 1355  
ID ABB4422 standard; peptide; 226 AA.  
DE Rat SCCE protein N-terminal fragment SEQ ID 48.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 33.8%; Score 464.5; DB 5; Length 226;  
Best Local Similarity 42.7%; Pred. No. 5.8e-28;  
RESULT 1356  
ID ADJ59028 standard; protein; 261 AA.  
DE Human PSA analogue (Y155/Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.8%; Score 464.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 6.8e-28;  
RESULT 1357  
ID ADA50549 standard; protein; 237 AA.  
DE Rhesus macaque prostate specific antigen (PSA/CLK3), SEQ ID NO:4.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.8%; Score 464; DB 6; Length 237;  
Best Local Similarity 42.6%; Pred. No. 6.7e-28;  
RESULT 1358  
ID ADM12395 standard; protein; 261 AA.  
DE Human prostate-specific antigen protein.  
PN US2003235594-A1.  
PD 25-DEC-2003.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Query Match 33.7%; Score 463.5; DB 8; Length 261;  
Best Local Similarity 40.8%; Pred. No. 8.1e-28;  
RESULT 1359  
ID ADR66838 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1360  
ID ADR66277 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1361  
ID ADR66934 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1362  
ID ADR66036 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1363  
ID ADP27546 standard; protein; 281 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 281;  
Best Local Similarity 41.0%; Pred. No. 1.1e-27;  
RESULT 1364  
ID ADP27545 standard; protein; 297 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 297;  
Best Local Similarity 41.0%; Pred. No. 1.2e-27;  
RESULT 1365  
ID AAR84668 standard; protein; 261 AA.  
DE Prepro-hk2 kallikrein.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1366  
ID AAW10600 standard; protein; 261 AA.  
DE Human prepro-Trp226-glandular kallikrein-2.  
PN WO9701630-A1.  
PD 16-JAN-1997.  
PA (ORIN ) ORION YHTYMAE OY.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1367  
ID AAU98921 standard; protein; 245 AA.  
DE Human prostate specific antigen (PSA) variant.  
PN WO200240059-A2.  
PD 23-MAY-2002.  
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.  
PA (MINC/) MINCHEFF M S.  
PA (LOUK/) LOUKINOV D I.  
PA (ZOUB/) ZOUBAK S.  
Query Match 33.4%; Score 459.5; DB 5; Length 245;  
Best Local Similarity 41.4%; Pred. No. 1.5e-27;  
RESULT 1368  
ID AAY08894 standard; protein; 238 AA.  
DE Chimeric serine protease FXT protein.  
PN EP927764-A2.  
PD 07-JUL-1999.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
Query Match 33.4%; Score 459; DB 2; Length 238;  
Best Local Similarity 40.5%; Pred. No. 1.6e-27;  
RESULT 1369  
ID AAB21314 standard; protein; 255 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 255;  
Best Local Similarity 40.8%; Pred. No. 1.9e-27;  
RESULT 1370  
ID AAW06971 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein prepro-hk2.  
PN WO9634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITECH INC.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1371  
ID AAW83203 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein protein pphk2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1372  
ID AAW45397 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein precursor prepro-hk2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1373  
ID AAW45397 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein precursor prepro-hk2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1374  
ID AAW6189 standard; protein; 261 AA.  
DE Prepro human Kallikrein 2 (preprohk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1375  
ID AAB21318 standard; protein; 261 AA.  
DE Human KLU2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1376  
ID AAU06279 standard; protein; 261 AA.  
DE Human kallikrein2 polypeptide.  
PN WO200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMUNE INC.  
Query Match 33.4%; Score 458.5; DB 4; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1377  
ID ADB75390 standard; protein; 261 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 33.4%; Score 458.5; DB 7; Length 261;

Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1378  
ID AAW83213 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hk3.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1379  
ID AAW56086 standard; protein; 237 AA.  
DE Human prostate specific antigen protein.  
PN WO9810292-A1.  
PD 12-MAR-1998.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1380  
ID AAW96187 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1381  
ID AAB11041 standard; peptide; 237 AA.  
DE Human prostate-specific antigen N-terminal fragment #2.  
PN EP1043394-A2.  
PD 11-OCT-2000.  
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.  
Query Match 33.3%; Score 457.5; DB 3; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1382  
ID AAB19819 standard; protein; 237 AA.  
DE Prostate specific antigen specific to benign prostatic hyperplasia.  
PN WO200067030-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1383  
ID AAB19818 standard; protein; 237 AA.  
DE Prostate specific antigen elevated in benign prostatic hyperplasia.  
PN WO200066718-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1384  
ID ADA50546 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1385  
ID ADA09840 standard; protein; 237 AA.  
DE Human mature prostate specific antigen (PSA).  
PN US2003059864-A1.  
PD 27-MAR-2003.  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (RITT/) RITTENHOUSE H G.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1386



ID ADJ59023 standard; protein; 237 AA.  
DE Human PSA mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.3%; Score 457.5; DB 7; Length 237;  
Best Local Similarity 41.8%; Pred. No. 2.1e-27;  
RESULT 1387  
ID ADF60980 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA).  
PN US2003166036-A1.  
PD 04-SEP-2003.  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (KITTT/) RITTENHOUSE H G.  
Query Match 33.3%; Score 457.5; DB 8; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1388  
ID AAP70677 standard; protein; 245 AA.  
DE Human kallikrein gene product.  
PN WO8702709-A.  
PD 07-MAY-1987.  
PA (BIOT-) BIOTECHN RES PARTN.  
PA (CALB-) CALIF BIOTECHNOL INC.  
Query Match 33.2%; Score 456; DB 1; Length 245;  
Best Local Similarity 39.7%; Pred. No. 2.9e-27;  
RESULT 1389  
ID AAW45398 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hK3 (PSA).  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.2%; Score 455.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 3e-27;  
RESULT 1390  
ID ADJ59025 standard; protein; 237 AA.  
DE Human PSA mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.2%; Score 455.5; DB 7; Length 237;  
Best Local Similarity 41.6%; Pred. No. 3e-27;  
RESULT 1391  
ID AAW69972 standard; protein; 261 AA.  
DE Kallikrein prepro-hK2v217 variant.  
PN WO9634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITECH INC.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.2%; Score 455.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 3.3e-27;  
RESULT 1392  
ID AAW45400 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein hK2v217.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.2%; Score 455.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 3.3e-27;  
RESULT 1393  
ID AAW59129 standard; protein; 232 AA.  
DE Homo sapiens Tub Interactor (hTI-1) protein.  
PN WO9812302-A1.  
PD 26-MAR-1998.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 33.1%; Score 454.5; DB 2; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1394  
ID AAY72523 standard; protein; 232 AA.  
DE Human prostate antigen #1.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 33.1%; Score 454.5; DB 4; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1395  
ID AAU74769 standard; protein; 232 AA.  
DE Protein sequence of prostate homologue #1.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 33.1%; Score 454.5; DB 5; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1396  
ID AAU74930 standard; protein; 232 AA.  
DE Amino acid sequence of prostate protein fragment #1.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 33.1%; Score 454.5; DB 5; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1397  
ID AAR84669 standard; protein; 244 AA.  
DE Pro-hK2 kallikrein.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.1%; Score 454.5; DB 2; Length 244;  
Best Local Similarity 41.2%; Pred. No. 3.7e-27;  
RESULT 1398  
ID ADO38617 standard; protein; 261 AA.  
DE Prostate Specific Antigen (PSA).  
PN US2004058881-A1.  
PD 25-MAR-2004.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Query Match 33.1%; Score 454.5; DB 8; Length 261;  
Best Local Similarity 39.6%; Pred. No. 4e-27;  
RESULT 1399  
ID ADJ59027 standard; protein; 237 AA.  
DE Human PSA analogue (Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.0%; Score 453.5; DB 7; Length 237;  
Best Local Similarity 41.6%; Pred. No. 4.3e-27;  
RESULT 1400  
ID AAW83204 standard; protein; 244 AA.  
DE Prostate-specific glandular kallikrein protein phK2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;  
Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1401  
ID AAW45396 standard; protein; 244 AA.  
DE Prostate-specific glandular kallikrein precursor pro-hK2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;  
Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1402  
ID AAW96188 standard; protein; 244 AA.  
DE Pro human Kallikrein 2 (prohK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;

Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1403  
ID AAW03130 standard; protein; 250 AA.  
DE Prostate-specific antigen.  
PN WO9821042-A2.  
PD 11-JUL-1996.  
PA (UYBO-) UNIV BOSTON.  
Query Match 32.9%; Score 452.5; DB 2; Length 250;  
Best Local Similarity 40.5%; Pred. No. 5.4e-27;  
RESULT 1404  
ID ADP27538 standard; protein; 281 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 281;  
Best Local Similarity 41.8%; Pred. No. 6.1e-27;  
RESULT 1405  
ID ADP27537 standard; protein; 297 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 297;  
Best Local Similarity 41.8%; Pred. No. 6.5e-27;  
RESULT 1406  
ID ADJ59029 standard; protein; 236 AA.  
DE Human PSA analogue (L155/Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 32.9%; Score 451.5; DB 7; Length 236;  
Best Local Similarity 41.6%; Pred. No. 6.1e-27;  
RESULT 1407  
ID AAR77098 standard; protein; 237 AA.  
DE Prostate-specific antigen.  
PN WO9528498-A1.  
PD 26-OCT-1995.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 40.7%; Pred. No. 7.4e-27;  
RESULT 1408  
ID AAW83202 standard; protein; 237 AA.  
DE Prostate-specific glandular kallikrein protein hK2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYO) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1409  
ID AAW45395 standard; protein; 237 AA.  
DE Mature prostate-specific glandular kallikrein hK2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1410  
ID AAW96186 standard; protein; 237 AA.  
DE Mature human kallikrein 2 (hK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG-) YOUNG C Y F.  
PA (TIND-) TINDALL D J.  
PA (KLEE-) KLEE G G.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1411  
ID ADA50561 standard; protein; 237 AA.  
DE Kallikrein KLK2, SEQ ID NO:16.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 32.8%; Score 450.5; DB 6; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1412  
ID AAR84667 standard; protein; 237 AA.  
DE Mature kallikrein hK2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.6%; Score 448.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1e-26;  
RESULT 1413  
ID ADI17277 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 813.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1414  
ID ADI17269 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 805.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1415  
ID ADJ83076 standard; protein; 217 AA.  
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO-) ALSOBROOK J P.  
PA (TCHE-) TCHERNEV V T.  
PA (LIUX-) LIU X.  
PA (SPYT-) SPYTEK K A.  
PA (ZERH-) ZERHUSEN B D.  
PA (PATT-) PATTURAJAN M.  
PA (LEPL-) LEPLEY D M.  
PA (BURG-) BURGESS C E.  
PA (SHIM-) SHIMKETS R A.  
PA (GROS-) GROSSE W M.  
PA (SZEK-) SZEKERES E S.  
PA (VERN-) VERNET C A M.  
PA (LILL-) LI L.  
PA (CASM-) CASMAN S J.  
PA (BOLD-) BOLDOG F L.  
PA (GORM-) GORMAN L.  
PA (GANG-) GANGOLLI E A.  
PA (FERN-) FERNANDES E R.  
PA (RIEG-) RIEGER D K.  
PA (EDIN-) EDINGER S R.  
PA (GUNT-) GUNTHER E.  
PA (MILL-) MILLET I.  
PA (SCIO-) SCIORE P.  
PA (ELDE-) ELLERMAN K.  
PA (MACD-) MACDOUGALL J R.  
PA (SMIT-) SMITHSON G.  
Query Match 32.6%; Score 447.5; DB 7; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1416  
ID AAW83212 standard; protein; 237 AA.  
DE hK2 variant A217V.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1417

ID AAW49087 standard; protein; 237 AA.  
DE Mutant human kallikrein 2 (hk2) A217V.  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1418  
ID AAW96190 standard; protein; 237 AA.  
DE Variant human kallikrein 2 (hk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG-) YOUNG C Y F.  
PA (TINDALL-) TINDALL D J.  
PA (KLEE-) KLEE G G.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1419  
ID AAW11023 standard; protein; 240 AA.  
DE Human prostate specific antigen.  
PN WO9640754-A1.  
PD 19-DEC-1996.  
PA (TEXAS) UNIV TEXAS SYSTEM.  
Query Match 32.4%; Score 445; DB 2; Length 240;  
Best Local Similarity 41.0%; Pred. No. 2e-26;  
RESULT 1420  
ID AAR84671 standard; protein; 237 AA.  
DE Mature kallikrein hk3.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.4%; Score 444.5; DB 2; Length 237;  
Best Local Similarity 41.1%; Pred. No. 2.1e-26;  
RESULT 1421  
ID ABM82643 standard; protein; 227 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2892.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 32.2%; Score 443; DB 8; Length 227;  
Best Local Similarity 39.6%; Pred. No. 2.7e-26;  
RESULT 1422  
ID AAR84670 standard; protein; 238 AA.  
DE Mature kallikrein hk2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.1%; Score 441.5; DB 2; Length 238;  
Best Local Similarity 40.9%; Pred. No. 3.6e-26;  
RESULT 1423  
ID AAR94526 standard; protein; 279 AA.  
DE Korean Viper Salmons thrombin-like protease, Halybin.  
PN EP07067-A2.  
PD 17-APR-1996.  
PA (MOGAM) MOGAM BIOTECHNOLOGY RES INST.  
Query Match 32.0%; Score 439; DB 2; Length 279;  
Best Local Similarity 37.7%; Pred. No. 6.7e-26;  
RESULT 1424  
ID AAG79000 standard; protein; 233 AA.  
DE Mamushi fibrinolytic enzyme, brevinase.  
PN KR2001045716-A.  
PD 05-JUN-2001.  
PA (LEEJ-) LEE J W.  
PA (PARK-) PARK W.  
Query Match 31.8%; Score 436.5; DB 4; Length 233;  
Best Local Similarity 37.9%; Pred. No. 8.7e-26;  
RESULT 1425  
ID AAM52944 standard; protein; 260 AA.  
DE Agkistrodon halys brevicaudus thrombin-like protease, salmobin.

PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 31.7%; Score 436; DB 2; Length 260;  
Best Local Similarity 36.1%; Pred. No. 1.1e-25;  
RESULT 1426  
ID AAB50447 standard; protein; 205 AA.  
DE Human prostate cancer-related intracellular protein #1.  
PN WO200071711-A2.  
PD 30-NOV-2000.  
PA (SAAT/) SAATCIOGLU F.  
Query Match 31.4%; Score 431.5; DB 4; Length 205;  
Best Local Similarity 44.2%; Pred. No. 1.8e-25;  
RESULT 1427  
ID ADE78966 standard; protein; 227 AA.  
DE Human protein modification and maintenance molecule (PMMW)-4.  
PN WO2003063688-A2.  
PD 07-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 430; DB 7; Length 227;  
Best Local Similarity 39.2%; Pred. No. 2.7e-25;  
RESULT 1428  
ID AAW69388 standard; protein; 205 AA.  
DE Prostate tumour specific gene clone DE13 protein.  
PN WO9837418-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1429  
ID AAW71872 standard; protein; 205 AA.  
DE Protein encoded by prostate tumour clone P703 splice variant DE13.  
PN WO9837093-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1430  
ID AAY82005 standard; protein; 205 AA.  
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.  
PN WO200004149-A2.  
PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1431  
ID ABG94414 standard; protein; 205 AA.  
DE Human prostate tumour protein partial variant sequence #2.  
PN US2002090372-A1.  
PD 11-JUL-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1432  
ID AAM01120 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1433  
ID AAU69766 standard; protein; 205 AA.  
DE Human prostate cDNA encoded protein #6.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1434  
ID AAB74803 standard; protein; 205 AA.  
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.

PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1435  
ID AAG99005 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1436  
ID ABU71656 standard; protein; 205 AA.  
DE Prostate cancer specific antigen P703P #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1437  
ID AAU04964 standard; protein; 205 AA.  
DE Human prostate tumour protein DE13.  
PN US6262245-B1.  
PD 17-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1438  
ID ABB95225 standard; protein; 205 AA.  
DE Human P703P-DE13 protein SEQ ID NO 176.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Query Match 31.0%; Score 426.5; DB 5; Length 205;

Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1439  
ID ABG76668 standard; protein; 205 AA.  
DE Prostate tumour protein #6.  
PN US2002081580-A1.  
PD 27-JUN-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 31.0%; Score 426.5; DB 5; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1440  
ID ABR54337 standard; protein; 205 AA.  
DE Prostate tumour specific protein sequence SEQ ID 176.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 6; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1441  
ID ADB13626 standard; protein; 205 AA.  
DE Human prostate specific protein P703P-DE13.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 7; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1442  
ID ADG26042 standard; protein; 205 AA.  
DE Human prostate-specific polypeptide #6.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 7; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1443  
ID ABB09589 standard; protein; 234 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 30.7%; Score 422.5; DB 5; Length 234;  
Best Local Similarity 36.4%; Pred. No. 1e-24;  
RESULT 1444  
ID ADK36957 standard; protein; 281 AA.  
DE Novel human polypeptide SeqID9039.  
PN WO200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 30.7%; Score 422.5; DB 5; Length 281;  
Best Local Similarity 39.3%; Pred. No. 1.3e-24;  
RESULT 1445  
ID ABU92024 standard; protein; 218 AA.  
DE Human protein modification and maintenance molecule-4 (PMMW-4).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 30.7%; Score 422; DB 6; Length 218;  
Best Local Similarity 37.8%; Pred. No. 1.1e-24;  
RESULT 1446  
ID AAB31579 standard; peptide; 225 AA.  
DE Amino acid sequence of cod trypsin isozyms.  
PN WO200078332-A2.  
PD 28-DEC-2000.  
PA (BJAR/) BJARNASON J B.  
Query Match 30.6%; Score 421; DB 4; Length 225;  
Best Local Similarity 44.3%; Pred. No. 1.3e-24;  
RESULT 1447  
ID ADE15982 standard; protein; 218 AA.  
DE G-coupled protein receptor related polypeptide, SEQ ID NO 12.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 30.6%; Score 420; DB 7; Length 218;

Best Local Similarity 37.8%; Pred. No. 1.5e-24;  
ID ADL93921 standard; protein; 218 AA.  
DE Human G-coupled protein receptor-related protein #6.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL//) LI L.  
PA (GERL//) GERLACH V.  
PA (LIUX//) LIU X.  
PA (MILL//) MILLER C E.  
PA (SPVT//) SPYTEK K A.  
PA (ZERH//) ZERHUSEN B D.  
PA (PENA//) PENA C E A.  
PA (SHEN//) SHENOY S G.  
PA (ZHON//) ZHONG H.  
PA (SMIT//) SMITHSON G.  
PA (CASM//) CASMAN S J.  
PA (BOLD//) BOLDOG F L.  
PA (VOSS//) VOSS E Z.  
PA (VERN//) VERNET C A.  
PA (MACD//) MACDOUGALL J R.  
PA (RAST//) RASTELLI L.  
PA (ANDE//) ANDERSON D W.  
PA (ZHON//) ZHONG M.  
PA (MEZE//) MEZES P S.  
PA (FURT//) FURTAK K.  
PA (PATT//) PATTURAJAN M.  
PA (BURG//) BURGESS C E.  
PA (MALY//) MALYANKAR U M.  
PA (SHIM//) SHIMKETS R A.  
PA (TAUP//) TAUPIER R J.  
PA (EDIN//) EDINGER S.  
PA (MAZU//) MAZUR A.  
Query Match 30.6%; Score 420; DB 8; Length 218;  
Best Local Similarity 37.8%; Pred. No. 1.5e-24;  
RESULT 1449  
ID AAY28641 standard; protein; 207 AA.  
DE Human secreted protein from cDNA clone HKAET41.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 30.4%; Score 418; DB 2; Length 207;  
Best Local Similarity 46.1%; Pred. No. 2e-24;  
RESULT 1450  
ID AAW46773 standard; protein; 233 AA.  
DE Amino acid sequence of Salmonase.  
PN EP814164-A2.  
PD 29-DEC-1997.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match 30.4%; Score 417.5; DB 2; Length 233;  
Best Local Similarity 36.6%; Pred. No. 2.5e-24;  
RESULT 1451  
ID AAE21442 standard; protein; 226 AA.  
DE Human trypsin domain consensus protein #2.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 30.3%; Score 416.5; DB 5; Length 226;  
Best Local Similarity 42.6%; Pred. No. 2.9e-24;  
RESULT 1452  
ID ABG75786 standard; protein; 226 AA.  
DE Trypsin domain consensus sequence, SMART.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Query Match 30.3%; Score 416.5; DB 6; Length 226;  
Best Local Similarity 42.6%; Pred. No. 2.9e-24;  
RESULT 1453  
ID ADA05736 standard; protein; 198 AA.  
DE Human NOV18c protein SEQ ID NO:96.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.

Query Match 30.0%; Score 412.5; DB 6; Length 198;  
Best Local Similarity 36.8%; Pred. No. 5.2e-24;  
RESULT 1454  
ID ADNG2900 standard; protein; 198 AA.  
DE Human NOV18c.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT//) SMITHSON G.  
PA (MILL//) MILLET I.  
PA (PEYM//) PEYMAN J A.  
PA (KEKU//) KEKUDA R.  
PA (JUJU//) JU J.  
PA (LILL//) LI L.  
PA (GUOX//) GUO X.  
PA (PATT//) PATTURAJAN M.  
PA (SPYT//) SPYTEK K A.  
PA (EDIN//) EDINGER S R.  
PA (ELLE//) ELLERMAN K.  
PA (MALY//) MALYANKAR U M.  
PA (ORTT//) ORT T.  
PA (GORM//) GORMAN L.  
PA (ZERH//) ZERHUSEN B D.  
PA (ANDE//) ANDERSON D W.  
PA (ZHON//) ZHONG M.  
PA (CATT//) CATTERTON E.  
PA (JIWW//) JI W.  
PA (MILL//) MILLER C E.  
PA (RAST//) RASTELLI L.  
PA (STON//) STONE D J.  
PA (PENA//) PENA C E A.  
PA (SHEN//) SHENOY S G.  
PA (SHIM//) SHIMKETS R A.  
PA (ROTH//) ROTHENBERG M E.  
PA (LEAC//) LEACH M D.  
PA (AGEE//) AGEE M L.  
PA (BERG//) BERGHS C.  
PA (DIP//) DIPPO V A.  
PA (EISE//) EISEN A.  
PA (GANG//) GANGOLLI E A.  
PA (RIEG//) RIEGER D K.  
PA (SPAD//) SPADERNA S K.  
Query Match 30.0%; Score 412.5; DB 8; Length 198;  
Best Local Similarity 36.8%; Pred. No. 5.2e-24;  
RESULT 1455  
ID ADA50560 standard; protein; 194 AA.  
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 29.8%; Score 409; DB 6; Length 194;  
Best Local Similarity 38.7%; Pred. No. 9.5e-24;  
RESULT 1456  
ID ADG75684 standard; protein; 215 AA.  
DE Human protein modification and maintenance molecule polypeptide SeqID8.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 29.8%; Score 409; DB 7; Length 215;  
Best Local Similarity 37.1%; Pred. No. 1.1e-23;  
RESULT 1457  
ID ABM82829 standard; protein; 215 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3078.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.8%; Score 409; DB 8; Length 215;  
Best Local Similarity 37.1%; Pred. No. 1.1e-23;  
RESULT 1458  
ID ABM83248 standard; protein; 299 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3497.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

Query Match 29.8%; Score 409; DB 8; Length 299;  
Best Local Similarity 38.6%; Pred. No. 1.5e-23;  
RESULT 1459  
ID ADA05738 standard; protein; 181 AA.  
DE Human NOV18d protein SEQ ID NO:198.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 29.7%; Score 408.5; DB 6; Length 181;  
Best Local Similarity 37.4%; Pred. No. 9.6e-24;  
RESULT 1460  
ID ADNG2902 standard; protein; 181 AA.  
DE Human NOV18d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 29.7%; Score 408.5; DB 8; Length 181;  
Best Local Similarity 37.4%; Pred. No. 9.6e-24;  
RESULT 1461  
ID ABM82641 standard; protein; 222 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.6%; Score 407; DB 8; Length 222;  
Best Local Similarity 36.7%; Pred. No. 1.6e-23;  
RESULT 1462  
ID AAB08510 standard; protein; 230 AA.  
DE A recombinant protein C activator polypeptide.  
PN WO200050613-A2.  
PD 31-AUG-2000.  
PA (INLI) INSTRUMENTATION LAB.  
Query Match 29.6%; Score 406.5; DB 3; Length 230;  
Best Local Similarity 36.2%; Pred. No. 1.8e-23;  
RESULT 1463  
ID AAW76538 standard; protein; 231 AA.  
DE A. contortrix protein C activator protein fragment.  
PN WO9842850-A1.  
PD 01-OCT-1998.  
PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match 29.6%; Score 406.5; DB 2; Length 231;  
Best Local Similarity 36.2%; Pred. No. 1.8e-23;  
RESULT 1464  
ID AB09590 standard; protein; 218 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 29.5%; Score 405.5; DB 5; Length 218;  
Best Local Similarity 36.5%; Pred. No. 2e-23;  
RESULT 1465  
ID ABM84665 standard; protein; 220 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.5%; Score 405; DB 8; Length 220;  
Best Local Similarity 36.7%; Pred. No. 2.2e-23;  
RESULT 1466  
ID AAB08511 standard; protein; 230 AA.  
DE Biosynthetic variant of protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI) INSTRUMENTATION LAB.  
Query Match 29.4%; Score 403.5; DB 3; Length 230;  
Best Local Similarity 37.0%; Pred. No. 3e-23;  
RESULT 1467  
ID AAR20557 standard; protein; 234 AA.  
DE Fibrinogenolytic protein #4 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (BADI) BASF AG.  
Query Match 29.3%; Score 403; DB 2; Length 234;  
Best Local Similarity 36.7%; Pred. No. 3.3e-23;  
RESULT 1468  
ID AAP81333 standard; protein; 255 AA.  
DE Batroxobin.  
PN JP63049084-A.  
PD 01-MAR-1988.  
PA (YAMA/) YAMASHINA I.  
Query Match 29.3%; Score 402; DB 1; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1469  
ID AAR05436 standard; protein; 255 AA.  
DE Batroxobin gene product.  
PN JP02124092-A.  
PD 11-MAY-1990.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 29.3%; Score 402; DB 2; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1470  
ID AAV17869 standard; protein; 255 AA.  
DE Araraca batroxobin.  
PN WO9929838-A1.  
PD 17-JUN-1999.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 29.3%; Score 402; DB 2; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1471  
ID AAE21441 standard; protein; 249 AA.  
DE Human trypsin domain consensus protein #1.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 29.2%; Score 401.5; DB 5; Length 249;  
Best Local Similarity 40.3%; Pred. No. 4.6e-23;  
RESULT 1472  
ID AAM52946 standard; protein; 231 AA.  
DE Batroxobin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 29.1%; Score 400; DB 2; Length 231;

Best Local Similarity 34.2%; Pred. No. 5.6e-23;  
RESULT 1473  
ID AAB11711 standard; protein; 264 AA.  
DE Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 28.8%; Score 395.5; DB 3; Length 264;  
Best Local Similarity 39.1%; Pred. No. 1.4e-22;  
RESULT 1474  
ID AAM52945 standard; protein; 236 AA.  
DE Flabobobin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 28.7%; Score 394; DB 2; Length 236;  
Best Local Similarity 36.8%; Pred. No. 1.7e-22;  
RESULT 1475  
ID AAR20556 standard; protein; 236 AA.  
DE Fibrinogenolytic protein #3 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (BADI ) BASF AG.  
Query Match 28.6%; Score 393; DB 2; Length 236;  
Best Local Similarity 37.3%; Pred. No. 2e-22;  
RESULT 1476  
ID ABM62831 standard; protein; 233 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.5%; Score 392; DB 8; Length 233;  
Best Local Similarity 36.8%; Pred. No. 2.3e-22;  
RESULT 1477  
ID AAE39993 standard; protein; 253 AA.  
DE Human adipsin protein #2.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.5%; Score 391; DB 7; Length 253;  
Best Local Similarity 38.0%; Pred. No. 3e-22;  
RESULT 1478  
ID ABG75785 standard; protein; 227 AA.  
DE Trypsin domain consensus sequence, PFAM.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Query Match 28.3%; Score 389; DB 6; Length 227;  
Best Local Similarity 40.4%; Pred. No. 3.9e-22;  
RESULT 1479  
ID ADE58223 standard; protein; 253 AA.  
DE Human Protein P00746, SEQ ID NO 4094.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 28.3%; Score 389; DB 7; Length 253;  
Best Local Similarity 38.5%; Pred. No. 4.3e-22;  
RESULT 1480  
ID AAP70758 standard; protein; 269 AA.  
DE Pig pancreas elastase-2.  
PN JP62000276-A.  
PD 06-JAN-1987.  
PA (SANY ) SANKYO CO LTD.  
Query Match 28.2%; Score 388; DB 1; Length 269;  
Best Local Similarity 38.5%; Pred. No. 5.5e-22;  
RESULT 1481  
ID AAE39992 standard; protein; 253 AA.  
DE Human adipsin protein #1.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.2%; Score 387; DB 7; Length 253;

Best Local Similarity 38.5%; Pred. No. 6.2e-22;  
RESULT 1482  
ID AAB11710 standard; protein; 264 AA.  
DE Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 28.1%; Score 386.5; DB 3; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1483  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSSET polypeptide clone name VCTRL-1.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.1%; Score 386.5; DB 6; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1484  
ID ABU09382 standard; protein; 271 AA.  
DE Consensus sequence of trypsin-like domain.  
PN WO2003031463-A2.  
PD 17-APR-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 28.1%; Score 386; DB 6; Length 271;  
Best Local Similarity 39.1%; Pred. No. 7.9e-22;  
RESULT 1485  
ID ABM62830 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1486  
ID ABM62644 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1487  
ID ABM81778 standard; protein; 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 28.1%; Score 385.5; DB 8; Length 264;  
Best Local Similarity 36.8%; Pred. No. 8.4e-22;  
RESULT 1488  
ID ADR66037 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;  
RESULT 1489  
ID ADR66935 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;

RESULT 1490  
ID AAP61724 standard; protein; 269 AA.  
DE Porcine elastase II.  
PN JP61192289-A.  
PD 26-AUG-1986.  
PA (KIRI ) KIRIN BREWERY KK.  
Query Match 27.9%; Score 384; DB 1; Length 269;  
Best Local Similarity 38.4%; Pred. No. 1.1e-21;  
RESULT 1491  
ID AAR07513 standard; protein; 258 AA.  
DE Ancrod-like polypeptide #2.  
PN EP395375-A.  
PD 31-OCT-1990.  
PA (GLAX ) GLAXO INC.  
PA (KNOL ) KNOLL AG.  
Query Match 27.9%; Score 383; DB 2; Length 258;  
Best Local Similarity 34.3%; Pred. No. 1.3e-21;  
RESULT 1492  
ID AAR05775 standard; protein; 272 AA.  
DE Snake venom ancrod polypeptide.  
PN WO9006362-A.  
PD 14-JUN-1990.  
PA (BADI ) BASF AG.  
PA (BACH/) BACH A.  
Query Match 27.9%; Score 383; DB 2; Length 272;  
Best Local Similarity 33.9%; Pred. No. 1.4e-21;  
RESULT 1493  
ID AAU79393 standard; protein; 171 AA.  
DE Novel human kallikrein KLIK15, splice variant #3.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 5; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1494  
ID ADNI0933 standard; protein; 171 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 8; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1495  
ID ABM82642 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2891.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 27.8%; Score 382; DB 8; Length 212;  
Best Local Similarity 35.5%; Pred. No. 1.2e-21;  
RESULT 1496  
ID AAR05772 standard; protein; 250 AA.  
DE Human adipin gene product from the clone phg31.  
PN WO9006365-A.  
PD 14-JUN-1990.  
PA (DANA-) DANA-FARBER CANCER INST.  
PA (META-) METABOLIC BIOSYSTEMS INC.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 37.2%; Pred. No. 1.5e-21;  
RESULT 1497  
ID AAR05421 standard; protein; 250 AA.  
DE Human adipin/D encoded by a cDNA.  
PN WO9001540-A.  
PD 22-FEB-1990.  
PA (CALB-) CALIF BIOTECHN INC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 38.4%; Pred. No. 1.5e-21;  
RESULT 1498  
ID ADE58221 standard; protein; 263 AA.  
DE Rat Protein AAB31922, SEQ ID NO 4092.  
PN WO2003016475-A2.

PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 27.7%; Score 381; DB 7; Length 263;  
Best Local Similarity 37.6%; Pred. No. 1.9e-21;  
RESULT 1499  
ID ADN99596 standard; protein; 187 AA.  
DE Novel human protein sequence #412.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 27.6%; Score 379.5; DB 8; Length 187;  
Best Local Similarity 42.7%; Pred. No. 1.7e-21;  
RESULT 1500  
ID ABU92049 standard; protein; 220 AA.  
DE Human protein modification and maintenance molecule-29 (PMM-29).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 27.6%; Score 379; DB 6; Length 220;  
Best Local Similarity 37.2%; Pred. No. 2.2e-21;



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OM protein - protein search, using sw model

Run on: March 5, 2005, 20:31:44 ; Search time 42 Seconds  
(without alignments)  
440.785 Million cell u

**Title:** US-10-015-385A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVITYICKYVDWIRMIRNN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

FOC-Processing: Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*

1: /cqn2 6/ptodata/1/iaa/5A COMB.pep:\*

```
1: /cgn2_5/ptodata/1/1aa/5B COMB.pcp:
2: /cgn2_6/ptodata/1/1aa/5B COMB.pcp: *
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3: /cgn2 6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pcp:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1359.5	98.9	249	4	US-09-949-016-8151	Sequence 8151, Ap
2	1301.94	94.7	254	4	US-09-949-016-6948	Sequence 6948, Ap
3	881	59.0	162	4	US-09-244-111-6	Sequence 6, Appli
4	630.5	45.9	260	4	US-09-618-259-7	Sequence 7, Appli
5	626.5	45.6	260	3	US-09-070-526-2	Sequence 2, Appli
6	622.5	45.3	260	3	US-09-025-059-3	Sequence 3, Appli
7	622.5	45.3	260	3	US-09-008-271A-7	Sequence 7, Appli
8	622.5	45.3	260	4	US-09-618-259-8	Sequence 8, Appli
9	618.5	45.0	250	4	US-09-205-258-427	Sequence 427, App
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11	602.5	43.9	288	4	US-09-386-642-13	Sequence 13, Appl
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13	597.5	43.5	248	3	US-08-944-483-24	Sequence 24, Appl
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15	567	41.3	290	4	US-09-949-016-8166	Sequence 8166, Ap
16	564.5	41.1	270	4	US-09-949-016-7712	Sequence 7712, Ap
17	564.5	41.1	293	4	US-09-509-908-2	Sequence 2, Appli
18	564	41.0	276	1	US-08-467-155A-1	Sequence 1, Appli
19	564	41.0	276	2	US-08-628-198-1	Sequence 1, Appli
20	564	41.0	276	3	US-09-201-038-1	Sequence 1, Appli
21	564	41.0	276	5	PCF-US96-07343-1	Sequence 1, Appli
22	563	41.0	325	4	US-09-949-016-7713	Sequence 7713, Ap
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24	555	40.4	253	2	US-08-557-146-2	Sequence 2, Appli
25	555	40.4	253	2	US-08-824-874-3	Sequence 3, Appli
26	555	40.4	253	2	US-09-154-344-2	Sequence 2, Appli
27	555	40.4	253	3	US-08-930-188-2	Sequence 2, Appli

101	494	36.0	254	4	US-09-685-166A-523	Sequence 523, App	174	458	33.3	228	2	US-08-296-149-7	Sequence 7, Appli
102	494	36.0	254	4	US-09-679-426-523	Sequence 523, App	175	458	33.3	228	2	US-08-801-499-7	Sequence 7, Appli
103	494	36.0	254	4	US-09-759-143-523	Sequence 523, App	176	458	33.3	228	2	US-08-615-271-7	Sequence 7, Appli
104	494	36.0	254	4	US-09-651-236-523	Sequence 523, App	177	458	33.3	228	3	US-09-074-660-7	Sequence 7, Appli
105	493	35.9	262	2	US-08-790-131-1	Sequence 1, Appli	178	458	33.3	228	3	US-09-074-659-7	Sequence 7, Appli
106	493	35.9	262	2	US-08-790-137-3	Sequence 3, Appli	179	458	33.3	228	3	US-09-106-468-7	Sequence 7, Appli
107	493	35.9	262	2	US-08-681-151-4	Sequence 4, Appli	180	458	33.3	228	3	US-09-106-466A-7	Sequence 7, Appli
108	493	35.9	262	2	US-08-824-874-4	Sequence 4, Appli	181	458	33.3	228	3	US-09-106-467-7	Sequence 7, Appli
109	493	35.9	262	3	US-08-807-151-4	Sequence 4, Appli	182	457.5	33.3	237	3	US-08-768-859A-1	Sequence 1, Appli
110	493	35.9	262	3	US-09-210-084-4	Sequence 4, Appli	183	457.5	33.3	237	3	US-08-767-820A-1	Sequence 1, Appli
111	493	35.9	262	3	US-09-478-957-4	Sequence 4, Appli	184	457.5	33.3	237	3	US-08-622-046B-7	Sequence 7, Appli
112	493	35.8	262	4	US-09-764-762-4	Sequence 4, Appli	185	457.5	33.3	237	3	US-08-622-046B-38	Sequence 38, Appli
113	492	35.8	225	2	US-09-027-337-5	Sequence 5, Appli	186	457.5	33.3	237	3	US-08-944-483-38	Sequence 3, Appli
114	492	35.8	225	4	US-09-644-600-5	Sequence 5, Appli	187	457.5	33.3	237	4	US-09-100-264-3	Sequence 2, Appli
115	492	35.8	225	4	US-09-654-600A-5	Sequence 5, Appli	188	457.5	33.3	237	4	US-08-303-339-2	Sequence 7, Appli
116	492	35.8	262	1	US-08-744-026-4	Sequence 4, Appli	189	457.5	33.3	237	4	US-08-843-076D-7	Sequence 1, Appli
117	492	35.8	262	2	US-09-102-732-4	Sequence 4, Appli	190	455.5	33.2	237	1	US-09-303-208-1	Sequence 11, Appli
118	492	35.8	262	3	US-09-261-767-4	Sequence 4, Appli	191	455.5	33.2	237	5	PCT-US94-07329-11	Sequence 11, Appli
119	491	35.7	221	4	US-09-959-392-33	Sequence 33, Appli	192	455.5	33.2	237	5	PCT-US95-06157-1	Sequence 1, Appli
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121	487.5	35.5	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	33.2	261	3	US-08-767-820A-19	Sequence 19, Appli
122	487.5	35.5	449	4	US-09-685-168A-617	Sequence 617, App	195	455.5	33.2	261	3	US-08-622-046B-3	Sequence 3, Appli
123	487.5	35.5	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	33.1	232	2	US-08-897-340-31	Sequence 31, Appli
124	487.5	35.5	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	33.1	232	3	US-09-252-329-31	Sequence 31, Appli
125	487.5	35.5	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	33.1	244	5	PCT-US95-06157-10	Sequence 10, Appli
126	487	35.4	224	2	US-08-766-982-13	Sequence 13, Appli	199	452.5	32.9	238	5	PCT-US95-06157-8	Sequence 8, Appli
127	487	35.4	224	3	US-08-944-483-36	Sequence 36, Appli	200	452.5	32.9	244	3	US-08-768-859A-10	Sequence 10, Appli
128	487	35.4	224	3	US-09-296-219-13	Sequence 13, Appli	201	452.5	32.9	244	3	US-08-767-820A-10	Sequence 10, Appli
129	478	34.4	224	3	US-08-944-483-35	Sequence 35, Appli	202	452.5	32.9	244	3	US-08-622-046B-16	Sequence 16, Appli
130	472.5	34.4	220	3	US-09-439-313-327	Sequence 327, App	203	452.5	32.9	244	3	US-09-100-264-5	Sequence 5, Appli
131	472.5	34.4	220	3	US-09-352-616A-327	Sequence 327, App	204	452.5	32.9	244	4	US-08-843-076D-5	Sequence 5, Appli
132	472.5	34.4	220	4	US-09-232-149A-327	Sequence 327, App	205	450.5	32.8	237	2	US-08-844-024-2	Sequence 2, Appli
133	472.5	34.4	220	4	US-09-636-215-327	Sequence 327, App	206	450.5	32.8	237	2	US-08-718-547-2	Sequence 2, Appli
134	472.5	34.4	220	4	US-09-685-168A-327	Sequence 327, App	207	450.5	32.8	237	3	US-08-768-859A-16	Sequence 16, Appli
135	472.5	34.4	220	4	US-09-688-488-327	Sequence 327, App	208	450.5	32.8	237	3	US-08-767-820A-16	Sequence 16, Appli
136	472.5	34.4	220	4	US-09-679-426-327	Sequence 327, App	209	450.5	32.8	237	3	US-08-622-046B-12	Sequence 12, Appli
137	472.5	34.4	220	4	US-09-759-143-327	Sequence 327, App	210	450.5	32.8	237	3	US-08-944-483-37	Sequence 37, Appli
138	472.5	34.4	220	4	US-09-651-236-327	Sequence 327, App	211	450.5	32.8	237	4	US-09-100-264-1	Sequence 1, Appli
139	472.5	34.4	262	4	US-09-618-259-9	Sequence 9, Appli	212	450.5	32.8	237	4	US-08-843-076D-1	Sequence 1, Appli
140	470.5	34.2	261	1	US-08-744-026-5	Sequence 5, Appli	213	450.5	32.8	238	3	US-08-768-859A-8	Sequence 8, Appli
141	470.5	34.2	261	2	US-09-102-732-5	Sequence 5, Appli	214	450.5	32.8	238	3	US-08-767-820A-8	Sequence 8, Appli
142	470.5	34.2	261	3	US-09-083-521-6	Sequence 6, Appli	215	450	32.8	260	3	US-08-983-075D-9	Sequence 9, Appli
143	470.5	34.2	261	3	US-09-261-767-5	Sequence 5, Appli	216	449.5	32.7	244	3	US-08-622-046B-5	Sequence 10, Appli
144	470.5	34.2	261	4	US-09-413-049-1	Sequence 1, Appli	217	448.5	32.6	237	1	US-08-096-946-10	Sequence 10, Appli
145	470.5	34.2	261	4	US-09-907-402-1	Sequence 1, Appli	218	448.5	32.6	237	5	PCT-US94-07329-10	Sequence 10, Appli
146	470.5	34.2	261	4	US-09-618-259-10	Sequence 10, Appli	219	448.5	32.6	237	5	PCT-US95-06157-16	Sequence 16, Appli
147	470.5	34.2	375	4	US-09-755-100A-11	Sequence 11, Appli	220	447.5	32.6	237	3	US-08-768-859A-21	Sequence 21, Appli
148	470	34.2	238	3	US-08-944-483-39	Sequence 39, Appli	221	447.5	32.6	237	3	US-08-767-820A-21	Sequence 21, Appli
149	469.5	34.2	271	1	US-08-467-155A-10	Sequence 10, Appli	222	447.5	32.6	237	3	US-08-622-046B-1	Sequence 1, Appli
150	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	223	447.5	32.6	237	4	US-08-843-076D-8	Sequence 8, Appli
151	469.5	34.2	271	3	US-09-201-038-10	Sequence 10, Appli	224	447.5	32.6	237	4	US-08-472-228A-1	Sequence 1, Appli
152	469.5	34.2	271	5	PCT-US96-07343-10	Sequence 10, Appli	225	445	32.4	240	3	US-09-146-831-1	Sequence 1, Appli
153	469	34.1	284	4	US-09-386-642-54	Sequence 54, Appli	226	445	32.4	240	3	PCT-US96-09303-1	Sequence 1, Appli
154	464.5	33.8	286	1	US-08-467-155A-9	Sequence 9, Appli	227	445	32.4	240	5	US-08-467-155A-8	Sequence 8, Appli
155	464.5	33.8	286	2	US-08-628-198-9	Sequence 9, Appli	228	430	31.3	299	1	US-08-628-198-8	Sequence 8, Appli
156	464.5	33.8	286	5	PCT-US96-07343-9	Sequence 9, Appli	229	430	31.3	299	2	US-09-201-038-8	Sequence 8, Appli
157	464.5	33.5	261	5	US-09-201-038-9	Sequence 9, Appli	230	430	31.3	299	5	PCT-US96-07343-8	Sequence 8, Appli
158	460.5	33.5	261	5	US-09-651-236-6	Sequence 6, Appli	231	430	31.3	299	5	US-09-020-956-176	Sequence 176, App
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162	458.5	33.4	261	3	US-08-768-859A-6	Sequence 6, Appli	235	426.5	31.0	205	3	US-09-233-149A-176	Sequence 176, App
163	458.5	33.4	261	3	US-08-767-820A-6	Sequence 6, Appli	236	426.5	31.0	205	4	US-09-159-813-176	Sequence 176, App
164	458.5	33.4	261	3	US-08-622-046B-14	Sequence 14, Appli	237	426.5	31.0	205	4	US-09-636-215-176	Sequence 176, App
165	458.5	33.4	261	3	US-09-100-264-7	Sequence 7, Appli	238	426.5	31.0	205	4	US-09-683-166A-176	Sequence 176, App
166	458.5	33.4	261	3	US-08-983-075D-7	Sequence 7, Appli	239	426.5	31.0	205	4	US-09-115-453-176	Sequence 176, App
167	458.5	33.4	261	4	US-08-843-076D-3	Sequence 3, Appli	240	426.5	31.0	205	4	US-09-688-489-176	Sequence 176, App
168	458.5	33.4	278	4	US-09-949-016-7711	Sequence 7711, Ap	241	426.5	31.0	205	4	US-09-679-426-176	Sequence 176, App
169	458	33.3	228	1	US-08-278-091-7	Sequence 7, Appli	242	426.5	31.0	205	4	US-09-759-143-176	Sequence 176, App
170	458	33.3	228	1	US-08-483-859-7	Sequence 7, Appli	243	426.5	31.0	205	4	US-09-651-236-176	Sequence 176, App
171	458	33.3	228	1	US-08-472-173-7	Sequence 7, Appli	244	426.5	31.0	205	4	US-09-244-111-4	Sequence 4, Appli
172	458	33.3	228	2	US-08-487-167-7	Sequence 7, Appli	245	418	30.4	207	4	US-08-738-413B-9	Sequence 9, Appli
173	458	33.3	228	2	US-08-482-816-7	Sequence 7, Appli	246	417.5	30.4	233	2		

247	406.5	29.6	231	4	US-09-402-515A-16	Sequence 16, Appl	320	354	25.8	461	6	5270178-18	Patent No. 5270178
248	404	29.4	234	1	US-08-684-862-6	Sequence 6, Appl	321	354	25.8	461	6	5270178-17	Patent No. 5270178
249	393	28.6	236	1	US-08-684-862-5	Sequence 5, Appl	322	354	25.8	461	6	5270178-18	Patent No. 5270178
250	389	28.3	236	2	US-08-738-413B-10	Sequence 10, Appl	323	353.5	25.7	230	3	US-08-944-483-62	Sequence 62, Appl
251	387	28.2	253	6	5223425-8	Patent No. 5223425	324	353.5	25.7	270	2	US-08-978-404B-8	Sequence 8, Appl
252	387	28.2	253	6	5223425-8	Patent No. 5223425	325	353	25.7	274	2	US-08-978-404B-5	Sequence 5, Appl
253	385.5	28.1	267	4	US-09-949-016-9575	Sequence 9575, Ap	326	353	25.7	314	3	US-09-008-271A-3	Sequence 3, Appl
254	385	28.0	232	2	US-08-738-413B-11	Sequence 11, Appl	327	353	25.7	314	4	US-09-023-942A-6	Sequence 6, Appl
255	385	28.0	250	6	5223425-4	Patent No. 5223425	328	353	25.7	314	4	US-09-907-794A-257	Sequence 257, App
256	385	28.0	250	6	5223425-4	Patent No. 5223425	329	353	25.7	314	4	US-09-905-125A-257	Sequence 257, App
257	377.5	27.3	154	3	US-09-261-416-5	Sequence 5, Appl	330	353	25.7	314	4	US-09-902-775A-257	Sequence 257, App
258	374.5	27.3	238	6	5223425-5	Patent No. 5223425	331	353	25.7	314	4	US-09-906-700-257	Sequence 257, App
259	374.5	27.3	238	6	5223425-5	Patent No. 5223425	332	353	25.7	314	4	US-09-903-603A-257	Sequence 257, App
260	374.5	27.3	259	6	5223425-2	Patent No. 5223425	333	353	25.7	314	4	US-09-904-920A-257	Sequence 257, App
261	374.5	27.3	259	6	5223425-2	Patent No. 5223425	334	353	25.7	314	4	US-09-909-064-257	Sequence 257, App
262	374	27.2	260	6	5223425-10	Patent No. 5223425	335	353	25.7	314	4	US-09-905-381A-257	Sequence 257, App
263	374	27.2	260	6	5223425-10	Patent No. 5223425	336	353	25.7	314	4	US-09-906-618-257	Sequence 257, App
264	370.5	27.0	228	3	US-08-944-483-44	Sequence 44, Appl	337	351.5	25.6	814	1	US-08-750-711-1	Sequence 1, Appl
265	370	26.9	418	4	US-09-370-838-62	Sequence 62, Appl	338	349.5	25.4	166	4	US-09-636-215-838	Sequence 838, App
266	370	26.9	418	4	US-09-854-133-62	Sequence 62, Appl	339	349.5	25.4	166	4	US-09-685-166A-838	Sequence 838, App
267	368	26.8	418	1	US-08-508-448C-25	Sequence 25, Appl	340	349.5	25.4	166	4	US-09-679-426-838	Sequence 838, App
268	368	26.8	418	4	US-09-370-838-82	Sequence 82, Appl	341	349.5	25.4	166	4	US-09-759-143-838	Sequence 838, App
269	368	26.8	418	4	US-09-370-838-83	Sequence 83, Appl	342	349.5	25.4	166	4	US-09-651-236-838	Sequence 838, App
270	368	26.8	418	4	US-09-854-133-82	Sequence 82, Appl	343	349	25.4	159	3	US-09-020-955-172	Sequence 172, App
271	368	26.8	418	4	US-09-854-133-83	Sequence 83, Appl	344	349	25.4	159	3	US-09-030-607-172	Sequence 172, App
272	366.5	26.7	149	3	US-09-518-046-20	Sequence 20, Appl	345	349	25.4	159	3	US-09-439-313-172	Sequence 172, App
273	366	26.6	232	1	US-08-508-448C-19	Sequence 19, Appl	346	349	25.4	159	3	US-09-352-616A-172	Sequence 172, App
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278	365.5	26.6	245	3	US-08-639-075A-121	Sequence 121, App	351	349	25.4	159	4	US-09-115-453-172	Sequence 172, App
279	365.5	26.6	245	3	US-09-012-431-121	Sequence 121, App	352	349	25.4	159	4	US-09-688-489-172	Sequence 172, App
280	365.5	26.6	245	3	US-08-906-613-121	Sequence 121, App	353	349	25.4	159	4	US-09-679-426-172	Sequence 172, App
281	364.5	26.5	400	3	US-09-004-731-30	Sequence 30, Appl	354	349	25.4	159	4	US-09-759-143-172	Sequence 172, App
282	364.5	26.5	400	3	US-09-004-731-33	Sequence 33, Appl	355	349	25.4	159	4	US-09-651-236-172	Sequence 172, App
283	364.5	26.5	400	3	US-08-749-693-30	Sequence 30, Appl	356	349	25.4	1019	1	US-08-296-014A-4	Sequence 4, Appl
284	364.5	26.5	400	3	US-08-749-693-33	Sequence 33, Appl	357	349	25.4	1019	2	US-08-596-405-4	Sequence 4, Appl
285	364.5	26.5	400	3	US-09-004-729-30	Sequence 30, Appl	358	349	25.4	1019	2	US-08-877-620-4	Sequence 4, Appl
286	364.5	26.5	400	4	US-09-004-729-33	Sequence 33, Appl	359	349	25.4	1019	4	US-09-287-368-4	Sequence 4, Appl
287	362.5	26.4	242	3	US-09-004-731-36	Sequence 36, Appl	360	349	25.4	1019	4	US-09-626-795-4	Sequence 4, Appl
288	362.5	26.4	242	3	US-08-749-693-36	Sequence 36, Appl	361	349	25.4	1083	1	US-08-296-014A-2	Sequence 2, Appl
289	362.5	26.4	242	4	US-09-004-729-36	Sequence 36, Appl	362	349	25.4	1083	2	US-08-596-405-2	Sequence 2, Appl
290	362.5	26.4	319	4	US-09-386-642-12	Sequence 12, Appl	363	349	25.4	1083	2	US-08-877-620-2	Sequence 2, Appl
291	362.5	26.4	328	4	US-09-386-642-11	Sequence 11, Appl	364	349	25.4	1083	4	US-09-287-368-2	Sequence 2, Appl
292	361.5	26.3	387	3	US-09-032-215-8	Sequence 8, Appl	365	349	25.4	1083	4	US-09-626-795-2	Sequence 2, Appl
293	361.5	26.3	387	3	US-09-032-215-13	Sequence 13, Appl	366	348	25.3	461	6	5460953-3	Patent No. 5460953
294	361	26.3	236	1	US-08-684-862-4	Sequence 4, Appl	367	348	25.3	461	6	5460953-3	Patent No. 5460953
295	360.5	26.2	299	3	US-08-944-483-66	Sequence 66, Appl	368	347	25.3	262	1	US-07-720-189-1	Sequence 1, Appl
296	358.5	26.1	232	4	US-09-959-392-31	Sequence 31, Appl	369	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
297	358	26.1	812	4	US-08-991-761A-7	Sequence 7, Appl	370	347	25.3	409	3	US-09-065-872-2	Sequence 2, Appl
298	357.5	26.0	232	3	US-08-906-769-81	Sequence 81, Appl	371	347	25.3	409	4	US-09-667-570A-2	Sequence 2, Appl
299	357.5	26.0	232	3	US-08-906-616-81	Sequence 81, Appl	372	347	25.3	410	3	US-09-065-872-1	Sequence 1, Appl
300	357.5	26.0	232	3	US-08-817-795-81	Sequence 81, Appl	373	347	25.3	410	4	US-09-667-570A-1	Sequence 1, Appl
301	357.5	26.0	232	3	US-08-639-075A-81	Sequence 81, Appl	374	347	25.3	419	1	US-08-295-411-1	Sequence 1, Appl
302	357.5	26.0	232	3	US-09-012-431-81	Sequence 81, Appl	375	347	25.3	419	2	US-08-955-471-1	Sequence 1, Appl
303	357.5	26.0	232	3	US-09-012-692-81	Sequence 81, Appl	376	347	25.3	419	4	US-09-667-570A-3	Sequence 3, Appl
304	357.5	26.0	232	3	US-08-906-613-81	Sequence 81, Appl	377	347	25.3	419	4	US-10-182-263-1	Sequence 1, Appl
305	357.5	26.0	232	5	PCT-US95-14442A-81	Sequence 81, Appl	378	347	25.3	419	5	PCT-US92-10242-1	Sequence 1, Appl
306	357	26.0	268	4	US-09-949-016-10712	Sequence 10712, A	379	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appl
307	356.5	25.9	248	3	US-08-944-483-63	Sequence 63, Appl	380	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appl
308	355.5	25.9	148	4	US-09-618-259-2	Sequence 2, Appl	381	347	25.3	461	4	US-10-182-263-2	Sequence 2, Appl
309	355.5	25.9	231	2	US-09-027-337-6	Sequence 6, Appl	382	347	25.3	461	4	US-09-054-272-32	Sequence 32, Appl
310	355.5	25.9	231	4	US-09-644-600-6	Sequence 6, Appl	383	347	25.3	461	4	US-09-949-016-5921	Sequence 5921, Ap
311	355.5	25.9	231	4	US-09-654-600A-6	Sequence 6, Appl	384	347	25.3	461	6	5225537-2	Patent No. 5225537
312	355.5	25.9	276	2	US-09-016-366A-15	Sequence 15, Appl	385	347	25.3	461	6	5225537-2	Patent No. 5225537
313	355.5	25.9	276	2	US-08-978-404B-21	Sequence 21, Appl	386	347	25.3	485	4	US-09-949-016-10882	Sequence 10882, A
314	354.5	25.8	461	6	5270178-2	Patent No. 5270178	387	346.5	25.2	791	1	US-08-643-219-1	Sequence 1, Appl
315	354.5	25.8	461	6	5270178-2	Patent No. 5270178	388	346.5	25.2	791	3	US-08-851-350-1	Sequence 1, Appl
316	354	25.8	229	2	US-08-557-146-13	Sequence 13, Appl	389	346	25.2	234	3	US-08-944-483-46	Sequence 46, Appl
317	354	25.8	229	2	US-09-154-344-13	Sequence 13, Appl	390	346	25.2	241	3	US-08-944-483-59	Sequence 59, Appl
318	354	25.8	312	4	US-09-023-942A-4	Sequence 4, Appl	391	346	25.2	419	4	US-10-182-263-5	Sequence 5, Appl
319	354	25.8	461	6	5270178-17	Patent No. 5270178	392	346	25.2	419	4	US-10-182-263-6	Sequence 6, Appl

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334	345.5	25.1	248	3	US-08-906-616-111	Sequence 111, App	467	339.5	24.7	258	1	US-07-990-301A-2	Sequence 2, Appli
335	345.5	25.1	248	3	US-08-817-795-111	Sequence 111, App	468	339.5	24.7	333	4	US-08-991-761A-8	Sequence 8, Appli
336	345.5	25.1	248	3	US-08-633-075A-111	Sequence 111, App	469	339	24.7	419	4	US-10-182-263-4	Sequence 4, Appli
337	345.5	25.1	248	3	US-09-012-431-111	Sequence 111, App	470	339	24.7	461	3	US-08-742-877-2	Sequence 2, Appli
338	345.5	25.1	248	3	US-09-012-692-111	Sequence 111, App	471	339	24.7	461	3	US-08-083-871A-21	Sequence 21, Appli
339	345.5	25.1	248	3	US-08-906-613-111	Sequence 111, App	472	339	24.7	461	6	US-10-133-907-5	Sequence 5, Appli
400	345.5	25.1	248	5	PCT-US95-14442A-111	Sequence 111, App	473	339	24.7	461	6	5521070-2	Patent No. 5521070
401	344	25.0	274	2	US-09-016-366A-21	Sequence 21, Appli	474	339	24.7	461	6	5521070-2	Patent No. 5521070
402	344	25.0	274	2	US-08-978-404B-16	Sequence 16, Appli	475	339	24.7	480	4	US-09-949-016-11123	Sequence 11123, A
403	343.5	25.0	273	2	US-08-978-404B-3	Sequence 3, Appli	476	339	24.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
404	343.5	25.0	460	6	5270178-13	Patent No. 5270178	477	339	24.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
405	343.5	25.0	460	6	5270178-14	Patent No. 5270178	478	339	24.7	637	4	US-09-949-016-11538	Sequence 11538, A
406	343.5	25.0	460	6	5270178-15	Patent No. 5270178	479	339	24.7	637	4	US-09-949-016-11539	Sequence 11539, A
407	343.5	25.0	460	6	5270178-16	Patent No. 5270178	480	338.5	24.6	230	1	US-08-379-621-2	Sequence 2, Appli
408	343.5	25.0	460	6	5270178-13	Patent No. 5270178	481	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appli
409	343.5	25.0	460	6	5270178-14	Patent No. 5270178	482	338.5	24.6	230	2	US-08-889-078-2	Sequence 2, Appli
410	343.5	25.0	460	6	5270178-15	Patent No. 5270178	483	338.5	24.6	261	6	5270178-5	Patent No. 5270178
411	343.5	25.0	460	6	5270178-16	Patent No. 5270178	484	338.5	24.6	261	6	5270178-5	Patent No. 5270178
412	343	25.0	284	4	US-09-387-375-7	Sequence 7, Appli	485	338.5	24.6	308	3	US-08-705-875A-10	Sequence 10, Appli
413	343	25.0	284	4	US-10-041-000A-7	Sequence 7, Appli	486	338.5	24.6	308	4	US-09-242-999-10	Sequence 10, Appli
414	343	25.0	284	4	US-10-042-091A-7	Sequence 7, Appli	487	338	24.6	250	3	US-08-944-483-51	Sequence 51, Appli
415	342.5	24.9	248	3	US-09-032-215-37	Sequence 37, Appli	488	337.5	24.6	267	4	US-09-949-016-10711	Sequence 10711, A
416	342.5	24.9	249	3	US-09-079-970A-5	Sequence 5, Appli	489	337	24.5	235	3	US-08-944-483-48	Sequence 48, Appli
417	342.5	24.9	273	2	US-08-978-404B-6	Sequence 6, Appli	490	337	24.5	406	4	US-09-851-588-6	Sequence 6, Appli
418	342.5	24.9	546	6	5200340-6	Patent No. 5200340	491	337	24.5	423	4	US-09-656-002-2	Sequence 2, Appli
419	342.5	24.9	546	6	5200340-6	Patent No. 5200340	492	337	24.5	435	4	US-09-607-745-2	Sequence 2, Appli
420	342.5	24.9	713	4	US-09-949-016-9983	Sequence 9983, Ap	493	337	24.5	437	4	US-09-851-588-8	Sequence 8, Appli
421	342.5	24.9	790	1	US-08-469-486-54	Sequence 54, Appli	494	337	24.5	812	1	US-08-248-629A-1	Sequence 1, Appli
422	342.5	24.9	790	1	US-08-469-658-54	Sequence 54, Appli	495	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appli
423	342.5	24.9	791	2	US-09-131-995-1	Sequence 1, Appli	496	337	24.5	812	1	US-08-452-260-1	Sequence 1, Appli
424	342.5	24.9	791	2	US-08-832-087B-1	Sequence 1, Appli	497	337	24.5	812	1	US-08-326-785-1	Sequence 1, Appli
425	342.5	24.9	791	3	US-09-132-154-1	Sequence 1, Appli	498	337	24.5	812	2	US-08-612-788-1	Sequence 1, Appli
426	342.5	24.9	791	4	US-08-991-761A-6	Sequence 6, Appli	499	337	24.5	812	2	US-08-605-598B-1	Sequence 1, Appli
427	342.5	24.9	791	4	US-08-924-287A-1	Sequence 1, Appli	500	337	24.5	812	2	US-08-429-743-1	Sequence 1, Appli
428	342.5	24.9	810	1	US-07-854-603-2	Sequence 2, Appli	501	337	24.5	812	2	US-08-866-735-1	Sequence 1, Appli
429	342.5	24.9	810	1	US-08-147-000B-29	Sequence 29, Appli	502	337	24.5	812	3	US-09-066-028-1	Sequence 1, Appli
430	342.5	24.9	810	3	US-09-086-514-1	Sequence 1, Appli	503	337	24.5	812	4	US-09-192-012-3	Sequence 3, Appli
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432	342.5	24.9	810	4	US-09-403-736-1	Sequence 1, Appli	505	337	24.5	812	4	US-08-991-761A-12	Sequence 12, Appli
433	342.5	24.9	810	4	US-09-701-265-1	Sequence 1, Appli	506	337	24.5	812	5	PCT-US95-05107-1	Sequence 1, Appli
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435	342.5	24.9	810	6	5200340-8	Patent No. 5200340	508	336	24.5	415	1	US-08-073-531B-1	Sequence 1, Appli
436	342	24.9	234	1	US-08-684-862-3	Sequence 3, Appli	509	336	24.5	415	2	US-08-766-288-1	Sequence 1, Appli
437	342	24.9	273	2	US-09-016-366A-19	Sequence 19, Appli	510	336	24.5	790	4	US-08-991-761A-13	Sequence 13, Appli
438	342	24.9	273	2	US-08-978-404B-14	Sequence 14, Appli	511	334.5	24.3	446	4	US-10-177-661-4	Sequence 4, Appli
439	341.5	24.9	156	3	US-09-261-416-6	Sequence 6, Appli	512	334.5	24.3	477	4	US-10-177-661-2	Sequence 2, Appli
440	341.5	24.9	261	6	5270178-19	Patent No. 5270178	513	334.5	24.3	562	4	US-09-879-792-12	Sequence 12, Appli
441	341.5	24.9	261	6	5270178-20	Patent No. 5270178	514	334	24.3	316	4	US-09-387-375-9	Sequence 9, Appli
442	341.5	24.9	261	6	5270178-19	Patent No. 5270178	515	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appli
443	341.5	24.9	261	6	5270178-20	Patent No. 5270178	516	334	24.3	316	4	US-10-042-091A-9	Sequence 9, Appli
444	341	24.8	261	6	5270178-21	Patent No. 5270178	517	333.5	24.3	290	4	US-09-386-653A-7	Sequence 7, Appli
445	341	24.8	261	6	5270178-21	Patent No. 5270178	518	333.5	24.3	302	3	US-09-220-731-26	Sequence 26, Appli
446	341	24.8	306	4	US-09-386-642-53	Sequence 53, Appli	519	333.5	24.3	302	4	US-09-242-999-22	Sequence 22, Appli
447	341	24.8	230	1	US-09-118-748-2	Sequence 2, Appli	520	333	24.2	415	1	US-08-295-411-2	Sequence 2, Appli
448	340.5	24.8	230	1	US-08-456-840-47	Sequence 47, Appli	521	333	24.2	415	2	US-08-955-471-2	Sequence 2, Appli
449	340.5	24.8	230	1	US-08-266-407A-47	Sequence 47, Appli	522	333	24.2	415	5	PCT-US92-10242-2	Sequence 2, Appli
450	340.5	24.8	230	2	US-08-892-544-47	Sequence 47, Appli	523	332.5	24.2	638	2	US-08-681-151-3	Sequence 3, Appli
451	340.5	24.8	230	2	US-08-766-982-12	Sequence 12, Appli	524	332.5	24.2	810	4	US-08-991-761A-11	Sequence 11, Appli
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453	340.5	24.8	230	3	US-09-296-219-12	Sequence 12, Appli	526	331	24.1	579	1	US-08-295-411-4	Sequence 4, Appli
454	340.5	24.8	244	4	US-09-601-318-4	Sequence 4, Appli	527	331	24.1	579	2	US-08-955-471-4	Sequence 4, Appli
455	340.5	24.8	244	4	US-09-601-318-5	Sequence 5, Appli	528	331	24.1	579	3	US-09-117-708-14	Sequence 14, Appli
456	340.5	24.8	244	4	US-09-601-318-6	Sequence 6, Appli	529	331	24.1	579	5	PCT-US92-10242-4	Sequence 4, Appli
457	340.5	24.8	244	4	US-09-601-318-7	Sequence 7, Appli	530	331	24.1	615	1	US-07-998-972A-3	Sequence 3, Appli
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459	340.5	24.8	245	4	US-09-601-318-1	Sequence 1, Appli	532	331	24.1	615	5	PCT-US92-11357-3	Sequence 3, Appli
460	340.5	24.8	267	2	US-09-016-366A-23	Sequence 23, Appli	533	331	24.1	622	3	US-08-952-967-8	Sequence 8, Appli
461	340.5	24.8	267	2	US-08-978-404B-18	Sequence 18, Appli	534	331	24.1	622	4	US-09-054-272-42	Sequence 42, Appli
462	340.5	24.8	267	4	US-09-917-254-101	Sequence 101, App	535	331	24.1	560	4	US-09-949-016-6458	Sequence 6458, Ap
463	340.5	24.8	300	3	US-08-705-875A-6	Sequence 6, Appli	536	330.5	24.1	560	4	US-09-912-559-3	Sequence 3, Appli
464	340.5	24.8	300	4	US-09-242-999-6	Sequence 6, Appli	537	330.5	24.1	560	4	US-09-912-559-3	Sequence 3, Appli
465	340	24.7	419	4	US-10-182-263-3	Sequence 3, Appli	538	330	24.0	221	3	US-08-944-483-54	Sequence 54, Appli

539	330	24.0	222	1	US-08-456-840-46	Sequence 46, Appl	612	321	23.4	300	1	US-08-448-937A-1	Sequence 1, Appl
540	330	24.0	222	1	US-08-266-407A-46	Sequence 46, Appl	613	321	23.4	315	4	US-09-386-653A-9	Sequence 9, Appl
541	330	24.0	222	2	US-08-892-544-46	Sequence 46, Appl	614	321	23.4	655	1	US-08-148-910-12	Sequence 12, Appl
542	330	24.0	222	6	5223425-6	Patent No. 5223425	615	321	23.4	655	1	US-08-448-937A-12	Sequence 12, Appl
543	330	24.0	222	6	5223425-6	Patent No. 5223425	616	321	23.4	809	4	US-08-991-761A-9	Sequence 9, Appl
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545	329.5	24.0	376	2	US-08-558-269-10	Sequence 10, Appl	618	319.5	23.3	240	1	US-08-483-853-11	Sequence 11, Appl
546	329.5	24.0	376	3	US-09-410-882-10	Sequence 10, Appl	619	319.5	23.3	240	1	US-08-472-173-11	Sequence 11, Appl
547	329	23.9	238	3	US-08-944-483-52	Sequence 52, Appl	620	319.5	23.3	240	2	US-08-487-167-11	Sequence 11, Appl
548	328.5	23.9	238	3	US-08-944-483-64	Sequence 64, Appl	621	319.5	23.3	240	2	US-08-483-816-11	Sequence 11, Appl
549	328.5	23.9	338	4	US-08-991-761A-10	Sequence 10, Appl	622	319.5	23.3	240	2	US-08-296-149-11	Sequence 11, Appl
550	327.5	23.8	151	3	US-09-518-046-21	Sequence 21, Appl	623	319.5	23.3	240	2	US-08-801-493-11	Sequence 11, Appl
551	327.5	23.8	154	3	US-09-261-416-7	Sequence 7, Appl	624	319.5	23.3	240	2	US-08-615-271-11	Sequence 11, Appl
552	327	23.8	241	3	US-08-944-483-60	Sequence 60, Appl	625	319.5	23.3	240	3	US-09-074-660-11	Sequence 11, Appl
553	327	23.8	255	1	US-08-650-129-5	Sequence 5, Appl	626	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
554	327	23.8	255	3	US-08-984-417-5	Sequence 5, Appl	627	319.5	23.3	240	3	US-09-106-468-11	Sequence 11, Appl
555	326.5	23.8	144	4	US-09-618-259-1	Sequence 1, Appl	628	319.5	23.3	240	3	US-09-106-466A-11	Sequence 11, Appl
556	325.5	23.7	261	3	US-08-163-919A-2	Sequence 2, Appl	629	319.5	23.3	240	3	US-09-106-467-11	Sequence 11, Appl
557	325.5	23.7	261	4	US-08-462-515-2	Sequence 2, Appl	630	319.5	23.3	254	3	US-08-944-483-50	Sequence 50, Appl
558	325.5	23.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	631	318	23.1	295	4	US-10-165-442-3	Sequence 3, Appl
559	325	23.7	226	1	US-08-650-129-4	Sequence 4, Appl	632	317.5	23.1	245	3	US-08-944-483-69	Sequence 69, Appl
560	325	23.7	226	3	US-08-984-417-4	Sequence 4, Appl	633	317	23.1	232	3	US-08-944-483-45	Sequence 45, Appl
561	324.5	23.6	228	1	US-08-278-091-10	Sequence 10, Appl	634	317	23.1	295	4	US-10-165-442-1	Sequence 1, Appl
562	324.5	23.6	228	1	US-08-483-859-10	Sequence 10, Appl	635	316.5	23.0	226	1	US-07-929-198-2	Sequence 2, Appl
563	324.5	23.6	228	1	US-08-472-173-10	Sequence 10, Appl	636	316.5	23.0	226	1	US-07-929-198-6	Sequence 6, Appl
564	324.5	23.6	228	2	US-08-487-167-10	Sequence 10, Appl	637	316.5	23.0	226	2	US-08-557-146-15	Sequence 15, Appl
565	324.5	23.6	228	2	US-08-482-816-10	Sequence 10, Appl	638	316.5	23.0	226	2	US-09-154-344-15	Sequence 15, Appl
566	324.5	23.6	228	2	US-08-296-149-10	Sequence 10, Appl	639	316.5	23.0	226	3	US-08-944-483-43	Sequence 43, Appl
567	324.5	23.6	228	2	US-08-801-499-10	Sequence 10, Appl	640	316	23.0	246	3	US-08-906-769-127	Sequence 127, App
568	324.5	23.6	228	2	US-08-615-271-10	Sequence 10, Appl	641	316	23.0	246	3	US-08-906-616-127	Sequence 127, App
569	324.5	23.6	228	3	US-09-074-660-10	Sequence 10, Appl	642	316	23.0	246	3	US-08-639-075A-127	Sequence 127, App
570	324.5	23.6	228	3	US-09-074-659-10	Sequence 10, Appl	643	316	23.0	246	3	US-09-012-431-127	Sequence 127, App
571	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	644	316	23.0	246	3	US-09-012-692-127	Sequence 127, App
572	324.5	23.6	228	3	US-09-106-466A-10	Sequence 10, Appl	645	316	23.0	246	3	US-08-906-613-127	Sequence 127, App
573	324.5	23.6	228	3	US-09-106-467-10	Sequence 10, Appl	646	316	23.0	259	4	US-10-165-442-4	Sequence 4, Appl
574	323.5	23.5	275	2	US-09-016-366A-17	Sequence 17, Appl	647	315.5	23.0	254	3	US-09-578-303-5	Sequence 5, Appl
575	323.5	23.5	275	2	US-08-978-404B-12	Sequence 12, Appl	648	315.5	23.0	292	4	US-09-607-745-9	Sequence 9, Appl
576	323.5	23.5	406	1	US-08-293-778-24	Sequence 24, Appl	649	315.5	23.0	300	3	US-08-705-875A-4	Sequence 4, Appl
577	323.5	23.5	406	1	US-08-955-471-5	Sequence 5, Appl	650	315.5	23.0	300	3	US-09-220-731-21	Sequence 21, Appl
578	323.5	23.5	406	2	US-08-955-471-5	Sequence 5, Appl	651	315.5	23.0	300	4	US-09-243-999-4	Sequence 4, Appl
579	323.5	23.5	406	4	US-09-782-587B-1	Sequence 1, Appl	652	315.5	23.0	487	1	US-08-469-486-53	Sequence 53, Appl
580	323.5	23.5	406	4	US-09-782-587B-3	Sequence 3, Appl	653	315.5	23.0	487	2	US-08-469-658-53	Sequence 53, Appl
581	323.5	23.5	406	5	PCT-US92-10242-5	Sequence 5, Appl	654	315.5	23.0	492	1	US-08-469-486-2	Sequence 2, Appl
582	323.5	23.5	444	1	US-08-475-845-2	Sequence 2, Appl	655	315.5	23.0	492	2	US-08-469-658-2	Sequence 2, Appl
583	323.5	23.5	444	2	US-08-327-690-2	Sequence 2, Appl	656	315	22.9	259	4	US-10-165-442-2	Sequence 2, Appl
584	323.5	23.5	444	2	US-08-660-289-2	Sequence 2, Appl	657	315	22.9	691	4	US-09-949-016-7775	Sequence 7775, Ap
585	323.5	23.5	444	2	US-08-537-807-2	Sequence 2, Appl	658	314.5	22.9	283	4	US-09-244-111-2	Sequence 2, Appl
586	323.5	23.5	444	2	US-08-871-003-2	Sequence 2, Appl	659	314	22.9	855	2	US-09-027-337-2	Sequence 2, Appl
587	323.5	23.5	444	3	US-08-464-233-2	Sequence 2, Appl	660	314	22.9	855	4	US-09-644-600-2	Sequence 2, Appl
588	323.5	23.5	444	3	US-09-189-607-2	Sequence 2, Appl	661	313.5	22.8	855	4	US-09-654-600A-2	Sequence 2, Appl
589	323.5	23.5	444	3	US-09-378-907-2	Sequence 2, Appl	662	313.5	22.8	226	1	US-07-929-198-4	Sequence 4, Appl
590	323.5	23.5	444	5	PCT-US94-05779-2	Sequence 2, Appl	663	312.5	22.7	798	4	US-09-959-392-34	Sequence 34, Appl
591	323.5	23.5	461	4	US-09-949-016-8839	Sequence 8839, Ap	664	312	22.7	248	3	US-08-944-483-71	Sequence 71, Appl
592	323.5	23.5	466	1	US-07-882-202A-4	Sequence 4, Appl	665	311.5	22.7	251	3	US-08-944-483-47	Sequence 47, Appl
593	323.5	23.5	466	1	US-08-021-615A-4	Sequence 4, Appl	666	311	22.6	383	2	US-08-558-269-6	Sequence 6, Appl
594	323.5	23.5	466	1	US-08-321-777-4	Sequence 4, Appl	667	311	22.6	383	3	US-09-410-882-6	Sequence 6, Appl
595	323.5	23.5	466	3	US-09-009-217-14	Sequence 14, Appl	668	311	22.6	798	1	US-08-200-900A-2	Sequence 2, Appl
596	323.5	23.5	466	3	US-09-009-656-14	Sequence 14, Appl	669	311	22.6	798	4	US-08-794-042-2	Sequence 2, Appl
597	323.5	23.5	466	5	PCT-US93-04493-4	Sequence 4, Appl	670	311	22.6	798	5	PCT-US94-00616-2	Sequence 2, Appl
598	323.5	23.5	483	4	US-09-949-016-9523	Sequence 9523, Ap	671	311	22.6	812	4	US-09-192-012-9	Sequence 9, Appl
599	322.5	23.5	285	4	US-09-023-942A-26	Sequence 26, Appl	672	311	22.6	1042	4	US-09-959-392-2	Sequence 2, Appl
600	322.5	23.5	560	4	US-09-912-559-4	Sequence 4, Appl	673	310.5	22.6	247	2	US-08-978-404B-47	Sequence 47, Appl
601	322	23.4	207	4	US-10-000-489-54	Sequence 54, Appl	674	309.5	22.5	241	4	US-09-657-986B-2	Sequence 2, Appl
602	322	23.4	699	4	US-09-949-016-6138	Sequence 6138, Ap	675	309.5	22.5	492	4	US-09-685-166A-895	Sequence 895, App
603	322	23.4	717	4	US-09-949-016-11182	Sequence 11182, A	676	309.5	22.5	492	4	US-09-879-792-14	Sequence 14, Appl
604	321.5	23.4	255	2	US-09-027-337-7	Sequence 7, Appl	677	309.5	22.5	492	4	US-09-679-426-895	Sequence 895, App
605	321.5	23.4	255	4	US-09-644-600-7	Sequence 7, Appl	678	309.5	22.5	492	4	US-09-759-143-895	Sequence 895, App
606	321.5	23.4	255	4	US-09-654-600A-7	Sequence 7, Appl	679	308.5	22.5	243	3	US-08-944-483-70	Sequence 70, Appl
607	321.5	23.4	418	4	US-10-177-661-6	Sequence 6, Appl	680	308.5	22.5	319	4	US-09-270-761-42672	Sequence 42672, A
608	321	23.4	248	2	US-08-851-974-3	Sequence 3, Appl	681	308	22.4	232	4	US-09-959-392-32	Sequence 32, Appl
609	321	23.4	248	2	US-09-213-390-3	Sequence 3, Appl	682	308	22.4	317	4	US-09-386-629-7	Sequence 7, Appl
610	321	23.4	269	2	US-08-978-404B-10	Sequence 10, Appl	683	308	22.4	317	4	US-09-907-794A-263	Sequence 263, App
611	321	23.4	300	1	US-08-148-910-1	Sequence 1, Appl	684	308	22.4	317	4	US-09-905-125A-263	Sequence 263, App

685	308	22.4	317	4	US-09-902-775A-263	Sequence 263, App	758	304	22.1	562	6	5185259-3	Patent No. 5185259
686	308	22.4	317	4	US-09-906-700-263	Sequence 263, App	759	304	22.1	562	6	5200340-2	Patent No. 5200340
687	308	22.4	317	4	US-09-903-603A-263	Sequence 263, App	760	304	22.1	562	6	5244676-5	Patent No. 5244676
688	308	22.4	317	4	US-09-904-920A-263	Sequence 263, App	761	304	22.1	562	6	5344773-2	Patent No. 5344773
689	308	22.4	317	4	US-09-905-064-263	Sequence 263, App	762	304	22.1	562	6	5185259-3	Patent No. 5185259
690	308	22.4	317	4	US-09-905-381A-263	Sequence 263, App	763	304	22.1	562	6	5200340-2	Patent No. 5200340
691	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	764	304	22.1	562	6	5244676-5	Patent No. 5244676
692	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	765	304	22.1	562	6	5344773-2	Patent No. 5344773
693	307.5	22.4	376	4	US-08-681-151-1	Sequence 1, Appli	766	304	22.1	587	4	US-09-949-016-11501	Sequence 11501, A
694	307	22.3	268	1	US-09-820-002-2	Sequence 2, Appli	767	303.5	22.1	234	4	US-09-513-999C-7815	Sequence 7815, Ap
695	307	22.3	268	1	US-08-568-031-2	Sequence 2, Appli	768	303.5	22.1	278	1	US-08-352-828C-4	Sequence 4, Appli
696	307	22.3	268	1	US-08-966-319-2	Sequence 2, Appli	769	303.5	22.1	278	3	US-09-330-945-4	Sequence 4, Appli
697	307	22.3	268	3	US-09-153-304-2	Sequence 2, Appli	770	303	22.1	258	4	US-09-949-016-10661	Sequence 10661, A
698	307	22.3	355	2	US-08-811-949-47	Sequence 47, Appl	771	303	22.1	355	2	US-08-811-949-53	Sequence 53, Appl
699	307	22.3	355	2	US-08-811-949-59	Sequence 59, Appl	772	303	22.1	389	2	US-08-811-949-67	Sequence 67, Appl
700	307	22.3	417	4	US-08-820-002-4	Sequence 4, Appli	773	303	22.1	437	2	US-08-811-949-55	Sequence 55, Appl
701	307	22.3	437	2	US-08-811-949-51	Sequence 51, Appl	774	303	22.1	527	4	US-09-600-985-1	Sequence 1, Appli
702	307	22.3	452	4	US-09-949-016-7182	Sequence 7182, Ap	775	302.5	22.0	1113	4	US-09-959-392-4	Sequence 4, Appli
703	306	22.3	527	2	US-08-811-949-39	Sequence 39, Appl	776	302	22.0	389	2	US-08-811-949-65	Sequence 65, Appl
704	306	22.3	256	2	US-09-337-3	Sequence 3, Appli	777	302	22.0	477	2	US-08-560-098A-51	Sequence 51, Appl
705	306	22.3	256	4	US-09-644-600-3	Sequence 3, Appli	778	302	22.0	527	4	US-09-600-985-2	Sequence 2, Appli
706	306	22.3	437	2	US-08-811-949-57	Sequence 57, Appl	779	302	22.0	527	4	US-09-600-985-3	Sequence 3, Appli
707	305.5	22.2	146	4	US-09-618-259-3	Sequence 3, Appli	780	301.5	21.9	226	3	US-08-944-483-41	Sequence 41, Appl
708	305	22.2	247	2	US-08-851-974-1	Sequence 1, Appli	781	301	21.9	255	1	US-08-208-007A-14	Sequence 14, Appl
709	305	22.2	247	2	US-08-851-974-4	Sequence 4, Appli	782	301	21.9	255	3	US-08-915-095A-14	Sequence 14, Appl
710	305	22.2	247	2	US-09-213-390-1	Sequence 1, Appli	783	301	21.9	255	3	US-08-798-096-14	Sequence 14, Appl
711	305	22.2	247	2	US-09-213-390-4	Sequence 4, Appli	784	301	21.9	255	4	US-08-798-096-14	Sequence 14, Appl
712	305	22.2	247	2	US-09-949-016-6457	Sequence 6457, Ap	785	301	21.9	255	4	US-09-953-956-14	Sequence 14, Appl
713	305	22.2	247	2	US-08-811-949-49	Sequence 49, Appl	786	301	21.9	255	4	US-08-553-125A-14	Sequence 14, Appl
714	304.5	22.2	437	2	US-09-004-731-16	Sequence 16, Appl	787	301	21.9	255	4	US-10-114-464-14	Sequence 14, Appl
715	304.5	22.2	258	3	US-09-004-731-19	Sequence 19, Appl	788	301	21.9	257	6	US-09-949-016-10662	Sequence 10662, A
716	304.5	22.2	258	3	US-08-749-699-16	Sequence 16, Appl	789	301	21.9	527	6	5520913-1	Patent No. 5520913
717	304.5	22.2	258	3	US-08-749-699-19	Sequence 19, Appl	790	301	21.9	527	6	5520913-1	Patent No. 5520913
718	304.5	22.2	258	4	US-09-004-723-16	Sequence 16, Appl	791	300	21.8	233	4	US-09-636-382A-24	Sequence 24, Appl
719	304.5	22.2	258	4	US-09-004-723-19	Sequence 19, Appl	792	298	21.7	347	2	US-08-811-949-1	Sequence 1, Appli
720	304.5	22.2	314	3	US-09-636-382A-2	Sequence 2, Appli	793	297	21.6	237	3	US-08-163-919A-3	Sequence 3, Appli
721	304.5	22.2	384	3	US-09-032-215-22	Sequence 22, Appl	794	297	21.6	237	4	US-08-462-515-3	Sequence 3, Appli
722	304.5	22.2	393	4	US-09-759-143-934	Sequence 934, App	795	297	21.6	237	5	PCT-US94-14073-3	Sequence 3, Appli
723	304.5	22.2	492	3	US-09-342-749-2	Sequence 2, Appli	796	297	21.6	252	3	US-08-944-483-72	Sequence 72, Appl
724	304.5	22.2	492	4	US-09-691-840-2	Sequence 2, Appli	797	297	21.6	253	2	US-09-027-337-8	Sequence 8, Appli
725	304.5	22.2	492	4	US-09-759-143-932	Sequence 932, App	798	297	21.6	253	4	US-09-644-600A-8	Sequence 8, Appli
726	304.5	22.2	510	4	US-09-949-016-11074	Sequence 11074, A	799	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appli
727	304	22.1	232	1	US-07-990-301A-4	Sequence 4, Appli	800	297	21.6	256	3	US-09-032-215-27	Sequence 27, Appl
728	304	22.1	235	3	US-08-944-483-65	Sequence 65, Appl	801	297	21.6	323	4	US-09-880-503-7	Sequence 7, Appli
729	304	22.1	255	3	US-08-944-483-67	Sequence 67, Appl	802	297	21.6	354	2	US-08-811-949-61	Sequence 61, Appl
730	304	22.1	268	4	US-09-613-822B-2	Sequence 2, Appli	803	297	21.6	411	3	US-09-181-816-1	Sequence 1, Appli
731	304	22.1	327	4	US-09-386-623-8	Sequence 8, Appli	804	297	21.6	521	4	US-09-949-016-11081	Sequence 11081, A
732	304	22.1	355	1	US-08-137-116-1	Sequence 1, Appli	805	297	21.6	521	4	US-09-949-016-11082	Sequence 11082, A
733	304	22.1	355	1	US-08-217-618-1	Sequence 1, Appli	806	297	21.6	521	4	US-09-949-016-11083	Sequence 11083, A
734	304	22.1	355	1	US-08-427-640-2	Sequence 2, Appli	807	296.5	21.6	224	1	US-08-278-091-12	Sequence 12, Appl
735	304	22.1	355	1	US-08-427-640-6	Sequence 6, Appli	808	296.5	21.6	224	1	US-08-483-859-12	Sequence 12, Appl
736	304	22.1	355	1	US-08-217-617A-1	Sequence 1, Appli	809	296.5	21.6	224	1	US-08-472-173-12	Sequence 12, Appl
737	304	22.1	355	2	US-08-217-616-1	Sequence 1, Appli	810	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appl
738	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appl	811	296.5	21.6	224	2	US-08-483-816-12	Sequence 12, Appl
739	304	22.1	355	6	US-08-794-528-1	Sequence 1, Appli	812	296.5	21.6	224	2	US-08-296-149-12	Sequence 12, Appl
740	304	22.1	355	6	5223256-1	Patent No. 5223256	813	296.5	21.6	224	2	US-08-801-499-12	Sequence 12, Appl
741	304	22.1	355	6	5223256-1	Patent No. 5223256	814	296.5	21.6	224	2	US-08-615-271-12	Sequence 12, Appl
742	304	22.1	356	1	US-08-427-640-4	Sequence 4, Appli	815	296.5	21.6	224	3	US-09-074-660-12	Sequence 12, Appl
743	304	22.1	356	1	US-08-427-640-8	Sequence 8, Appli	816	296.5	21.6	224	3	US-09-074-659-12	Sequence 12, Appl
744	304	22.1	378	3	US-09-553-498-10	Sequence 10, Appl	817	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
745	304	22.1	378	4	US-09-618-869-10	Sequence 10, Appl	818	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
746	304	22.1	433	4	US-09-949-016-8220	Sequence 8220, Ap	819	296.5	21.6	224	3	US-09-106-468A-12	Sequence 12, Appl
747	304	22.1	472	2	US-08-811-949-63	Sequence 63, Appl	820	296.5	21.6	246	4	US-09-205-258-1149	Sequence 1149, Ap
748	304	22.1	527	1	US-07-609-510B-16	Sequence 16, Appl	821	296.5	21.6	276	4	US-08-560-098A-49	Sequence 49, Appl
749	304	22.1	527	4	US-09-612-314A-51	Sequence 51, Appl	822	296.5	21.6	306	2	US-09-880-503-5	Sequence 5, Appli
750	304	22.1	527	5	PCT-US91-01025A-2	Sequence 2, Appli	823	296.5	21.6	306	2	US-08-560-098A-45	Sequence 45, Appl
751	304	22.1	527	6	5185259-8	Patent No. 5185259	824	296.5	21.6	331	2	US-08-560-098A-46	Sequence 46, Appl
752	304	22.1	527	6	5185259-8	Patent No. 5185259	825	296.5	21.6	365	1	US-08-093-741-83	Sequence 83, Appl
753	304	22.1	562	2	US-08-811-949-43	Sequence 43, Appl	826	296.5	21.6	365	1	US-08-720-012-83	Sequence 83, Appl
754	304	22.1	562	2	US-08-560-098A-50	Sequence 50, Appl	827	296.5	21.6	393	2	US-08-560-098A-44	Sequence 44, Appl
755	304	22.1	562	2	US-08-883-795A-38	Sequence 38, Appl	828	296.5	21.6	393	3	US-08-967-024C-24	Sequence 24, Appl
756	304	22.1	562	4	US-09-703-695A-4	Sequence 4, Appli	829	296.5	21.6	393	3	US-08-967-024C-25	Sequence 25, Appl
757	304	22.1	562	4	US-10-443-701-4	Sequence 4, Appli	830	296.5	21.6	403	4	US-09-880-503-6	Sequence 6, Appli

831	296.5	21.6	411	1	US-08-087-163-1	Sequence 1, Appli	904	282	20.5	244	3	US-08-944-483-74	Sequence 74, Appl
832	296.5	21.6	411	1	US-08-286-748B-18	Sequence 18, Appl	905	279	20.3	902	4	US-09-644-600-10	Sequence 10, Appl
833	296.5	21.6	411	1	US-08-153-799-18	Sequence 18, Appl	906	279	20.3	902	4	US-09-654-600A-10	Sequence 10, Appl
834	296.5	21.6	411	2	US-08-560-098A-48	Sequence 48, Appl	907	277.5	20.2	902	4	US-08-944-483-58	Sequence 58, Appl
835	296.5	21.6	411	4	US-08-560-098A-48	Sequence 3, Appli	908	277	20.2	488	4	US-09-367-777-44	Sequence 44, Appl
836	296.5	21.6	430	6	5219569-2	Patent No. 5219569	909	277	20.2	488	4	US-09-367-791A-27	Sequence 27, Appl
837	296.5	21.6	430	6	5219569-2	Patent No. 5219569	910	276	20.1	306	1	US-08-330-978-1	Sequence 1, Appli
838	296.5	21.6	431	4	US-09-101-272G-1	Sequence 1, Appli	911	276	20.1	306	1	US-08-474-042-1	Sequence 1, Appli
839	296.5	21.6	431	6	5188829-1	Patent No. 5188829	912	276	20.1	306	1	US-08-484-558-1	Sequence 1, Appli
840	296.5	21.6	431	6	5188829-1	Patent No. 5188829	913	276	20.1	306	1	US-08-774-592-1	Sequence 1, Appli
841	296.5	21.6	432	4	US-08-560-098A-47	Sequence 47, Appl	914	276	20.1	437	1	US-08-487-037-2	Sequence 2, Appli
842	296	21.5	269	4	US-09-715-994-2	Sequence 2, Appli	915	276	20.1	437	1	US-08-295-411-3	Sequence 3, Appli
843	295.5	21.5	283	3	US-08-807-151-1	Sequence 1, Appli	916	276	20.1	448	2	US-08-955-471-3	Sequence 3, Appli
844	295.5	21.5	283	3	US-09-478-957-1	Sequence 1, Appli	917	276	20.1	448	5	PCT-US92-10068-1	Sequence 1, Appli
845	295.5	21.5	454	3	US-09-518-046-2	Sequence 2, Appli	918	276	20.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
846	294	21.4	256	3	US-09-032-215-32	Sequence 32, Appl	919	276	20.1	488	1	US-08-487-037-1	Sequence 1, Appli
847	293.5	21.4	239	3	US-08-944-483-61	Sequence 61, Appl	920	276	20.1	488	1	US-09-949-016-9524	Sequence 9524, Ap
848	293.5	21.4	411	4	US-09-403-736-2	Sequence 2, Appli	921	274.5	20.0	211	3	US-09-220-731-25	Sequence 25, Appl
849	293.5	21.4	430	1	US-07-942-157A-3	Sequence 3, Appli	922	274.5	20.0	211	4	US-09-242-99B-20	Sequence 20, Appl
850	292	21.3	237	3	US-09-004-731-22	Sequence 22, Appl	923	274	19.9	241	1	US-08-330-978-4	Sequence 4, Appli
851	292	21.3	237	3	US-08-749-699-22	Sequence 22, Appl	924	274	19.9	241	1	US-08-474-042-4	Sequence 4, Appli
852	292	21.3	237	4	US-09-004-729-22	Sequence 22, Appl	925	274	19.9	241	1	US-08-484-558-4	Sequence 4, Appli
853	292	21.3	256	3	US-08-906-769-89	Sequence 89, Appl	926	274	19.9	241	1	US-08-774-592-4	Sequence 4, Appli
854	292	21.3	256	3	US-08-906-616-89	Sequence 89, Appl	927	274	19.9	254	1	US-08-330-978-3	Sequence 3, Appli
855	292	21.3	256	3	US-08-817-795-89	Sequence 89, Appl	928	274	19.9	254	1	US-08-474-042-3	Sequence 3, Appli
856	292	21.3	256	3	US-08-639-075A-89	Sequence 89, Appl	929	274	19.9	254	1	US-08-484-558-3	Sequence 3, Appli
857	292	21.3	256	3	US-09-012-431-89	Sequence 89, Appl	930	274	19.9	254	1	US-08-774-592-3	Sequence 3, Appli
858	292	21.3	256	3	US-09-012-692-89	Sequence 89, Appl	931	272	19.8	253	3	US-08-906-769-131	Sequence 131, App
859	292	21.3	256	3	US-08-906-613-89	Sequence 89, Appl	932	272	19.8	253	3	US-08-906-616-131	Sequence 131, App
860	292	21.3	256	5	PCT-US95-14442A-89	Sequence 89, Appl	933	272	19.8	253	3	US-08-639-075A-131	Sequence 131, App
861	292	21.3	414	4	US-09-270-767-46426	Sequence 46426, A	934	272	19.8	253	3	US-09-012-431-131	Sequence 131, App
862	291.5	21.2	242	3	US-08-944-483-57	Sequence 57, Appl	935	272	19.8	253	3	US-09-012-692-131	Sequence 131, App
863	291.5	21.2	253	3	US-08-944-483-73	Sequence 73, Appl	936	272	19.8	253	3	US-08-906-613-131	Sequence 131, App
864	291	21.2	416	2	US-09-000-846-2	Sequence 2, Appli	937	270	19.7	251	3	US-08-944-483-28	Sequence 28, Appl
865	290	21.1	235	2	US-08-557-146-14	Sequence 14, Appl	938	269	19.6	256	4	US-08-395-456C-23	Sequence 23, Appl
866	290	21.1	235	2	US-09-154-344-14	Sequence 14, Appl	939	269	19.6	256	4	US-08-487-453A-23	Sequence 23, Appl
867	290	21.1	235	3	US-08-807-151-3	Sequence 3, Appli	940	268	19.5	256	2	US-08-230-428B-4	Sequence 4, Appli
868	290	21.1	235	3	US-08-944-483-42	Sequence 42, Appl	941	268	19.5	437	1	US-08-487-037-3	Sequence 3, Appli
869	290	21.1	235	3	US-09-478-957-3	Sequence 3, Appli	942	267.5	19.5	266	3	US-09-004-731-24	Sequence 24, Appl
870	289	21.0	223	1	US-07-956-848A-41	Sequence 41, Appl	943	267.5	19.5	266	3	US-08-749-699-24	Sequence 24, Appl
871	289	21.0	223	1	US-08-471-956-41	Sequence 41, Appl	944	267.5	19.5	266	4	US-09-004-729-24	Sequence 24, Appl
872	289	21.0	583	4	US-09-576-594-837	Sequence 837, App	945	265.5	19.3	197	1	US-08-456-840-48	Sequence 48, Appl
873	288.5	21.0	255	3	US-08-906-769-91	Sequence 91, Appl	946	265.5	19.3	197	1	US-08-266-407A-48	Sequence 48, Appl
874	288.5	21.0	255	3	US-08-906-616-91	Sequence 91, Appl	947	265.5	19.3	197	2	US-08-892-544-48	Sequence 48, Appl
875	288.5	21.0	255	3	US-08-906-616-91	Sequence 91, Appl	948	264.5	19.3	248	1	US-08-238-130-2	Sequence 2, Appli
876	288.5	21.0	255	3	US-08-817-795-91	Sequence 91, Appl	949	264.5	19.3	248	1	US-08-921-426-4	Sequence 4, Appli
877	288.5	21.0	255	3	US-09-012-431-91	Sequence 91, Appl	950	264.5	19.3	248	3	US-08-816-915-4	Sequence 4, Appli
878	288.5	21.0	255	3	US-09-012-692-91	Sequence 91, Appl	951	264.5	19.3	248	5	PCT-US95-07743-4	Sequence 4, Appli
879	288.5	21.0	255	3	US-08-906-613-91	Sequence 91, Appl	952	264.5	19.3	249	3	US-09-578-303-2	Sequence 2, Appli
880	288.5	21.0	255	5	PCT-US95-14442A-91	Sequence 91, Appl	953	264	19.2	250	3	US-08-944-483-68	Sequence 68, Appl
881	288	21.0	268	1	US-08-270-584A-2	Sequence 2, Appli	954	264	19.2	256	4	US-09-949-016-6271	Sequence 6271, Ap
882	288	21.0	268	2	US-08-765-192-2	Sequence 2, Appli	955	263.5	19.2	222	2	US-08-491-204A-18	Sequence 18, Appl
883	288	21.0	268	3	US-09-199-793-2	Sequence 2, Appli	956	263.5	19.2	251	4	US-09-949-016-6112	Sequence 6112, Ap
884	287	20.9	227	3	US-08-944-483-40	Sequence 40, Appl	957	263.5	19.2	255	4	US-09-949-016-9690	Sequence 9690, Ap
885	287	20.9	407	3	US-09-734-675-4	Sequence 4, Appli	958	263	19.1	252	3	US-08-906-769-103	Sequence 103, App
886	286.5	20.9	218	3	US-09-578-303-3	Sequence 3, Appli	959	263	19.1	252	3	US-08-906-616-103	Sequence 103, App
887	286.5	20.9	228	3	US-09-004-731-10	Sequence 10, Appl	960	263	19.1	252	3	US-08-817-795-103	Sequence 103, App
888	286.5	20.9	228	3	US-08-749-699-10	Sequence 10, Appl	961	263	19.1	252	3	US-08-639-075A-103	Sequence 103, App
889	286.5	20.9	228	4	US-09-004-729-10	Sequence 10, Appl	962	263	19.1	252	3	US-09-012-431-103	Sequence 103, App
890	286	20.8	228	4	US-09-205-258-1150	Sequence 1150, Ap	963	263	19.1	252	3	US-09-012-692-103	Sequence 103, App
891	284.5	20.7	225	3	US-09-004-731-13	Sequence 13, Appl	964	263	19.1	252	3	US-08-906-613-103	Sequence 103, App
892	284.5	20.7	225	3	US-08-749-699-13	Sequence 13, Appl	965	263	19.1	252	5	PCT-US95-14442A-103	Sequence 103, App
893	284.5	20.7	225	4	US-09-004-729-13	Sequence 13, Appl	966	262.5	19.1	233	3	US-09-004-731-27	Sequence 27, Appl
894	284.5	20.7	255	3	US-08-906-769-83	Sequence 83, Appl	967	262.5	19.1	233	3	US-08-749-699-27	Sequence 27, Appl
895	284.5	20.7	255	3	US-08-906-616-83	Sequence 83, Appl	968	262.5	19.1	233	4	US-09-004-729-27	Sequence 27, Appl
896	284.5	20.7	255	3	US-08-817-795-83	Sequence 83, Appl	969	261.5	19.0	222	1	US-07-969-931-9	Sequence 9, Appli
897	284.5	20.7	255	3	US-08-639-075A-83	Sequence 83, Appl	970	261.5	19.0	222	1	US-07-855-417A-9	Sequence 9, Appli
898	284.5	20.7	255	3	US-09-012-431-83	Sequence 83, Appl	971	261.5	19.0	225	3	US-08-944-483-32	Sequence 32, Appl
899	284.5	20.7	255	3	US-09-012-692-83	Sequence 83, Appl	972	257.5	18.7	224	1	US-08-553-516-2	Sequence 2, Appli
900	284.5	20.7	255	3	US-08-906-613-83	Sequence 83, Appl	973	256	18.6	267	3	US-08-906-769-145	Sequence 145, App
901	284.5	20.7	255	5	PCT-US95-14442A-83	Sequence 83, Appl	974	256	18.6	267	3	US-08-906-616-145	Sequence 145, App
902	283.5	20.6	268	3	US-09-032-215-42	Sequence 42, Appl	975	256	18.6	267	3	US-08-639-075A-145	Sequence 145, App
903	282.5	20.6	144	4	US-09-618-259-4	Sequence 4, Appli	976	256	18.6	267	3	US-09-004-731-67	Sequence 67, Appl



977	256	18.6	267	3	US-09-012-431-145	Sequence 145, App	1050	226	16.4	697	3	US-08-462-040-50	Sequence 50, Appl
978	256	18.6	267	3	US-08-749-699-67	Sequence 67, Appl	1051	226	16.4	723	1	US-07-838-410-1	Sequence 1, Appl
979	256	18.6	267	3	US-09-012-692-145	Sequence 145, App	1052	226	16.4	723	1	US-08-290-937B-1	Sequence 1, Appl
980	256	18.6	267	3	US-08-906-613-145	Sequence 145, App	1053	226	16.4	723	1	US-08-290-937B-2	Sequence 2, Appl
981	256	18.6	267	3	US-09-004-729-67	Sequence 67, Appl	1054	226	16.4	723	1	US-08-290-937B-3	Sequence 3, Appl
982	256	18.6	405	3	US-09-734-675-2	Sequence 2, Appl	1055	226	16.4	723	1	US-08-404-643-1	Sequence 1, Appl
983	254	18.5	242	3	US-09-004-731-41	Sequence 41, Appl	1056	226	16.4	723	3	US-09-194-326-1	Sequence 1, Appl
984	254	18.5	242	3	US-08-749-699-41	Sequence 41, Appl	1057	226	16.4	723	3	US-09-194-326-2	Sequence 2, Appl
985	254	18.5	242	4	US-09-004-729-41	Sequence 41, Appl	1058	226	16.4	723	3	US-09-194-326-3	Sequence 3, Appl
986	254	18.5	255	4	US-09-270-767-44361	Sequence 44361, A	1059	226	16.4	723	3	US-08-700-519J-19	Sequence 19, Appl
987	253	18.4	182	4	US-09-328-925-12	Sequence 12, Appl	1060	226	16.4	723	4	US-09-600-991-18	Sequence 18, Appl
988	253	18.4	231	4	US-08-395-456C-25	Sequence 25, Appl	1061	226	16.4	723	4	US-08-605-221-4	Sequence 4, Appl
989	253	18.4	242	3	US-09-032-215-47	Sequence 47, Appl	1062	226	16.4	723	4	US-09-601-040A-10	Sequence 10, Appl
990	252.5	18.4	221	2	US-08-925-708-1	Sequence 1, Appl	1063	226	16.4	728	1	US-07-815-333A-2	Sequence 2, Appl
991	252.5	18.4	239	3	US-09-004-731-44	Sequence 44, Appl	1064	226	16.4	728	1	US-08-087-783A-22	Sequence 22, Appl
992	252.5	18.4	239	3	US-08-749-699-44	Sequence 44, Appl	1065	226	16.4	728	3	US-08-605-221-2	Sequence 2, Appl
993	252.5	18.4	239	4	US-09-004-729-44	Sequence 44, Appl	1066	223	16.2	723	3	US-08-030-410-3	Sequence 3, Appl
994	252.5	18.4	247	3	US-08-944-483-49	Sequence 49, Appl	1067	222	16.2	213	3	US-08-906-769-149	Sequence 149, App
995	252	18.3	229	4	US-08-395-456C-27	Sequence 27, Appl	1068	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
996	251	18.3	229	2	US-08-394-600B-20	Sequence 20, Appl	1069	222	16.2	213	3	US-08-639-075A-149	Sequence 149, App
997	251	18.3	229	4	US-08-395-456C-20	Sequence 20, Appl	1070	222	16.2	213	3	US-09-012-431-149	Sequence 149, App
998	251	18.3	229	4	US-08-487-453A-20	Sequence 20, Appl	1071	222	16.2	213	3	US-09-012-692-149	Sequence 149, App
999	251	18.3	229	5	PCT-US95-02513-20	Sequence 20, Appl	1072	222	16.2	213	3	US-08-906-613-149	Sequence 149, App
1000	250	18.2	352	4	US-09-902-540-97996	Sequence 9796, Ap	1073	222	16.2	234	3	US-08-944-483-56	Sequence 56, Appl
1001	248.5	18.1	717	4	US-09-601-040A-6	Sequence 6, Appl	1074	220.5	16.0	267	2	US-08-978-404B-46	Sequence 46, Appl
1002	248.5	18.1	717	4	US-09-601-040A-8	Sequence 8, Appl	1075	220	16.0	278	4	US-09-270-767-48024	Sequence 48024, A
1003	247.5	18.0	729	4	US-09-601-040A-4	Sequence 4, Appl	1076	220	16.0	457	4	US-09-270-767-32807	Sequence 32807, A
1004	247.5	18.0	729	4	US-08-944-483-30	Sequence 30, Appl	1077	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1005	247	18.0	229	3	US-08-944-483-30	Sequence 30, Appl	1078	217.5	15.8	385	4	US-09-345-881-16	Sequence 16, Appl
1006	245	17.8	226	4	US-09-601-040A-28	Sequence 28, Appl	1079	216	15.7	185	3	US-08-906-769-141	Sequence 141, App
1007	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1080	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1008	245	17.8	228	3	US-08-944-483-55	Sequence 55, Appl	1081	216	15.7	185	3	US-08-639-075A-141	Sequence 141, App
1009	245	17.8	228	3	US-09-296-219-11	Sequence 11, Appl	1082	216	15.7	185	3	US-09-012-431-141	Sequence 141, App
1010	245	17.8	711	1	US-08-184-012C-8	Sequence 8, Appl	1083	216	15.7	185	3	US-09-012-692-141	Sequence 141, App
1011	245	17.8	711	1	US-08-334-177-2	Sequence 2, Appl	1084	216	15.7	185	3	US-08-906-613-141	Sequence 141, App
1012	245	17.8	711	2	US-08-666-082B-1	Sequence 1, Appl	1085	216	15.7	223	1	US-08-278-091-13	Sequence 13, Appl
1013	245	17.8	711	2	US-08-766-982-2	Sequence 2, Appl	1086	216	15.7	223	1	US-08-483-859-13	Sequence 13, Appl
1014	245	17.8	711	3	US-09-296-219-2	Sequence 2, Appl	1087	216	15.7	223	1	US-08-472-173-13	Sequence 13, Appl
1015	245	17.8	711	4	US-09-600-991-20	Sequence 20, Appl	1088	216	15.7	223	2	US-08-487-167-13	Sequence 13, Appl
1016	245	17.8	711	4	US-09-601-040A-12	Sequence 12, Appl	1089	216	15.7	223	2	US-08-482-816-13	Sequence 13, Appl
1017	245	17.8	711	4	US-09-949-016-6981	Sequence 6981, Ap	1090	216	15.7	223	2	US-08-296-149-13	Sequence 13, Appl
1018	245	17.8	711	5	PCT-US95-13830-2	Sequence 2, Appl	1091	216	15.7	223	2	US-08-801-499-13	Sequence 13, Appl
1019	244.5	17.8	716	3	US-08-766-982-1	Sequence 1, Appl	1092	216	15.7	223	2	US-08-615-271-13	Sequence 13, Appl
1020	244.5	17.8	716	3	US-09-296-219-1	Sequence 1, Appl	1093	216	15.7	223	2	US-09-074-660-13	Sequence 13, Appl
1021	242	17.6	214	6	5180819-3	Patent No. 5180819	1094	216	15.7	223	3	US-09-074-659-13	Sequence 13, Appl
1022	242	17.6	214	6	5180819-3	Patent No. 5180819	1095	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1023	242	17.6	435	3	US-09-261-416-2	Sequence 2, Appl	1096	216	15.7	223	3	US-09-106-466A-13	Sequence 13, Appl
1024	240	17.5	161	3	US-09-261-416-8	Sequence 8, Appl	1097	216	15.7	223	3	US-09-106-467-13	Sequence 13, Appl
1025	234	17.0	158	3	US-09-518-046-22	Sequence 22, Appl	1098	211	15.4	223	1	US-08-485-455D-17	Sequence 17, Appl
1026	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1099	211	15.4	223	1	US-08-482-130C-17	Sequence 17, Appl
1027	232.5	16.9	185	3	US-09-220-731-22	Sequence 22, Appl	1100	211	15.4	223	2	US-08-484-211C-17	Sequence 17, Appl
1028	232.5	16.9	185	4	US-09-242-999-5	Sequence 5, Appl	1101	211	15.4	223	2	US-08-817-795-17	Sequence 17, Appl
1029	231.5	16.8	219	2	US-08-925-708-2	Sequence 2, Appl	1102	211	15.4	223	3	US-08-485-443B-17	Sequence 17, Appl
1030	231	16.8	242	3	US-08-944-483-29	Sequence 29, Appl	1103	211	15.4	223	5	PCT-US95-14442A-17	Sequence 17, Appl
1031	230.5	16.8	304	3	US-09-088-651-2	Sequence 2, Appl	1104	211	15.4	224	3	US-08-906-769-17	Sequence 17, Appl
1032	228.5	16.6	287	4	US-09-270-767-33263	Sequence 33263, A	1105	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1033	228.5	16.6	287	4	US-09-270-767-48480	Sequence 48480, A	1106	211	15.4	224	3	US-08-639-075A-17	Sequence 17, Appl
1034	227	16.5	258	4	US-09-023-942A-8	Sequence 8, Appl	1107	211	15.4	224	3	US-09-012-431-17	Sequence 17, Appl
1035	227	16.5	259	3	US-08-906-769-190	Sequence 190, Appl	1108	211	15.4	224	3	US-09-012-692-17	Sequence 17, Appl
1036	227	16.5	259	3	US-08-906-616-190	Sequence 190, App	1109	211	15.4	224	3	US-08-906-613-17	Sequence 17, Appl
1037	227	16.5	259	3	US-08-639-075A-190	Sequence 190, App	1110	211	15.4	224	3	US-08-906-613-17	Sequence 17, Appl
1038	227	16.5	259	3	US-09-004-731-85	Sequence 85, Appl	1111	210.5	15.3	222	4	US-09-270-767-62005	Sequence 62005, A
1039	227	16.5	259	3	US-09-012-431-190	Sequence 190, App	1112	210.5	15.3	238	3	US-08-944-483-31	Sequence 31, Appl
1040	227	16.5	259	3	US-08-749-699-85	Sequence 85, Appl	1113	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1041	227	16.5	259	3	US-09-012-692-190	Sequence 190, App	1114	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1042	227	16.5	259	3	US-08-906-613-190	Sequence 190, App	1115	206	15.0	164	3	US-09-518-046-25	Sequence 25, Appl
1043	227	16.5	259	4	US-09-004-729-85	Sequence 85, Appl	1116	206	15.0	250	4	US-09-270-767-33709	Sequence 33709, A
1044	227	16.5	723	3	US-08-700-519J-18	Sequence 18, Appl	1117	204.5	14.9	157	3	US-09-518-046-23	Sequence 23, Appl
1045	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1118	204.5	14.9	178	3	US-08-906-769-107	Sequence 107, App
1046	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1119	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1047	226	16.4	697	2	US-08-460-890A-50	Sequence 50, Appl	1120	204.5	14.9	178	3	US-08-817-795-107	Sequence 107, App
1048	226	16.4	697	3	US-08-167-641C-50	Sequence 50, Appl	1121	204.5	14.9	178	3	US-08-639-075A-107	Sequence 107, App
1049	226	16.4	697	3	US-08-460-971A-50	Sequence 50, Appl	1122	204.5	14.9	178	3	US-09-012-431-107	Sequence 107, App



1123	204.5	14.9	178	3	US-09-012-692-107	Sequence 107, App	1196	160.5	11.7	178	3	US-09-220-731-24	Sequence 24, Appl
1124	204.5	14.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	11.7	178	4	US-09-242-999-24	Sequence 24, Appl
1125	204.5	14.9	178	5	PCT-US95-14442A-107	Sequence 107, App	1198	160	11.6	97	4	US-09-270-767-31931	Sequence 31931, A
1126	200.5	14.6	159	3	US-09-518-046-24	Sequence 24, Appl	1199	160	11.6	97	4	US-09-270-767-47148	Sequence 47148, A
1127	200	14.6	223	4	US-09-270-767-45768	Sequence 45768, A	1200	159	11.6	190	2	US-08-845-998-6	Sequence 6, Appl
1128	198.5	14.4	254	3	US-08-906-769-129	Sequence 129, App	1201	159	11.6	190	3	US-09-206-537-6	Sequence 6, Appl
1129	198.5	14.4	254	3	US-08-906-616-129	Sequence 129, App	1202	159	11.6	190	3	US-09-430-854-6	Sequence 6, Appl
1130	198.5	14.4	254	3	US-08-639-075A-129	Sequence 129, App	1203	158	11.5	357	4	US-09-270-767-43564	Sequence 43564, A
1131	198.5	14.4	254	3	US-09-012-431-129	Sequence 129, App	1204	158	11.5	357	4	US-09-270-767-58936	Sequence 58936, A
1132	198.5	14.4	254	3	US-09-012-692-129	Sequence 129, App	1205	157.5	11.5	764	2	US-08-177-109A-2	Sequence 2, Appl
1133	198.5	14.4	254	3	US-08-906-613-129	Sequence 129, App	1206	157.5	11.5	764	2	US-08-687-706-2	Sequence 2, Appl
1134	196.5	14.3	141	4	US-09-949-016-7265	Sequence 7265, App	1207	157.5	11.5	798	4	US-09-949-016-11021	Sequence 11021, A
1135	195	14.2	326	3	US-09-411-577-3	Sequence 3, Appl	1208	157	11.4	141	4	US-09-513-999C-4215	Sequence 4215, App
1136	195	14.2	326	4	US-10-057-951-3	Sequence 3, Appl	1209	156.5	11.4	163	4	US-09-270-767-60652	Sequence 60652, A
1137	192.5	14.0	260	3	US-08-906-769-139	Sequence 139, App	1210	156.5	11.4	286	4	US-09-270-767-45162	Sequence 45162, A
1138	192.5	14.0	260	3	US-08-906-616-139	Sequence 139, App	1211	156	11.4	112	4	US-09-270-767-33319	Sequence 33319, A
1139	192.5	14.0	260	3	US-08-639-075A-139	Sequence 139, App	1212	156	11.4	112	4	US-09-270-767-48536	Sequence 48536, A
1140	192.5	14.0	260	3	US-09-012-431-139	Sequence 139, App	1213	154.5	11.2	204	3	US-08-906-769-147	Sequence 147, App
1141	192.5	14.0	260	3	US-09-012-692-139	Sequence 139, App	1214	154.5	11.2	204	3	US-08-639-075A-147	Sequence 147, App
1142	192.5	14.0	260	3	US-08-906-613-139	Sequence 139, App	1215	154.5	11.2	204	3	US-09-012-431-147	Sequence 147, App
1143	191	13.9	74	4	US-09-205-258-1151	Sequence 1151, App	1216	154.5	11.2	204	3	US-09-012-692-147	Sequence 147, App
1144	191	13.9	138	6	5200340-4	Patent No. 5200340	1217	154.5	11.2	204	3	US-08-906-613-147	Sequence 147, App
1145	191	13.9	138	6	5200340-4	Patent No. 5200340	1218	154.5	11.2	204	3	US-08-906-613-147	Sequence 147, App
1146	190	13.8	90	4	US-09-270-767-57991	Sequence 57991, A	1219	153.5	11.2	151	4	US-09-270-767-33178	Sequence 33178, A
1147	187	13.6	312	4	US-09-636-382A-15	Sequence 15, Appl	1220	153.5	11.2	151	4	US-09-270-767-48395	Sequence 48395, A
1148	186.5	13.6	570	4	US-10-067-422-9	Sequence 9, Appl	1221	152.5	11.1	139	4	US-09-270-767-33648	Sequence 33648, A
1149	186	13.5	159	4	US-09-618-259-5	Sequence 5, Appl	1222	150.5	11.0	79	4	US-09-270-767-33666	Sequence 33666, A
1150	183	13.3	313	4	US-09-270-767-44375	Sequence 44375, A	1223	150.5	11.0	79	4	US-09-270-767-48883	Sequence 48883, A
1151	183	13.3	145	3	US-08-906-769-123	Sequence 123, App	1224	149	10.8	77	3	US-09-439-313-329	Sequence 329, App
1152	182	13.2	145	3	US-08-906-616-123	Sequence 123, App	1225	149	10.8	77	3	US-09-352-616A-329	Sequence 329, App
1153	182	13.2	145	3	US-08-639-075A-123	Sequence 123, App	1226	149	10.8	77	4	US-09-232-149A-329	Sequence 329, App
1154	182	13.2	145	3	US-09-012-692-123	Sequence 123, App	1227	149	10.8	77	4	US-09-636-215-329	Sequence 329, App
1155	182	13.2	145	3	US-08-906-613-123	Sequence 123, App	1228	149	10.8	77	4	US-09-685-166A-329	Sequence 329, App
1156	181	13.2	118	4	US-09-621-976-5522	Sequence 5522, App	1229	149	10.8	77	4	US-09-688-489-329	Sequence 329, App
1157	181	13.2	133	4	US-09-949-016-7471	Sequence 7471, App	1230	149	10.8	77	4	US-09-679-426-329	Sequence 329, App
1158	180	13.1	144	3	US-09-012-431-123	Sequence 123, App	1231	149	10.8	77	4	US-09-753-143-329	Sequence 329, App
1159	178.5	13.0	164	3	US-09-020-956-178	Sequence 178, App	1232	149	10.8	77	4	US-09-651-236-329	Sequence 329, App
1160	178.5	13.0	164	3	US-09-430-607-178	Sequence 178, App	1233	148.5	10.8	276	4	US-09-270-767-32048	Sequence 32048, A
1161	178.5	13.0	164	3	US-09-439-313-178	Sequence 178, App	1234	148.5	10.8	276	4	US-09-270-767-47265	Sequence 47265, A
1162	178.5	13.0	164	3	US-09-352-616A-178	Sequence 178, App	1235	143.5	10.4	72	3	US-08-906-769-87	Sequence 87, Appl
1163	178.5	13.0	164	4	US-09-232-149A-178	Sequence 178, App	1236	143.5	10.4	72	3	US-08-906-616-87	Sequence 87, Appl
1164	178.5	13.0	164	4	US-09-159-812-178	Sequence 178, App	1237	143.5	10.4	72	3	US-08-817-795-87	Sequence 87, Appl
1165	178.5	13.0	164	4	US-09-636-215-178	Sequence 178, App	1238	143.5	10.4	72	3	US-08-639-075A-87	Sequence 87, Appl
1166	178.5	13.0	164	4	US-09-685-166A-178	Sequence 178, App	1239	143.5	10.4	72	3	US-09-012-431-87	Sequence 87, Appl
1167	178.5	13.0	164	4	US-09-115-453-178	Sequence 178, App	1240	143.5	10.4	72	3	US-09-012-692-87	Sequence 87, Appl
1168	178.5	13.0	164	4	US-09-688-489-178	Sequence 178, App	1241	143.5	10.4	72	3	US-08-906-613-87	Sequence 87, Appl
1169	178.5	13.0	164	4	US-09-679-426-178	Sequence 178, App	1242	143.5	10.4	72	5	PCT-US95-14442A-87	Sequence 87, Appl
1170	178.5	13.0	164	4	US-09-759-143-178	Sequence 178, App	1243	142.5	10.4	208	3	US-08-906-769-151	Sequence 151, App
1171	178.5	13.0	164	4	US-09-651-236-178	Sequence 178, App	1244	142.5	10.4	208	3	US-08-906-616-151	Sequence 151, App
1172	178	13.0	346	4	US-09-949-016-9000	Sequence 9000, App	1245	142.5	10.4	208	3	US-08-639-075A-151	Sequence 151, App
1173	176	12.8	348	4	US-09-949-016-6979	Sequence 6979, App	1246	142.5	10.4	208	3	US-09-012-431-151	Sequence 151, App
1174	174.5	12.7	271	3	US-09-578-303-6	Sequence 6, Appl	1247	142.5	10.4	208	3	US-09-012-692-151	Sequence 151, App
1175	171.5	12.5	218	4	US-09-270-767-44299	Sequence 44299, A	1248	142.5	10.4	208	3	US-08-906-613-151	Sequence 151, App
1176	168	12.2	141	3	US-08-906-769-135	Sequence 135, App	1249	141.5	10.3	85	4	US-09-270-767-32321	Sequence 32321, A
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1178	168	12.2	141	3	US-08-639-075A-135	Sequence 135, App	1251	139	10.1	87	3	US-08-906-769-161	Sequence 161, App
1179	168	12.2	141	3	US-09-012-431-135	Sequence 135, App	1252	139	10.1	87	3	US-08-906-616-161	Sequence 161, App
1180	168	12.2	141	3	US-09-012-692-135	Sequence 135, App	1253	139	10.1	87	3	US-08-639-075A-161	Sequence 161, App
1181	168	12.2	141	3	US-08-906-613-135	Sequence 135, App	1254	139	10.1	87	3	US-09-012-431-161	Sequence 161, App
1182	166.5	12.1	178	3	US-08-705-875A-8	Sequence 8, Appl	1255	139	10.1	87	3	US-09-012-692-161	Sequence 161, App
1183	166.5	12.1	178	3	US-09-220-731-23	Sequence 23, Appl	1256	139	10.1	87	3	US-08-906-613-161	Sequence 161, App
1184	166.5	12.1	178	3	US-09-242-999-8	Sequence 8, Appl	1257	139	10.1	89	3	US-08-906-769-165	Sequence 165, App
1185	166	12.1	243	4	US-09-270-767-44348	Sequence 44348, A	1258	139	10.1	89	3	US-08-906-616-165	Sequence 165, App
1186	166	12.1	769	4	US-09-949-016-11019	Sequence 11019, A	1259	139	10.1	89	3	US-08-639-075A-165	Sequence 165, App
1187	165	12.0	198	3	US-08-906-769-133	Sequence 133, App	1260	139	10.1	89	3	US-09-012-431-165	Sequence 165, App
1188	165	12.0	198	3	US-08-906-616-133	Sequence 133, App	1261	139	10.1	89	3	US-09-012-692-165	Sequence 165, App
1189	165	12.0	198	3	US-08-639-075A-133	Sequence 133, App	1262	139	10.1	89	3	US-08-906-613-165	Sequence 165, App
1190	165	12.0	198	3	US-09-012-431-133	Sequence 133, App	1263	138	10.0	278	4	US-09-602-777A-76	Sequence 76, Appl
1191	165	12.0	198	3	US-09-012-692-133	Sequence 133, App	1264	134	9.8	203	4	US-09-270-767-32531	Sequence 32531, A
1192	165	12.0	198	3	US-08-906-613-133	Sequence 133, App	1265	134	9.8	203	4	US-09-270-767-47748	Sequence 47748, A
1193	163	11.9	190	2	US-08-845-998-4	Sequence 4, Appl	1266	129	9.4	200	3	US-09-008-271A-5	Sequence 5, Appl
1194	163	11.9	190	3	US-09-206-537-4	Sequence 4, Appl	1267	128	9.3	246	4	US-09-370-838-60	Sequence 60, Appl
1195	163	11.9	190	3	US-09-430-854-4	Sequence 4, Appl	1268	128	9.3	246	4	US-09-854-133-60	Sequence 60, Appl

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1270	126.5	9.2	160	4	US-09-270-767-48759	Sequence 48759, A	1343	117.5	8.6	396	4	US-09-800-729-86	Sequence 86, Appl
1271	126	9.2	142	3	US-08-906-769-155	Sequence 155, App	1344	115.5	8.4	138	4	US-09-270-767-32323	Sequence 32323, A
1272	126	9.2	142	3	US-08-906-616-155	Sequence 155, App	1345	115.5	8.4	138	4	US-09-270-767-47540	Sequence 47540, A
1273	126	9.2	142	3	US-08-639-075A-155	Sequence 155, App	1346	115	8.4	80	1	US-08-485-455D-69	Sequence 69, Appl
1274	126	9.2	142	3	US-09-004-731-83	Sequence 83, Appl	1347	115	8.4	80	2	US-08-482-130C-69	Sequence 69, Appl
1275	126	9.2	142	3	US-09-012-431-155	Sequence 155, App	1348	115	8.4	80	2	US-08-484-211C-69	Sequence 69, Appl
1276	126	9.2	142	3	US-08-749-699-83	Sequence 83, Appl	1349	114	8.3	330	4	US-09-270-767-32670	Sequence 32670, A
1277	126	9.2	142	3	US-09-012-692-155	Sequence 155, App	1350	114	8.3	330	4	US-09-270-767-47887	Sequence 47887, A
1278	126	9.2	142	3	US-08-906-613-155	Sequence 155, App	1351	113	8.2	137	4	US-09-270-767-61091	Sequence 61091, A
1279	126	9.2	142	3	US-09-004-729-83	Sequence 83, Appl	1352	112	8.2	80	3	US-08-906-769-69	Sequence 69, Appl
1280	124	9.0	125	3	US-08-906-769-97	Sequence 97, Appl	1353	112	8.2	80	3	US-08-906-616-69	Sequence 69, Appl
1281	124	9.0	125	3	US-08-906-616-97	Sequence 97, Appl	1354	112	8.2	80	3	US-08-817-795-69	Sequence 69, Appl
1282	124	9.0	125	3	US-08-817-795-97	Sequence 97, Appl	1355	112	8.2	80	3	US-08-485-443B-69	Sequence 69, Appl
1283	124	9.0	125	3	US-08-639-075A-97	Sequence 97, Appl	1356	112	8.2	80	3	US-08-639-075A-69	Sequence 69, Appl
1284	124	9.0	125	3	US-09-012-431-97	Sequence 97, Appl	1357	112	8.2	80	3	US-09-012-431-69	Sequence 69, Appl
1285	124	9.0	125	3	US-09-012-692-97	Sequence 97, Appl	1358	112	8.2	80	3	US-09-012-692-69	Sequence 69, Appl
1286	124	9.0	125	3	US-08-906-613-97	Sequence 97, Appl	1359	112	8.2	80	3	US-08-906-613-69	Sequence 69, Appl
1287	124	9.0	125	5	PCT-US95-14442A-97	Sequence 97, Appl	1360	112	8.2	80	5	PCT-US95-14442A-69	Sequence 69, Appl
1288	123.5	9.0	113	4	US-09-513-999C-4899	Sequence 4899, Ap	1361	111.5	8.1	179	4	US-09-270-767-31777	Sequence 31777, A
1289	123	9.0	193	4	US-09-270-767-32917	Sequence 32917, A	1362	111.5	8.1	179	4	US-09-270-767-46994	Sequence 46994, A
1290	123	9.0	193	4	US-09-270-767-48134	Sequence 48134, A	1363	110.5	8.0	99	3	US-08-906-769-93	Sequence 93, Appl
1291	121.5	8.8	86	1	US-08-485-455D-53	Sequence 53, Appl	1364	110.5	8.0	99	3	US-08-906-616-93	Sequence 93, Appl
1292	121.5	8.8	86	2	US-08-482-130C-53	Sequence 53, Appl	1365	110.5	8.0	99	3	US-08-817-795-93	Sequence 93, Appl
1293	121.5	8.8	86	2	US-08-484-211C-53	Sequence 53, Appl	1366	110.5	8.0	99	3	US-08-639-075A-93	Sequence 93, Appl
1294	121.5	8.8	86	3	US-08-906-769-53	Sequence 53, Appl	1367	110.5	8.0	99	3	US-09-012-431-93	Sequence 93, Appl
1295	121.5	8.8	86	3	US-08-906-616-53	Sequence 53, Appl	1368	110.5	8.0	99	3	US-09-012-692-93	Sequence 93, Appl
1296	121.5	8.8	86	3	US-08-817-795-53	Sequence 53, Appl	1369	110.5	8.0	99	3	US-08-906-613-93	Sequence 93, Appl
1297	121.5	8.8	86	3	US-08-485-443B-53	Sequence 53, Appl	1370	110.5	8.0	99	5	PCT-US95-14442A-93	Sequence 93, Appl
1298	121.5	8.8	86	3	US-08-639-075A-53	Sequence 53, Appl	1371	110	8.0	253	2	US-08-392-546C-2	Sequence 2, Appl
1299	121.5	8.8	86	3	US-09-012-431-53	Sequence 53, Appl	1372	109.5	8.0	33	4	US-09-270-767-47559	Sequence 47559, A
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1301	121.5	8.8	86	3	US-08-906-613-53	Sequence 53, Appl	1374	106	7.7	157	2	US-08-811-949-41	Sequence 41, Appl
1302	121.5	8.8	86	5	PCT-US95-14442A-53	Sequence 53, Appl	1375	105.5	7.7	36	3	US-08-944-483-26	Sequence 26, Appl
1303	120.5	8.8	45	3	US-09-070-526-4	Sequence 4, Appl	1376	105.5	7.7	97	4	US-09-270-767-32342	Sequence 32342, A
1304	120	8.7	130	1	US-08-485-455D-67	Sequence 67, Appl	1377	105.5	7.7	97	4	US-09-270-767-47559	Sequence 47559, A
1305	120	8.7	130	2	US-08-482-130C-67	Sequence 67, Appl	1378	105.5	7.7	136	3	US-08-906-769-137	Sequence 137, App
1306	120	8.7	130	2	US-08-484-211C-67	Sequence 67, Appl	1379	105.5	7.7	136	3	US-08-906-616-137	Sequence 137, App
1307	120	8.7	130	3	US-08-906-769-67	Sequence 67, Appl	1380	105.5	7.7	136	3	US-08-639-075A-137	Sequence 137, App
1308	120	8.7	130	3	US-08-906-616-67	Sequence 67, Appl	1381	105.5	7.7	136	3	US-09-004-731-79	Sequence 79, Appl
1309	120	8.7	130	3	US-08-817-795-67	Sequence 67, Appl	1382	105.5	7.7	136	3	US-09-012-431-137	Sequence 137, App
1310	120	8.7	130	3	US-08-485-443B-67	Sequence 67, Appl	1383	105.5	7.7	136	3	US-08-749-699-79	Sequence 79, Appl
1311	120	8.7	130	3	US-08-639-075A-67	Sequence 67, Appl	1384	105.5	7.7	136	3	US-09-012-692-137	Sequence 137, App
1312	120	8.7	130	3	US-09-012-431-67	Sequence 67, Appl	1385	105.5	7.7	136	3	US-08-906-613-137	Sequence 137, App
1313	120	8.7	130	3	US-09-012-692-67	Sequence 67, Appl	1386	105.5	7.7	136	4	US-09-004-729-79	Sequence 79, Appl
1314	120	8.7	130	3	US-08-906-613-67	Sequence 67, Appl	1387	104.5	7.6	441	4	US-09-949-016-10792	Sequence 10792, A
1315	120	8.7	130	5	PCT-US95-14442A-67	Sequence 67, Appl	1388	102.5	7.5	80	1	US-08-485-455D-59	Sequence 59, Appl
1316	119	8.7	97	1	US-08-485-455D-63	Sequence 63, Appl	1389	102.5	7.5	80	2	US-08-482-130C-59	Sequence 59, Appl
1317	119	8.7	97	2	US-08-482-130C-63	Sequence 63, Appl	1390	102.5	7.5	80	2	US-08-484-211C-59	Sequence 59, Appl
1318	119	8.7	97	2	US-08-484-211C-63	Sequence 63, Appl	1391	102.5	7.5	80	3	US-08-906-769-59	Sequence 59, Appl
1319	119	8.7	97	3	US-08-906-769-63	Sequence 63, Appl	1392	102.5	7.5	80	3	US-08-906-616-59	Sequence 59, Appl
1320	119	8.7	97	3	US-08-906-616-63	Sequence 63, Appl	1393	102.5	7.5	80	3	US-08-817-795-59	Sequence 59, Appl
1321	119	8.7	97	3	US-08-817-795-63	Sequence 63, Appl	1394	102.5	7.5	80	3	US-08-485-443B-59	Sequence 59, Appl
1322	119	8.7	97	3	US-08-485-443B-63	Sequence 63, Appl	1395	102.5	7.5	80	3	US-08-639-075A-59	Sequence 59, Appl
1323	119	8.7	97	3	US-08-639-075A-63	Sequence 63, Appl	1396	102.5	7.5	80	3	US-09-012-431-59	Sequence 59, Appl
1324	119	8.7	97	3	US-09-012-431-63	Sequence 63, Appl	1397	102.5	7.5	80	3	US-09-012-692-59	Sequence 59, Appl
1325	119	8.7	97	3	US-09-012-692-63	Sequence 63, Appl	1398	102.5	7.5	80	3	US-08-906-613-59	Sequence 59, Appl
1326	119	8.7	97	3	US-08-906-613-63	Sequence 63, Appl	1399	102.5	7.5	80	5	PCT-US95-14442A-59	Sequence 59, Appl
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1328	118	8.6	130	3	US-08-906-769-157	Sequence 157, App	1401	101.5	7.4	117	4	US-09-270-767-47534	Sequence 47534, A
1329	118	8.6	130	3	US-08-906-616-157	Sequence 157, App	1402	101	7.4	125	4	US-09-270-767-33002	Sequence 33002, A
1330	118	8.6	130	3	US-08-639-075A-157	Sequence 157, App	1403	101	7.4	125	4	US-09-270-767-48219	Sequence 48219, A
1331	118	8.6	130	3	US-09-012-431-157	Sequence 157, App	1404	101	7.4	339	4	US-09-543-681A-6965	Sequence 6965, Ap
1332	118	8.6	130	3	US-09-012-692-157	Sequence 157, App	1405	100.5	7.3	55	4	US-08-843-076D-22	Sequence 22, Appl
1333	118	8.6	130	3	US-08-906-613-157	Sequence 157, App	1406	100	7.3	68	1	US-08-485-455D-77	Sequence 77, Appl
1334	117.5	8.6	144	3	US-08-906-769-153	Sequence 153, App	1407	100	7.3	68	2	US-08-482-130C-77	Sequence 77, Appl
1335	117.5	8.6	144	3	US-08-906-616-153	Sequence 153, App	1408	100	7.3	68	2	US-08-484-211C-77	Sequence 77, Appl
1336	117.5	8.6	144	3	US-08-639-075A-153	Sequence 153, App	1409	100	7.3	68	3	US-08-906-769-77	Sequence 77, Appl
1337	117.5	8.6	144	3	US-09-004-731-81	Sequence 81, Appl	1410	100	7.3	68	3	US-08-906-616-77	Sequence 77, Appl
1338	117.5	8.6	144	3	US-09-012-431-153	Sequence 153, App	1411	100	7.3	68	3	US-08-817-795-77	Sequence 77, Appl
1339	117.5	8.6	144	3	US-08-749-699-81	Sequence 81, Appl	1412	100	7.3	68	3	US-08-485-443B-77	Sequence 77, Appl
1340	117.5	8.6	144	3	US-09-012-692-153	Sequence 153, App	1413	100	7.3	68	3	US-08-639-075A-77	Sequence 77, Appl
1341	117.5	8.6	144	3	US-08-906-613-153	Sequence 153, App	1414	100	7.3	68	3	US-09-012-431-77	Sequence 77, Appl

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1416	100	7.3	68	3	US-08-906-613-77	Sequence 77, Appl	1489	88	6.4	102	3	US-09-012-431-125	Sequence 125, App
1417	100	7.3	68	5	PCT-US95-14442A-77	Sequence 77, Appl	1490	88	6.4	102	3	US-09-012-692-125	Sequence 125, App
1418	100	7.3	69	3	US-08-906-769-101	Sequence 101, App	1491	88	6.4	102	3	US-08-906-613-125	Sequence 125, App
1419	100	7.3	69	3	US-08-906-616-101	Sequence 101, App	1492	88	6.4	238	4	US-09-270-767-44825	Sequence 44825, A
1420	100	7.3	69	3	US-08-817-795-101	Sequence 101, App	1493	87.5	6.4	64	1	US-08-485-455D-75	Sequence 75, Appl
1421	100	7.3	69	3	US-08-639-075A-101	Sequence 101, App	1494	87.5	6.4	64	2	US-08-482-130C-75	Sequence 75, Appl
1422	100	7.3	69	3	US-09-012-431-101	Sequence 101, App	1495	87.5	6.4	64	2	US-08-484-211C-75	Sequence 75, Appl
1423	100	7.3	69	3	US-09-012-692-101	Sequence 101, App	1496	87.5	6.4	64	3	US-08-906-769-75	Sequence 75, Appl
1424	100	7.3	69	3	US-08-906-613-101	Sequence 101, App	1497	87.5	6.4	64	3	US-08-906-616-75	Sequence 75, Appl
1425	100	7.3	69	3	PCT-US95-14442A-101	Sequence 101, App	1498	87.5	6.4	64	3	US-08-817-795-75	Sequence 75, Appl
1426	99.5	7.2	84	3	US-08-906-769-99	Sequence 99, Appl	1499	87.5	6.4	64	3	US-08-485-443B-75	Sequence 75, Appl
1427	98.5	7.2	84	3	US-08-906-616-99	Sequence 99, Appl	1500	87.5	6.4	64	3	US-08-639-075A-75	Sequence 75, Appl
1428	99.5	7.2	84	3	US-08-817-795-99	Sequence 99, Appl							
1429	99.5	7.2	84	3	US-08-639-075A-99	Sequence 99, Appl							
1430	99.5	7.2	84	3	US-09-012-431-99	Sequence 99, Appl							
1431	99.5	7.2	84	3	US-09-012-692-99	Sequence 99, Appl							
1432	99.5	7.2	84	3	US-08-906-613-99	Sequence 99, Appl							
1433	98.5	7.2	84	5	PCT-US95-14442A-99	Sequence 99, Appl							
1434	99.5	7.2	146	4	US-09-270-767-43546	Sequence 43546, A							
1435	99	7.2	50	1	US-07-666-913A-2	Sequence 2, Appl							
1436	98.5	7.2	128	3	US-08-906-769-143	Sequence 143, App							
1437	98.5	7.2	128	3	US-08-906-616-143	Sequence 143, App							
1438	98.5	7.2	128	3	US-08-639-075A-143	Sequence 143, App							
1439	98.5	7.2	128	3	US-09-012-431-143	Sequence 143, App							
1440	98.5	7.2	128	3	US-08-906-613-143	Sequence 143, App							
1441	98.5	7.2	108	4	US-09-270-767-33364	Sequence 33364, A							
1442	97.5	7.1	142	3	US-09-004-731-38	Sequence 38, Appl							
1443	97.5	7.1	142	3	US-08-749-699-38	Sequence 38, Appl							
1444	97.5	7.1	142	4	US-09-004-729-38	Sequence 38, Appl							
1445	97.5	7.1	149	4	US-09-270-767-46053	Sequence 46053, A							
1446	97.5	7.1	639	2	US-08-637-899-1	Sequence 1, Appl							
1447	97	7.1	93	4	US-09-621-976-4137	Sequence 4137, Ap							
1448	96	7.0	332	4	US-09-602-777A-42	Sequence 42, Appl							
1449	95	6.9	102	4	US-09-270-767-58913	Sequence 58913, A							
1450	94.5	6.9	119	3	US-08-906-769-109	Sequence 109, App							
1451	94.5	6.9	119	3	US-08-906-616-109	Sequence 109, App							
1452	94.5	6.9	119	3	US-08-817-795-109	Sequence 109, App							
1453	94.5	6.9	119	3	US-08-639-075A-109	Sequence 109, App							
1454	94.5	6.9	119	3	US-09-012-431-109	Sequence 109, App							
1455	94.5	6.9	119	3	US-09-012-692-109	Sequence 109, App							
1456	94.5	6.9	119	3	US-08-906-613-109	Sequence 109, App							
1457	94.5	6.9	119	5	PCT-US95-14442A-109	Sequence 109, App							
1458	94.5	6.9	123	4	US-09-949-016-93268	Sequence 9268, Ap							
1459	93.5	6.8	185	1	US-08-278-091-14	Sequence 14, Appl							
1460	93.5	6.8	185	1	US-08-483-859-14	Sequence 14, Appl							
1461	93.5	6.8	185	1	US-08-472-173-14	Sequence 14, Appl							
1462	93.5	6.8	185	2	US-08-487-167-14	Sequence 14, Appl							
1463	93.5	6.8	185	2	US-08-482-816-14	Sequence 14, Appl							
1464	93.5	6.8	185	2	US-08-296-149-14	Sequence 14, Appl							
1465	93.5	6.8	185	2	US-08-801-499-14	Sequence 14, Appl							
1466	93.5	6.8	185	2	US-08-615-271-14	Sequence 14, Appl							
1467	93.5	6.8	185	3	US-09-074-660-14	Sequence 14, Appl							
1468	93.5	6.8	185	3	US-09-106-468-14	Sequence 14, Appl							
1469	93.5	6.8	185	3	US-09-106-466A-14	Sequence 14, Appl							
1470	93.5	6.8	185	3	US-09-106-467-14	Sequence 14, Appl							
1471	93.5	6.8	185	6	5514590-10	Patent No. 5514590							
1472	93.5	6.8	185	6	5514590-10	Patent No. 5514590							
1473	93.5	6.8	185	6	5514590-4	Patent No. 5514590							
1474	93.5	6.8	220	4	US-09-270-767-42857	Sequence 42857, A							
1475	93.5	6.8	220	4	US-08-293-778-11	Sequence 11, Appl							
1476	93.5	6.8	163	4	US-09-270-767-32837	Sequence 32837, A							
1477	93	6.8	501	4	US-09-252-991A-19191	Sequence 19191, A							
1478	90	6.6	3594	4	US-09-911-842A-4	Sequence 4, Appl							
1479	89.5	6.5	294	3	US-09-518-046-4	Sequence 4, Appl							
1480	89.5	6.5	1935	4	US-09-949-016-10403	Sequence 10403, A							
1481	89	6.5	2205	1	US-08-093-453B-2	Sequence 2, Appl							
1482	88.5	6.4	52	4	US-09-270-767-59783	Sequence 59783, A							
1483	88.5	6.4	102	3	US-08-906-769-125	Sequence 125, App							
1484	88.5	6.4	102	3	US-08-906-616-125	Sequence 125, App							
1485	88	6.4											
1486	88	6.4											
1487	88	6.4											

## ALIGNMENTS

## RESULT 1

US-09-949-016-8151  
; Sequence 8151, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8151  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8151

Query Match 98.9%; Score 1359.5; DB 4; Length 249;

Best Local Similarity 99.6%; Pred. No. 3.1e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGLSIFLLCVLGLSQAATPKIFNCTGCRNSQPNQVGLFECTSLRCGGVLIDHRWLTA 60

Db 3 MGLSIFLLCVLGLSQAATPKIFNCTGCRNSQPNQVGLFECTSLRCGGVLIDHRWLTA 62

QY 61 AHCSGRYVVRLLGEHLSQLDWTQEIHRHSGFSVTHPGYLGASTSHEHDLRLRLPLVRV 120

Db 63 AHCSG-RYVVRLLGEHLSQLDWTQEIHRHSGFSVTHPGYLGASTSHEHDLRLRLPLVRV 121

QY 121 TSSVQPLPLNDCAATGTECHVSGWGIINHPNPPFDLLQCLNLSIVSHATGCHVYPGRI 180

Db 122 TSSVQPLPLNDCAATGTECHVSGWGIINHPNPPFDLLQCLNLSIVSHATGCHVYPGRI 181

QY 181 TSNMVACAGVPGQDACQDSDGGPLVCGVGLVSGVSGPCQDGIIPGVYTYCKYVDW 240

Db 182 TSNMVACAGVPGQDACQDSDGGPLVCGVGLVSGVSGPCQDGIIPGVYTYCKYVDW 241

QY 241 IRMINRNN 248

Db 242 IRMINRNN 249

RESULT 2

US-09-949-016-6948

; Sequence 6948, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6948  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6948

Query Match 94.7%; Score 1301; DB 4; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.5e-118;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSIRCCGVLIDHRWVLTAA 60  
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSIRCCGVLIDHRWVLTAA 60  
QY 61 AHCSGRYVWRLGHSLSOLDTEQIRHSGFVTHPGVYLGASTSHEHDLRLRLRPVRV 120  
DB 61 AHCSGRYVWRLGHSLSOLDTEQIRHSGFVTHPGVYLGASTSHEHDLRLRLRPVRV 120  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDILLQCLNLSIVSHATGCHGVYVPGRI 180  
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDILLQCLNLSIVSHATGCHGVYVPGRI 180  
QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGI PGVYTYICKYVDW 235  
DB 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGI PGVYTYICKYVDW 235

## RESULT 3

US-09-244-111-6  
; Sequence 6, Application US/09244111  
; Patent No. 6566498  
; GENERAL INFORMATION:

; APPLICANT: NI, et al.  
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides

; FILE REFERENCE: PF391  
; CURRENT APPLICATION NUMBER: US/09/244,111

; CURRENT FILING DATE: 1999-02-04

; EARLIER APPLICATION NUMBER: 60/073,961

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-244-111-6

Query Match 59.0%; Score 811; DB 4; Length 162;

Best Local Similarity 64.1%; Pred. No. 3.8e-71;

Matches 159; Conservative 0; Mismatches 3; Indels 86; Gaps 3;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSIRCCGVLIDHRWVLTAA 60  
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSIRCCGVLIDHRWVLTAA 60

QY 61 AHCSGRYVWRLGHSLSOLDTEQIRHSGFVTHPGVYLGASTSHEHDLRLRLRPVRV 120

DB 61 AH-----WQRO-----THS----- 69

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDILLQCLNLSIVSHATGCHGVYVPGRI 180  
DB 70 -----PDLQLCLNLSIVSHATGCHGVYVPGRI 94  
QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGI PGVYTYICKYVDW 240  
DB 95 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGI PGVYTYICKYVDW 154  
QY 241 IRMIMENN 248  
DB 155 IRMIMENN 162

## RESULT 4

US-09-618-259-7

; Sequence 7, Application US/09618259

; Patent No. 6642013

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Underwood, Lowell J.

; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease

; FILE REFERENCE: D6020CIP2

; CURRENT APPLICATION NUMBER: US/09/618,259

; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: US 09/127,444

; PRIOR FILING DATE: 1998-08-21

; NUMBER OF SEQ ID NOS: 72

; SEQ ID NO 7

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of TADG-14 protein

US-09-618-259-7

Query Match 45.9%; Score 630.5; DB 4; Length 260;

Best Local Similarity 50.2%; Pred. No. 2.5e-53;

Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSIRCCGVLIDHRWVLTAA 61  
DB 13 MFLLLGGAWAGHSAQEDKVLGGHECQPHSQPWAALFQGOQLLCGVLVGNWVLTAA 72

QY 62 HCSGRYVWRLGHSLSOLDTEQIRHSGFVTHPGVYLGAST-SHEHDLRLRLRPVRV 120

DB 73 HCKKPKYTVRLGDHSLQNKDQPEQI PVVQSTPHPCYNSDDVEDHNDLMLQLRDQASL 132

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPRNPFPDILLQCLNLSIVSHATGCHGVYVPGRI 180

DB 133 GSKVKPTSLADHCTQPGQKCTVSGWGTVPSTPRENPFDTLNCAEVKIFPQKCEDAYPGQI 192

QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGI PGVYTYICKYVDW 240

DB 193 TDGMVCAGSSKGADTCQDGGPLVCDGALQGITSWGSDPCGRSDKFGVYTNICRYLDW 251

QY 241 IRMIM 245

DB 252 IKKII 256

## RESULT 5

US-09-070-526-2

; Sequence 2, Application US/09070526

; Patent No. 6100059

; GENERAL INFORMATION:

; APPLICANT: SOUTHAN, CHRISTOPHER

; APPLICANT: CLINKENBEARD, HELEN

; APPLICANT: BURGESS, NICOLA

; TITLE OF INVENTION: No. 6100059el Compounds

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P. O. BOX 980

/ CITY: VALLEY FORGE  
/ STATE: PA  
/ COUNTRY: USA  
/ ZIP: 19482  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSEQ for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/070,526  
/ FILING DATE: 30-APR-1998  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: GB 9711952.3  
/ FILING DATE: 9-JUN-1997  
/ APPLICATION NUMBER: EP 97309646.4  
/ FILING DATE: 1-DEC-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: PRESTIA, PAUL F  
/ REGISTRATION NUMBER: 23,031  
/ REFERENCE/DOCKET NUMBER: GH-30353  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 610-407-0700  
/ TELEFAX: 610-407-0701  
/ TELEX: 846169  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 260 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-09-070-526-2

Query Match 45.6%; Score 626.5; DB 3; Length 260;  
Best Local Similarity 50.4%; Pred. No. 6.2e-53;  
Matches 122; Conservative 23; Mismatches 92; Indels 5; Gaps 3;  
  
QY 5 IFLLV---CVLGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWLTAA 61  
DB 13 MFLLLGGNAGHSRAQEDKVLGGECQPHSQPWAALFQGGQLCGVVGNNWLTAA 72  
  
QY 62 HCSGRYVRLGEHSLQSLDWTETQIRHSGFVTHPGYLGAST-SHEHDLRLRLPLRV 120  
DB 73 HCKKPKYTVRLGDHSLQNGDPEQEI PVVQSI PHPCYNSSDVEDHNDLMLQLRQASL 132  
  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDILLQCLNLSIVSHATCHGVYPGRI 180  
DB 133 GSKVPISLADHCTQPGQKTVSGMGTVTSPPNFPDITLNCFAEVKIFPOKKCEDAYPGQI 192  
  
QY 181 TSNMVCAGVPQDADACQDGGPLVCGGVLOGLVSGSVGPCQDGI PGVYTVICKYVDW 240  
DB 193 TGMVCAKSGKADTCQDGGPLVCGDGLQGITSWGSDPCGRSDKPGVYTNICRYLDW 251  
  
QY 241 IR 242  
DB 252 IK 253

RESULT 6  
US-09-025-059-3  
; Sequence 3, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.

/ CITY: Palo Alto  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94304  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSEQ for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/025,059  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Billings, Lucy J  
/ REGISTRATION NUMBER: 36,749  
/ REFERENCE/DOCKET NUMBER: PF-0481 US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 650-855-0555  
/ TELEFAX: 650-845-4166  
/ TELEX:  
/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 260 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ IMMEDIATE SOURCE:  
/ LIBRARY: GenBank  
/ CLONE: 1020091  
/ US-09-025-059-3

Query Match 45.3%; Score 622.5; DB 3; Length 260;  
Best Local Similarity 49.0%; Pred. No. 1.5e-52;  
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;  
  
QY 5 IFLLV---LGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWLTAA 61  
DB 13 ILLLLFMGNAGWAGTRAQSKILEGECIPHSPQWAALFQGERLICGGVLVGRWLTAA 72  
  
QY 62 HCSGRYVRLGEHSLQSLDWTETQIRHSGFVTHPGYLGAS-TSHEHDLRLRLPLRV 120  
DB 73 HCKKPKYTVRLGDHSLQSRDQPEQEIQAQSIQHPCYNNNSPEDHSHDMLRLONSA 132  
  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDILLQCLNLSIVSHATCHGVYPGRI 180  
DB 133 GSKVPIVQLANLCPKVQKCIISGMGTVTSPPNFPDITLNCFAEVKISQNKCEAYPGKI 192  
  
QY 181 TSNMVCAGVPQDADACQDGGPLVCGGVLOGLVSGSVGPCQDGI PGVYTVICKYVDW 240  
DB 193 TGMVCAKSGKADTCQDGGPLVCGDGLQGITSWGSDPCGKPKPGVYTKICRYTTW 251  
  
QY 241 IRMINRN 247  
DB 252 IKKTMND 258

RESULT 7  
US-09-008-271A-7  
; Sequence 7, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/008,271A  
 ; FILING DATE: 16-Jan-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mohan-Peterson, Sheela  
 ; REGISTRATION NUMBER: 41,201  
 ; REFERENCE/DOCKET NUMBER: PF-0458 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 260 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: COLANOT27  
 ; CLONE: 1798496  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :  
 US-09-008-271A-7

Query Match 45.3%; Score 622.5; DB 3; Length 260;  
 Best Local Similarity 49.8%; Pred. No. 1.5e-52;  
 Matches 122; Conservative 24; Mismatches 94; Indels 5; Gaps 3;  
 QY 5 IFLLLCV---CVLGLSQAATPKIFNGTECGRNSQPWQVGLPFGTSLRCGGVLIDHRWVLTAA 61  
 DB 13 IFLLLCV---CVLGLSQAATPKIFNGTECGRNSQPWQVGLPFGTSLRCGGVLIDHRWVLTAA 72  
 QY 62 HCSGRYVRLGEHLSQLDWTQIRHSGFSTVTHPGYLGAST-SHEHDLRLRLPLVRV 120  
 DB 73 HCKKPKYTVRLGDHSLQSDGSGPLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 132  
 QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHPNPPDILLQCLNLSIVSHATGCHGVYVPGRI 180  
 DB 133 GSKVAPISLADHCTQPGKCTVSGWGTVPSPNFPDILNCAEVKIFPKCKCEDAYPGQI 192  
 QY 181 TSNMVCAGVPGQDACQDGSGLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240  
 DB 193 TDGMVCAKSSKADTCQDGSGLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 251  
 QY 241 IRMIM 245  
 DB 252 IKKII 256

RESULT 8  
 US-09-618-259-8  
 ; Sequence 8, Application US/09618259  
 ; Patent No. 6642013  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Brien, Timothy J.  
 ; TITLE OF INVENTION: No. 6642013a1 Extracellular Serine Protease  
 ; FILE REFERENCE: D6020CIP2  
 ; CURRENT APPLICATION NUMBER: US/09/618,259

; CURRENT FILING DATE: 2000-07-18  
 ; PRIOR FILING DATE: US 09/127,444  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SEQ ID NO 8  
 ; LENGTH: 260  
 ; TYPE: PRT  
 ; ORGANISM: Mus sp.  
 ; FEATURE:  
 ; OTHER INFORMATION: Amino acid sequence of mouse neuropilin homologous  
 ; OTHER INFORMATION: to TADG-14; accession no. D30785  
 US-09-618-259-8

Query Match 45.3%; Score 622.5; DB 4; Length 260;  
 Best Local Similarity 49.0%; Pred. No. 1.5e-52;  
 Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;  
 QY 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLPFGTSLRCGGVLIDHRWVLTAA 61  
 DB 13 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLPFGTSLRCGGVLIDHRWVLTAA 72  
 QY 62 HCSGRYVRLGEHLSQLDWTQIRHSGFSTVTHPGYLGAS-TSHEHDLRLRLPLVRV 120  
 DB 73 HCKKPKYTVRLGDHSLQSDGSGPLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 132  
 QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHPNPPDILLQCLNLSIVSHATGCHGVYVPGRI 180  
 DB 133 GSKVAPISLADHCTQPGKCTVSGWGTVPSPNFPDILNCAEVKIFPKCKCEDAYPGQI 192  
 QY 181 TSNMVCAGVPGQDACQDGSGLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240  
 DB 193 TDGMVCAKSSKADTCQDGSGLVCGVGLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 251  
 QY 241 IRMIM 247  
 DB 252 IKKTM 258

RESULT 9  
 US-09-205-258-427  
 ; Sequence 427, Application US/09205258  
 ; Patent No. 6525174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young et al.  
 ; TITLE OF INVENTION: 207 Human Secreted Proteins  
 ; FILE REFERENCE: P2007P1  
 ; CURRENT APPLICATION NUMBER: US/09/205,258  
 ; CURRENT FILING DATE: 1998-12-04  
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422  
 ; EARLIER FILING DATE: 1998-06-04  
 ; EARLIER APPLICATION NUMBER: 60/048,885  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,375  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,881  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,880  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,896  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/049,020  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,876  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,895  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,884  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,894  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,971  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-427

Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 3.5e-52;  
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

OY 3 LSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62  
DB 4 LQILLLATGLVGGET-RIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAAH 62  
OY 63 CGSGSYRWRLGHSLSQLDWTEQIRHSGFSVTHPGYLG--STSHEDLRLRLPLRV 120

63 CLKPRYIVHLQOHNLQKEGCEQTRTATESPFGPGNNLPNKDHNRDMLVKMASPVSI 122  
121 TSSVQPLPLPNDCATAGTECHVSGMGITNHPRPDPDLQCLNLSIVSHATGHVYVPGRI 180  
123 TWAVRPLTLSSRCVTAGTSLISGWGSTSSPQLRPLPHTLRCANITIIHQKCNAYFGNI 182  
181 TSNMVCAG-GVPGQACQDSCGGLVCGGLVGLVSGVSGPGQDGIQGVVYIYCKYVD 239  
183 TDTMVCASVQEGGKDSQDSCGGLVCGGLVQSLQSIISWGO-DPCAIRKPGVYTKVKCYVD 241  
240 WIRMIMRNN 248  
242 WIQETWKN 250

RESULT 10  
US-09-025-059-1  
Sequence 1, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGTUT10  
CLONE: 2723646  
US-09-025-059-1

Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 4.1e-52;  
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

OY 3 LSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62  
DB 36 LQILLLATGLVGGET-RIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAAH 94  
OY 63 CGSGSYRWRLGHSLSQLDWTEQIRHSGFSVTHPGYLG--STSHEDLRLRLPLRV 120

Db 95 CLKPRYIVHLOQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHNRNDIMLVKMASPVSI 154  
QY 121 TSSVQPLPLNDCATAGTECHVSGWGITNHRNPPDILLQCLNLSIVSHATCHGVYPGRI 180  
Db 155 TWAVRPLTSSRCVTAGTSCLSISGWSSTSPQRLPHTLRNCANITIIHQKCNAYPGNI 214  
QY 181 TSNMVCAG-GVPGQACQDSGGLVCGGVLCGLVSGVSGPCGQDGPVGYTYICKYVD 239  
Db 215 TDTMVCASVQEGGKDCQCGSDGGLVVCNQLGIIISWGQ-DPCATRKPGVYTKVCKVD 273  
QY 240 WIRMTMRNN 248  
Db 274 WIQETMKN 282

## RESULT 11

US-09-386-642-13  
; Sequence 13, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; FILE OF INVENTION: Zymogen Activation System  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

Query Match 43.9%; Score 602.5; DB 4; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.5e-50;  
Matches 116; Conservative 21; Mismatches 87; Indels 3; Gaps 3;  
QY 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWLVTAHCSGSRVYVRLGSHLSQ 79  
Db 51 KIVGYNCLPHEPSQWQAALFQGLCGVLGCVGNWLVTAHCKPKYVRLGSHLSQ 110  
QY 80 LDWTEQIRHSGFVTHPGYLGA--STSHEDLRLRLPVRVTSSVQPLPNDCATAGT 138  
Db 111 KDGPEQEIPIVQVSIHPHCYNSSDVEDHNDLMLQLRDQASIGSKVKPISLADHCTQPGQ 170  
QY 139 ECHVSGWGITNHRNPPDILLQCLNLSIVSHATCHGVYPGRIITSNMVCAGGVPGQACQ 198  
Db 171 KCTVSGWGTVSPRENFDTLNCAEVKIFPQKCEDAPGGQITDGMVCAAGSKGADTCQG 230  
QY 199 DSGGLVCGGLVQGLVSGVSGPCGQDGPVGYTYICKYVDMIRMIM 245  
Db 231 DSGGLVCDGALQGITWSGS-DPCGRSDKPGVYTYICKYLDWIKKII 276

## RESULT 12

US-09-386-642-14  
; Sequence 14, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; FILE OF INVENTION: Zymogen Activation System  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14  
Query Match 43.6%; Score 598.5; DB 4; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.8e-50;  
Matches 114; Conservative 34; Mismatches 79; Indels 5; Gaps 4;  
QY 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWLVTAHCSGSRVYVRLGSHLSQ 79  
Db 51 KIVGYNCLPHEPSQWQAALFQGLCGVLGCVGNWLVTAHCKPKYVRLGSHLSQ 110  
QY 80 LDWTEQIRHSGFVTHPGYLGA--STSHEDLRLRLPVRVTSSVQPLPNDCATAGT 137  
Db 111 BEGCEQTRTATESFPHPGFNNSLPNKDHNRNDIMLVKMASPVSIWAVRPLTSSRCVTAG 170  
QY 138 TECHVSGWGITNHRNPPDILLQCLNLSIVSHATCHGVYPGRIITSNMVCAG-GVPGQAC 196  
Db 171 TSLISGWSSTSPQRLPHTLRNCANITIIHQKCNAYPGNITDTMVCASVQEGGKDC 230  
QY 197 QDSDGGLVCGGLVQGLVSGVSGPCGQDGPVGYTYICKYVDMIRMIRNN 248  
Db 231 QDSDGGLVVCNQLGIIISWGQ-DPCATRKPGVYTKVCKYVDIQTMKNN 281

## RESULT 13

US-08-944-483-24  
; Sequence 24, Application US/08944483  
; Patent No. 6232456  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STEWART, KENT D.  
; APPLICANT: STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; TITLE OF INVENTION: OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,483  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623



```
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-24

Query Match
Best Local Similarity 43.5%; Score 597.5; DB 3; Length 248;
Matches 119; Conservative 36; Mismatches 87; Indels 7; Gaps 6;

QY 3 LSIPLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db 4 LQILLALATGLVGGT-RIKGFEC-PHSQPMQALFK-TRLLCGATLIAPRWLLTAAH 60
QY 63 CSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGA--STSHEDLRLRLRPVTV 120
Db 61 CLKPRYIVHLGQHNKQEGCQTRTATESFFHPGFNNSLPNKDRNDIMLVKMASPVSI 120
QY 121 TSSVQPLPNDPCATAGTECHVSGWGITNHPRPFPDLLOCLNLSIVSHATCHGVYVGR 180
Db 121 TWAVRPLTLSSRCVTAGTSCLSGWSGSTSPQLRPLHTURCANITIIIEHKCENAYPGNI 180
QY 181 TSNMVCAG-GVPGQDACQGDGSGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYVD 239
Db 181 TDTMVCASVOEGGKDCQGDGSGPLVCGVLSQGLIISWGQ-DFCAITRKGVTYCKYVD 239
QY 240 WIRIMRN 248
Db 240 WIQETMKN 248

RESULT 14
US-08-956-267A-2
; Sequence 2, Application US/08956267A
; Patent No. 5945328
; GENERAL INFORMATION:
; APPLICANT: WOLDIKE, Helle Fabricius
; APPLICANT: KJELSEN, Thomas Borglum
; TITLE OF INVENTION: A Process For Producing Trypsin
; TITLE OF INVENTION: (Trypsinogen)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5945328o No. 5945328disk of No. 5945328th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,267A
; FILING DATE: 22-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4500.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-956-267A-2

Query Match
Best Local Similarity 41.7%; Score 573; DB 2; Length 247;
Matches 113; Conservative 42; Mismatches 83; Indels 10; Gaps 5;

QY 6 FLLLCVLGLSQA----ATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLTAA 61
Db 5 FVLLALLGAAPPTDDDDKIVGGYTCAANSIPYQVSLNSGSHF-CGGSLLNSQWVVSAA 63
QY 62 HCSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLCASTSHEHDLRLRLRPVTV 121
Db 64 HCYSRIQVRLGHNIDVLENEQFINAAKIITHPNFNG--NTLDDIMLILKSSPATLN 121
QY 122 SSVQPLPNDPCATAGTECHVSGWGITNHPRPFPDLLOCLNLSIVSHATCHGVYVGRIT 181
Db 122 SRVATVSLPRSCAAGTECLISGWNKTSKSSGYSPLLOCLKAPVLSDSCKSSYFGQIT 181
QY 182 SNMVCAGVP-GQDACQGDGSGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYVD 240
Db 182 GNMICVGFLEGGKDCQGDGSGPVVCGQLQGVISWGY--GCAQKNKPGVYTKVCYVNW 239
QY 241 IRMIMRN 248
Db 240 IQOTIAAN 247

RESULT 15
US-09-949-016-8166
; Sequence 8166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8166
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8166

Query Match
Best Local Similarity 41.3%; Score 567; DB 4; Length 290;
Matches 116; Conservative 36; Mismatches 80; Indels 16; Gaps 6;

QY 13 GLSQAATPKIFN-----GTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db 31 GVSQESS-KVLNTNGTSGFLPGGYTCFPHSQPMQALLVQGRLLCGGLVHPKWLTAH 89
QY 63 CSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGA--SHEHDLRLRLRPVTV 120
Db 90 CLKGLKVLKGLKHALGRVEAGEQVREVVHSIHPHYRRSPTHLNHDHIDIMLELQSPVL 149
QY 121 TSSVQPLP-NDCATAGTECHVSGWGITNHPRPFPDLLOCLNLSIVSHATCHGVYVGR 179
Db 150 TGYIOTPLSHNNRLTPGTTCRVSGWGTTSQVNPYKTLQCANIQLRDECRQVYPGK 209
QY 180 ITSNNVCAGVP-GQDACQGDGSGPLVCGGVLOGLVSWGSGVPGCGQDGIPIGVYTYICKYV 238
Db 210 ITDNMLCAGTKEGGKDCGSGGGLVNCNRTLYGIVSWGDF-PCGQDPGPGVYTVRSRV 268
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QY 239 DWIRIMR 246  
||| :  
Db 269 LWIRETIR 276

Search completed: March 5, 2005, 20:45:52  
Job time : 51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2005, 20:36:50 ; Search time 41 Seconds  
(without alignments)  
581.994 Million cell updates/sec

Title: US-10-015-385a-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCVLGLSQAATP.....GVYTYCKYDWMRMNRN 248

Scoring table: BLOSUMP2

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622.5	45.3	260	2 I56559	neuropsin - mouse
2	569.5	41.4	248	2 S55066	trypsin (EC 3.4.21
3	567	41.3	248	2 S55067	trypsin (EC 3.4.21
4	561	40.8	231	1 TRPOTR	trypsin (EC 3.4.21
5	555	40.4	243	2 A35871	serine proteinase
6	555	40.4	253	2 A53968	trypsin (EC 3.4.21
7	553	40.2	246	2 B25528	trypsin (EC 3.4.21
8	552	40.2	229	1 TRBOTR	trypsin (EC 3.4.21
9	550	40.0	247	2 S13813	trypsin (EC 3.4.21
10	546	39.7	247	1 TRDG	trypsin (EC 3.4.21
11	545	39.7	246	1 TRDGC	trypsin (EC 3.4.21
12	544.5	39.6	247	2 A27547	trypsin (EC 3.4.21
13	543	39.5	246	1 TRRT1	trypsin (EC 3.4.21
14	540	39.3	238	2 S31779	trypsin (EC 3.4.21
15	533.5	38.8	247	2 S05494	trypsin (EC 3.4.21
16	532	38.7	246	1 TRRT2	trypsin (EC 3.4.21
17	527.5	38.4	261	2 A31136	tissue kallikrein
18	524	38.1	232	1 KQPG	tissue kallikrein
19	520.5	37.9	261	2 A25606	tissue kallikrein
20	519	37.8	246	2 JQ1471	trypsin (EC 3.4.21
21	518	37.7	246	2 JQ1472	trypsin (EC 3.4.21
22	518	37.7	261	2 A34079	tissue kallikrein
23	513.5	37.4	231	2 S31778	trypsin (EC 3.4.21
24	513.5	37.4	239	2 A27207	tissue kallikrein
25	511.5	37.2	261	2 S45303	tissue kallikrein
26	510.5	37.2	261	1 NGMSG	7S nerve growth fa
27	508	37.0	242	2 S31776	trypsin (EC 3.4.21
28	508	37.0	242	2 S31775	trypsin (EC 3.4.21
29	503	36.6	260	2 A37938	tissue kallikrein

30	503	36.6	263	2 S15686	tissue kallikrein
31	502	36.5	259	2 B31136	tissue kallikrein
32	501	36.5	247	1 B25852	trypsin (EC 3.4.21
33	499.5	36.4	241	2 S39048	trypsin (EC 3.4.21
34	496.5	36.1	261	1 TRMSM5	tissue kallikrein
35	496	36.1	242	2 S49489	trypsin (EC 3.4.21
36	495.5	36.1	257	2 S33772	tissue kallikrein
37	495.5	36.1	261	2 S01971	tissue kallikrein
38	494.5	36.0	247	1 A25852	trypsin (EC 3.4.21
39	493	35.9	262	1 KQHU	tissue kallikrein
40	491.5	35.8	240	2 S39047	trypsin (EC 3.4.21
41	491	35.7	256	1 NGMSA	7S nerve growth fa
42	490.5	35.7	229	1 TRDFS	trypsin (EC 3.4.21
43	490.5	35.7	261	2 A41020	tissue kallikrein
44	489	35.6	244	2 A44284	tissue kallikrein
45	485.5	35.3	261	2 JE0236	tissue kallikrein
46	484.5	35.3	259	2 A29746	tissue kallikrein
47	484.5	35.3	304	2 S33496	trypsin (EC 3.4.21
48	483.5	35.2	265	1 KQRTF	tissue kallikrein
49	481.5	35.0	250	2 T01779	trypsin (EC 3.4.21
50	481.5	35.0	261	2 A29745	tissue kallikrein
51	479	34.9	261	1 S35711	seminogelase (EC 3
52	477.5	34.8	261	1 KQMS1	trypsin (EC 3.4.21
53	476	34.6	259	1 I38363	seminogelase (EC 3
54	470.5	34.2	261	1 A32297	trypsin (EC 3.4.21
55	469.5	34.2	261	2 A24378	tissue kallikrein
56	468	34.1	259	1 KQRTTN	tonin (EC 3.4.21.-
57	467.5	34.0	261	1 EGMSB	tissue kallikrein
58	467	34.0	247	2 S12764	trypsin (EC 3.4.21
59	461.5	33.6	259	2 D3863	tissue kallikrein
60	458.5	33.4	250	2 S31384	trypsin (EC 3.4.21
61	458.5	33.4	261	2 A29586	tissue kallikrein
62	449	32.7	258	2 A57290	venom plasminogen
63	436.5	31.8	250	2 S15685	kallikrein, glandu
64	436.5	31.8	257	1 JC2479	venombin B (EC 3.4
65	432	31.4	236	1 A32121	snake venom factor
66	431.5	31.4	261	2 A28062	gamma-amin (EC 3.
67	431	31.4	262	1 JC4803	venombin A (EC 3.4
68	422.5	30.7	233	1 JG0169	venombin A (EC 3.4
69	417	30.3	236	1 B32121	snake venom factor
70	411.5	29.9	228	1 S35689	venombin A (EC 3.4
71	408	28.7	235	1 S65621	venombin AB (EC 3.
72	406.5	29.6	231	2 A40468	venombin A (EC 3.4
73	402	29.3	255	1 A28169	venombin A (EC 3.4
74	394	28.7	236	1 A41456	pancreatic elastase
75	388	28.2	269	2 A26823	pancreatic elastase
76	386	28.1	232	1 A54361	venombin A (EC 3.4
77	385.5	28.1	188	2 B32340	tissue kallikrein
78	385.5	28.1	264	2 I38136	chymotrypsin-like
79	382.5	27.8	1524	2 T30337	polypeptide - Afri
80	382	27.8	246	1 DBHU	complement factor
81	381	27.7	263	1 I55608	complement factor
82	377	27.4	225	2 S45356	probable serine pr
83	374.5	27.3	259	1 WMS28	complement factor
84	371	27.0	271	1 ELRT2	pancreatic elastase
85	370.5	27.0	263	2 A21195	chymotrypsin (EC 3
86	370	26.9	234	1 S20407	venombin A (EC 3.4
87	368.5	26.8	343	1 A57014	proctasin (EC 3.4.
88	367.5	26.7	638	1 KQHUP	plasma kallikrein
89	366	26.6	258	1 S36783	venombin A (EC 3.4
90	364	26.5	156	2 B23863	tissue kallikrein
91	362.5	26.4	246	2 S64707	chymase (EC 3.4.21
92	359.5	26.2	277	2 S35340	trypsin (EC 3.4.21
93	359	26.1	443	2 I46932	coagulation factor
94	358	26.1	812	1 PLBO	plasma (EC 3.4.21
95	357	26.0	262	1 A31372	granzyme A (EC 3.4
96	357	26.0	263	2 A31299	chymotrypsin (EC 3
97	357	26.0	271	2 S29239	chymotrypsin (EC 3
98	357	26.0	1019	2 A38738	coagulation factor
99	355.5	25.9	276	2 A38654	mast cell proteina
100	354	25.8	271	2 A25528	pancreatic elastase
101	353.5	25.7	263	2 S47537	chymotrypsin (EC 3
102	353.5	25.7	270	2 S56160	mast cell tryptase

103	353	25.7	274	2	JC4171	trypsin (EC 3.4.21)	176	320.5	23.3	247	1	PRMSCL	granzyme B (EC 3.4.21)
104	352	25.6	260	1	A45061	granzyme A (EC 3.4.21)	177	319.5	23.3	559	1	A29941	t-plasminogen activator
105	352	25.6	461	1	JX0210	protein C (activator)	178	319	23.2	1034	1	A53663	enteropeptidase (EC 3.4.21)
106	351	25.5	456	1	KX80	protein C (activator)	179	318.5	23.2	460	2	B61545	plasmin (EC 3.4.21)
107	349.5	25.4	269	2	B26823	pancreatic elastase	180	318	23.1	265	2	T10495	chymotrypsin (EC 3.4.21)
108	348	25.3	267	2	S40006	trypsin (EC 3.4.21)	181	318	23.1	271	2	I46580	factor IX - pig (f)
109	347	25.3	461	1	KXHU	protein C (activator)	182	318	23.1	274	2	I47078	coagulation factor
110	346.5	25.2	244	2	S26042	chymase (EC 3.4.21)	183	318	23.1	618	2	A35827	thrombin (EC 3.4.21)
111	346.5	25.2	461	1	S18994	protein C (activator)	184	317.5	23.1	245	1	KYBOB	chymotrypsin (EC 3.4.21)
112	344	25.0	275	2	B35863	trypsin (EC 3.4.21)	185	317.5	23.1	246	2	A22692	cytotoxic T-lymphocyte
113	343.5	25.0	273	2	A47246	trypsin (EC 3.4.21)	186	317	23.1	249	2	A56534	granzyme M (EC 3.4.21)
114	343.5	25.0	274	2	S35339	trypsin (EC 3.4.21)	187	316.5	23.0	254	1	A46504	chymase (EC 3.4.21)
115	343	25.0	275	2	A32410	trypsin (EC 3.4.21)	188	315.5	23.0	256	1	TRWV3Y	trypsin-like protease
116	342.5	24.9	558	2	JC5878	plasma hyaluronan	189	315.5	23.0	266	1	ELRT1	pancreatic elastase
117	342.5	24.9	910	1	PLHU	plasmin (EC 3.4.21)	190	315.5	23.0	392	1	A30100	serine proteinase
118	342	24.9	275	2	C35863	trypsin (EC 3.4.21)	191	315.5	23.0	492	1	EXBO	coagulation factor
119	342	24.9	275	2	A35863	trypsin (EC 3.4.21)	192	315	22.9	248	2	S43259	granzyme-like protease
120	341.5	24.9	258	2	I56220	trypsin (EC 3.4.21)	193	315	22.9	617	2	S10511	thrombin (EC 3.4.21)
121	340.5	24.8	246	2	B38678	serine proteinase	194	315	22.9	686	1	A59271	Ra-reactive factor
122	339.5	24.7	258	2	A45161	probable pancreatin	195	314	22.9	275	2	S40005	trypsin (EC 3.4.21)
123	339.5	24.7	267	4	A56615	granzyme A (EC 3.4.21)	196	313	22.8	613	2	S15468	complement C3b/C4b
124	339	24.7	257	2	B45061	coagulation factor	197	313	22.8	855	2	JC7731	membrane-bound arginase
125	339	24.7	461	1	KFHU1	coagulation factor	198	312.5	22.7	274	2	S40004	trypsin-related protease
126	339	24.7	625	1	KFHU1	coagulation factor	199	312.5	22.7	615	1	KFHU12	brain-specific serine
127	338	24.6	625	1	TBBO	thrombin (EC 3.4.21)	200	311.5	22.7	761	2	JC5759	trypsin (EC 3.4.21)
128	337.5	24.6	238	1	TRWV5Y	trypsin-like protease	201	311	22.6	261	2	S40162	complement C3b/C4b
129	337.5	24.6	264	2	S65663	granzyme 3 (EC 3.4.21)	202	311	22.6	431	2	S47538	cathepsin G (EC 3.4.21)
130	337	24.5	434	1	A35005	granzyme 3 (EC 3.4.21)	203	311	22.6	433	1	JN0560	acrosin (EC 3.4.21)
131	337	24.5	812	1	PLMS	plasmin (EC 3.4.21)	204	311	22.6	1035	2	A43090	u-plasminogen activator
132	336.5	24.5	251	2	T10262	plasmin (EC 3.4.21)	205	310.5	22.6	247	1	PRRTG	enteropeptidase (EC 3.4.21)
133	336.5	24.5	251	2	PC1235	29K serine proteinase	206	310.5	22.6	559	1	A35029	mast cell protease
134	336.5	24.5	638	1	KOMSPL	plasma kallikrein	207	310	22.6	275	2	I46712	t-plasminogen activator
135	336	24.5	416	1	KFBO	coagulation factor	208	309.5	22.5	482	1	EXRT	factor IX - rabbit
136	336	24.5	790	1	PLRG	coagulation factor	209	307	22.5	250	2	S55493	coagulation factor
137	335.5	24.4	258	4	S70439	plasmin (EC 3.4.21)	210	307	22.3	259	2	S49129	serine proteinase
138	333	24.2	245	1	KYBOA	pancreatic elastase	211	307	22.3	259	1	S49129	chymotrypsin (EC 3.4.21)
139	333	24.2	285	1	I48144	chymotrypsin (EC 3.4.21)	212	306.5	22.3	375	1	S00845	hepsin (EC 3.4.21)
140	332.5	24.2	638	1	KORTPL	coagulation factor	213	305.5	22.2	236	2	I42696	limulus clotting enzyme
141	332.5	24.2	810	2	B30848	plasmin (EC 3.4.21)	214	305	22.2	281	1	A61021	thrombin (EC 3.4.21)
142	332.5	24.2	810	2	B30848	plasmin (EC 3.4.21)	215	304	22.1	149	1	KOMSM	granzyme B (EC 3.4.21)
143	331.5	24.1	256	1	TRFP	trypsin (EC 3.4.21)	216	304	22.1	236	2	C42696	tissue kallikrein
144	331.5	24.1	275	2	S40007	trypsin (EC 3.4.21)	217	304	22.1	268	2	S68825	thrombin (EC 3.4.21)
145	331	24.1	263	1	KYRTB	chymotrypsin (EC 3.4.21)	218	304	22.1	562	1	UKHUT	pancreatic elastase
146	331	24.1	622	1	TBHU	thrombin (EC 3.4.21)	219	303.5	22.1	244	2	A46721	t-plasminogen activator
147	330.5	24.1	247	1	KYHUCM	chymase (EC 3.4.21)	220	303.5	22.1	309	2	B49878	coagulation factor
148	330.5	24.1	560	1	JC4795	plasma hyaluronan	221	303	22.1	196	2	T08808	hypothetical protease
149	330	24.0	282	2	I84621	coagulation factor	222	302.5	22.0	244	2	A4910	mast cell protease
150	330	24.0	458	1	S00657	apoptin(a) (EC 3.4.21)	223	302.5	22.0	273	2	S40003	trypsin-related protease
151	329.5	24.0	226	2	JEO151	myonase (EC 3.4.21)	224	302.5	22.0	1004	2	T30338	oviductin (EC 3.4.21)
152	329.5	24.0	237	2	S68702	trypsin (EC 3.4.21)	225	302.5	22.0	1113	2	JEO315	low-density lipoprotein
153	329.5	24.0	269	2	C26823	pancreatic elastase	226	302	22.0	268	2	S68826	pancreatic elastase
154	329.5	24.0	1420	2	A32869	apolipoprotein(a)	227	302	22.0	394	2	J06060	t-plasminogen activator
155	328.5	23.9	455	2	A61545	plasmin (EC 3.4.21)	228	302	22.0	477	1	A34369	t-plasminogen activator
156	328.5	23.9	786	1	A47547	serine proteinase	229	302	22.0	477	2	J05098	t-plasminogen activator
157	328	23.8	452	1	A30351	coagulation factor	230	301	21.9	255	2	A27122	cathepsin G (EC 3.4.21)
158	327.5	23.8	266	2	S54146	trypsin (EC 3.4.21)	231	301	21.9	431	2	J05059	t-plasminogen activator
159	327	23.8	244	2	S72219	chymotrypsin B - A	232	300.5	21.9	442	1	UKPG	u-plasminogen activator
160	327	23.8	259	2	S68424	allergen der f III	233	300	21.8	245	2	A48598	kallikrein-like serine
161	326.5	23.8	248	1	PRMSC2	granzyme C (EC 3.4.21)	234	299.5	21.8	235	2	E42696	thrombin (EC 3.4.21)
162	326.5	23.8	266	1	ELFG	pancreatic elastase	235	299.5	21.8	246	2	A38678	mast cell protease
163	326	23.7	248	2	S33755	granzyme-like protease	236	299.5	21.8	258	1	S44184	chymotrypsin (EC 3.4.21)
164	324	23.6	274	2	A45754	trypsin (EC 3.4.21)	237	299.5	21.8	436	2	JX0172	acrosin (EC 3.4.21)
165	324	23.6	459	2	JQ0419	coagulation factor	238	299	21.8	437	2	S18407	complement factor
166	324	23.6	1019	1	A56318	enteropeptidase (EC 3.4.21)	239	298.5	21.7	191	2	S54115	chymase (EC 3.4.21)
167	323.5	23.5	466	1	KFHU7	coagulation factor	240	298.5	21.7	249	1	A35842	pancreatic elastase
168	323	23.4	699	1	I54763	Ra-reactive factor	241	298.5	21.7	270	2	B29934	coagulation factor
169	321.5	23.4	251	2	JC2125	chymase (EC 3.4.21)	242	298.5	21.7	407	1	KFBOY	trypsin (EC 3.4.21)
170	321	23.4	226	1	KCUF	bradykinin (EC 3.4.21)	243	297	21.6	237	1	TRCY1	chymase (EC 3.4.21)
171	321	23.4	226	2	S69370	duodenase - bovine	244	297	21.6	260	2	S26043	acrosin (EC 3.4.21)
172	321	23.4	247	2	S64708	chymase (EC 3.4.21)	245	297	21.6	418	2	A37344	chymase (EC 3.4.21)
173	321	23.4	248	2	A43520	natural killer cell	246	297	21.6	477	2	J05097	t-plasminogen activator
174	321	23.4	269	2	B32410	mastocytoma protein	247	296.5	21.6	248	1	S01007	granzyme F (EC 3.4.21)
175	321	23.4	655	1	A46688	hepatocyte growth factor	248	296	21.5	281	2	T13596	trypsin homolog

249	295.5	21.5	239	2	G42696	thrombin (EC 3.4.2	322	220.5	16.0	267	1	ELHUL	leukocyte elastase
250	295.5	21.5	433	1	UKMS	u-plasminogen acti	323	217.5	15.8	710	1	I51283	hepatocyte growth
251	294	21.4	247	2	S23504	chymase (EC 3.4.21	324	216	15.7	728	1	A35644	hepatocyte growth
252	294	21.4	303	2	T13598	trypsin homolog -	325	216	15.7	728	1	A60185	hepatocyte growth
253	293.5	21.4	431	1	UKHU	u-plasminogen acti	326	204.5	14.9	177	2	S23505	chymase (EC 3.4.21
254	293	21.3	234	2	F42696	thrombin (EC 3.4.2	327	201	14.6	214	2	S17680	fibrinolytic prote
255	293	21.3	247	2	S59135	mast cell proteina	328	197.5	14.4	213	2	S17537	chymotrypsin (EC 3
256	293	21.3	265	2	A38894	serine proteinase	329	196	14.3	248	2	S49323	chymotrypsin (EC 3
257	293	21.3	265	2	JSQ0260	serine proteinase	330	192.5	14.0	763	2	I50807	complement factor
258	293	21.3	433	1	UKBAY	u-plasminogen acti	331	189.5	13.8	94	2	PC2013	tissue kallikrein
259	292.5	21.3	236	2	A28566	T-cell suppressor	332	182	13.2	104	2	S15395	tissue kallikrein-
260	291.5	21.2	216	1	KYVH20	chymotrypsin (EC 3	333	180	13.1	258	2	G02959	haptoglobin - rhes
261	291	21.2	271	2	S41308	serine proteinase	334	179.5	13.1	149	2	S35208	serine proteinase
262	289.5	21.1	248	2	A33412	cytotoxic T-lympho	335	178	13.0	348	1	HPHU1	haptoglobin-relate
263	289	21.0	583	2	A29154	complement factor	336	177	12.9	347	1	HPHU1	haptoglobin precu
264	288.5	21.0	270	2	A29934	pancreatic elastas	337	177	12.9	406	1	HPHU2	haptoglobin precu
265	288.5	21.0	1047	2	A55617	masquerade precurs	338	176.5	12.8	760	1	C3MS	classical compleme
266	288	21.0	268	2	JQ1473	pancreatic elastas	339	176	12.8	735	2	T35778	probable fusidic a
267	288	21.0	421	2	S29599	u-plasminogen acti	340	174.5	12.7	377	2	C88710	protein C43G2.5 [1
268	287.5	20.9	235	2	H42696	thrombin (EC 3.4.2	341	174	12.7	161	2	I48158	coagulation factor
269	287.5	20.9	235	2	S28941	thrombin (EC 3.4.2	342	174	12.7	330	2	B82415	probable serine pr
270	286.5	20.9	618	1	KYVH2C	chymotrypsin (EC 3	343	172	12.5	346	2	I36942	haptoglobin - chim
271	286	20.8	254	2	S35585	chymotrypsin-like	344	171	12.4	159	2	S35202	proteinase 2 - buf
272	285.5	20.8	235	2	D42696	thrombin (EC 3.4.2	345	171	12.4	258	2	I36945	haptoglobin Hp - c
273	282.5	20.6	331	2	T27906	hypothetical prote	346	171	12.4	345	2	I36941	haptoglobin - chim
274	282	20.5	416	1	S33777	hepsin (EC 3.4.21	347	170	12.4	347	2	G00006	haptoglobin - blac
275	280	20.4	254	2	S65465	trypsin-like prote	348	169	12.3	329	1	HPDG	haptoglobin precu
276	278.5	20.3	593	2	S45281	coagulation factor	349	168	12.2	66	2	I52972	kallikrein - mouse
277	277.5	20.2	266	2	JC4850	trypsin-like prote	350	168	12.2	154	2	S35207	proteinase 7 - buf
278	276	20.1	430	1	A24702	serine proteinase	351	166	12.1	258	2	I36947	haptoglobin Hpp -
279	276	20.1	488	1	EXHU	coagulation factor	352	166	12.1	349	2	I36944	haptoglobin - chim
280	275.5	20.1	240	1	CPBOA3	procarboxypeptidas	353	166	12.1	752	1	C2HU	complement C2 prec
281	275	20.0	237	2	S53378	serine proteinase	354	165	12.0	161	2	I62744	coagulation factor
282	274.5	20.0	695	1	S05008	complement subcomp	355	165	12.0	347	1	HPMS	serine proteinase
283	273	19.9	247	2	S45113	granzyme-like prot	356	159.5	11.6	152	2	S35209	chymotrypsin-like
284	273	19.9	265	2	T15451	hypothetical prote	357	159	11.6	126	2	A23473	pancreatic elastas
285	272.5	19.8	432	1	S18932	u-plasminogen acti	358	158.5	11.5	264	2	A28942	complement factor
286	272	19.8	475	1	EXCH	coagulation factor	359	157.5	11.5	764	1	BBHU	complement factor
287	272	19.8	688	1	CHUS	complement subcomp	360	154.5	11.2	747	2	I51579	complement factor
288	271	19.7	2616	2	A57096	nudel protein prec	361	153.5	11.2	761	1	BBMS	complement factor
289	270	19.7	694	2	JC6554	complement subcomp	362	152.5	11.1	159	2	I84615	coagulation factor
290	269.5	19.6	248	2	S33756	granzyme-like prot	363	152	11.1	181	2	T08805	hypothetical prote
291	269	19.6	256	1	PRHU3	proteinase 3 (EC 3	364	151.5	11.0	152	2	S35203	serine proteinase
292	268.5	19.5	420	2	A55283	acrosin (EC 3.4.21	365	148	10.8	81	2	A18966	tissue kallikrein
293	265	19.3	415	1	A34170	acrosin (EC 3.4.21	366	145.5	10.6	82	2	T46510	hypothetical prote
294	264.5	19.3	256	2	T10109	trypsin (EC 3.4.21	367	138.5	10.1	158	2	S35201	serine proteinase
295	264.5	19.3	264	2	S23794	trypsin-like prote	368	138	10.0	153	2	S35204	proteinase 4 buf
296	263.5	19.2	251	1	TRHUAZ	azurocidin precurs	369	137	10.0	743	2	S34853	probable fusidic a
297	261.5	19.0	366	2	JE0105	testicular serine	370	136.5	9.9	152	2	S35206	serine proteinase
298	261.5	19.0	421	1	S11674	acrosin (EC 3.4.21	371	135.5	9.9	46	2	I49416	glandular kallikre
299	259	18.9	248	2	S01006	cytotoxic T-lympho	372	132	9.6	347	1	HPRT	haptoglobin precu
300	258.5	18.8	252	2	A36172	procytotoxic T-lym	373	129.5	9.4	396	1	KYBOZ	plasma protein Z -
301	258.5	18.8	285	2	T35195	probable serine pr	374	127.5	9.3	69	2	S28195	tissue kallikrein
302	257.5	18.7	254	2	S49329	trypsin-like prote	375	127.5	9.3	72	2	S28196	tissue kallikrein
303	256	18.6	403	2	C82228	probable trypsin V	376	126	9.2	80	2	A05324	gamma-tenin (EC 3
304	252	18.3	400	1	A48050	coagulation factor	377	123.5	9.0	137	2	S55364	serine proteinase
305	248	18.0	367	2	JE0104	testicular serine	378	123.5	9.0	151	2	S35205	proteinase 5 - buf
306	247	18.0	243	2	A56338	venom proteinase (	379	122.5	8.9	75	2	A37002	catroboxin I (EC 3
307	245	17.8	711	1	A47136	macrophage-stimula	380	115.5	8.4	422	1	KXHUZ	plasma protein Z p
308	244.5	17.8	716	1	A40332	macrophage-stimula	381	114.5	8.3	85	2	S44461	elastase (EC 3.4.2
309	239.5	17.4	265	2	I48679	neutrophil elastas	382	109.5	8.0	61	2	PS0049	serine proteinase
310	237.5	17.3	232	2	S32398	serine proteinase	383	108	7.9	333	2	T15257	hypothetical prote
311	235.5	17.1	198	2	S06176	cytotoxic T-lympho	384	104.5	7.6	256	2	A56593	trypsin-related pr
312	235.5	17.1	716	1	JC5061	macrophage-stimula	385	104	7.6	49	2	B24696	tissue kallikrein
313	235	17.1	96	2	A05308	tissue kallikrein	386	103.5	7.5	64	2	A30981	prostatic arginine
314	235	17.1	230	2	A27802	hyaluronidase (EC 3	387	99.5	7.2	340	2	T34423	hypothetical prote
315	234.5	17.1	219	1	TRFGAZ	azurocidin <sup>+</sup> -pig <sup>+</sup>	388	97	7.1	388	2	S34672	alkaline serine pr
316	233	17.0	705	1	CHURB	complement subcomp	389	96.5	7.0	416	2	AH2387	hypothetical prote
317	231.5	16.8	230	2	I48685	mast cell proteina	390	94.5	6.9	416	2	G71965	glycine hydroxymet
318	227.5	16.6	272	2	JC4170	trypsin-like prote	391	93.5	6.8	73	2	S44462	elastase (EC 3.4.2
319	227	16.5	259	1	TRSMG	trypsin (EC 3.4.21	392	93.5	6.8	299	1	PRSMBG	streptogrisin B (E
320	226	16.4	728	1	JH0579	hepatocyte growth	393	92.5	6.7	416	2	G64542	glycine hydroxymet
321	225	16.4	548	2	D82175	probable trypsin V	394	91	6.6	31	2	A18671	tissue kallikrein

395	90.5	6.6	48	2	A61331	trypsin (EC 3.4.21	468	78	5.7	4006	2	T09070	probable tenascin
396	90	6.6	1746	1	S19694	tenascin precursor	469	77.5	5.6	438	2	S53787	collagen alpha 1(I)
397	90	6.6	2825	2	T14271	Doc4 protein, stre	470	77.5	5.6	921	2	S42617	collagen alpha 1(I)
398	89	6.5	457	2	A53669	streptogrisin C (E	471	77.5	5.6	1669	1	CGMS4B	collagen alpha 1(I)
399	89	6.5	1737	2	T00209	MEGF8 protein - hu	472	77.5	5.6	1691	1	CGH06B	collagen alpha 6(I)
400	88.5	6.4	2205	1	MNWRN	nonstructural poly	473	77.5	5.6	2907	2	A57278	fibrillin-2 precu
401	88.5	6.4	3002	2	A47221	fibrillin 1 precu	474	77	5.6	517	2	T47134	hypothetical prote
402	87.5	6.4	278	2	AH0282	probable pepetidas	475	77	5.6	553	2	F75407	probable transport
403	87.5	6.4	1582	2	T15308	hypothetical prote	476	77	5.6	668	2	A41234	melanocyte-specifi
404	86.5	6.3	34	2	I49417	nerve growth facto	477	77	5.6	710	2	T31502	hypothetical prote
405	86.5	6.3	38	2	I70029	kallikrein, exon 2	478	77	5.6	1104	2	T38869	transcription fact
406	86.5	6.3	38	2	I70016	kallikrein - mouse	479	77	5.6	3566	1	A40701	tenascin-X precurs
407	86.5	6.3	38	2	I70036	kallikrein - mouse	480	76.5	5.6	295	2	A44984	collagen - nematod
408	86	6.3	70	2	A56784	kallikrein-like se	481	76.5	5.6	315	2	H83096	probable pyrophosp
409	86	6.3	502	2	A48679	kallikrein-like se	482	76.5	5.6	348	2	A34705	collagen - Caenorh
410	86	6.3	2704	2	S09118	G surface protein	483	76.5	5.6	382	2	PC2053	alkaline proteinas
411	85	6.2	398	2	B75254	acetate kinase - D	484	76.5	5.6	469	1	S29126	properdin precursor
412	85	6.2	411	2	T34585	probable secreted	485	76.5	5.6	1042	1	CGH1S	collagen alpha 1(I)
413	85	6.2	2718	2	A23475	G surface protein	486	76.5	5.6	1453	2	S21626	collagen alpha 1(I)
414	84.5	6.1	287	2	T22637	hypothetical prote	487	76.5	5.6	1532	2	A61262	collagen alpha 1(X
415	84.5	6.1	1023	2	T30257	IGG Fc binding pro	488	76	5.5	257	2	T52298	squamosa promoter
416	84.5	6.1	2871	2	A55567	fibrillin 1 - bovi	489	76	5.5	301	2	C84474	hypothetical prote
417	84	6.1	273	2	E85765	hypothetical prote	490	76	5.5	361	2	S30325	hypothetical prote
418	84	6.1	305	2	S44767	C29E4.1 protein -	491	76	5.5	465	2	AF2949	ornithine decarbox
419	84	6.1	458	2	T36442	probable serine pr	492	76	5.5	512	2	E98333	probable ornithine
420	84	6.1	725	2	E96596	hypothetical prote	493	76	5.5	608	2	T05442	glycine-rich prote
421	83.5	6.1	133	2	T17300	hypothetical prote	494	76	5.5	677	2	S23296	collagen alpha 2(I
422	83.5	6.1	788	2	A37057	integrin beta-6 ch	495	76	5.5	920	2	B34493	collagen alpha 1(I
423	83.5	6.1	1433	2	A46053	bullous pemphigoid	496	76	5.5	986	1	OXURGA	speract receptor p
424	83	6.0	266	2	T21597	hypothetical prote	497	76	5.5	3396	1	A42551	genome polyprotein
425	83	6.0	273	2	H64915	Putative protease	498	75.5	5.5	396	2	S22909	interleukin-3 rece
426	82.5	6.0	522	2	T29767	hypothetical prote	499	75.5	5.5	481	2	A35628	loricrin - mouse
427	82.5	6.0	644	2	C75457	alpha-amylyase - De	500	75.5	5.5	596	2	T26950	hypothetical prote
428	82.5	6.0	4936	2	AH2515	hypothetical prote	501	75.5	5.5	621	2	T50024	hypothetical prote
429	82	6.0	90	2	JB0210	proteinase (EC 3.4	502	75.5	5.5	653	2	A46362	amyloid precursor-
430	82	6.0	357	2	T21152	hypothetical prote	503	75.5	5.5	677	2	T37310	Pi1f protein - Cae
431	82	6.0	418	2	A46076	staphylytic prot	504	75.5	5.5	688	2	A53330	collagen alpha 2(I
432	82	6.0	418	2	F83411	LaaA proteinase pr	505	75.5	5.5	697	2	T18681	hypothetical prote
433	81.5	5.9	244	2	JC4708	gelatin-binding 28	506	75.5	5.5	1142	2	JX0369	collagen alpha 1(X
434	81.5	5.9	323	2	T27450	hypothetical prote	507	75	5.5	291	2	T20083	hypothetical prote
435	81.5	5.9	779	1	CG8018	collagen alpha 1(I	508	75	5.5	291	2	T26576	hypothetical prote
436	81.5	5.9	2229	1	T16199	hypothetical prote	509	75	5.5	310	2	I50696	collagen alpha 1(I
437	81	5.9	247	2	T26688	hypothetical prote	510	75	5.5	437	2	I50478	properdin - mouse
438	80.5	5.9	428	2	T24769	hypothetical prote	511	75	5.5	809	1	IJB0DD	desmocollin 2b pre
439	80.5	5.9	283	2	T29837	hypothetical prote	512	75	5.5	863	1	IJB0DC	desmocollin 2a pre
440	80.5	5.9	290	2	T46470	hypothetical prote	513	75	5.5	864	1	EART	elastin precursor
441	80.5	5.9	294	2	T23839	hypothetical prote	514	75	5.5	902	2	T26775	hypothetical prote
442	80.5	5.9	812	2	S31521	collagen Col1f - f	515	75	5.5	1140	2	AS0180	probable membrane
443	80.5	5.9	1464	1	CGH1S	collagen alpha 1(I	516	75	5.5	1236	1	VHWVME	structural polypro
444	80.5	5.9	2871	2	A55624	fibrillin-1 precu	517	75	5.5	1514	2	T52080	multi resistance p
445	80	5.8	248	2	A48853	pulmonary surfacta	518	75	5.5	1752	2	A45407	collagen alpha 3(I
446	80	5.8	333	2	T23618	hypothetical prote	519	74.5	5.4	177	2	AB3269	outer membrane lip
447	79.5	5.8	550	2	E90723	probable fumarate	520	74.5	5.4	246	2	S30144	osmotin-like prote
448	79.5	5.8	550	2	E85574	probable fumarate	521	74.5	5.4	601	2	G70983	probable glycosyl
449	79	5.7	274	2	T20435	hypothetical prote	522	74.5	5.4	638	1	A31845	nitrous-oxide redu
450	79	5.7	295	2	T19220	hypothetical prote	523	74.5	5.4	791	2	G71885	probable iron-regu
451	79	5.7	333	2	T20436	hypothetical prote	524	74.5	5.4	832	2	A31246	neurogenic protein
452	79	5.7	782	2	A61625	tenascin-like prot	525	74.5	5.4	833	2	S19087	gene Delta protein
453	79	5.7	921	2	S40495	collagen alpha 1(I	526	74.5	5.4	880	2	S00670	neurogenic repetit
454	79	5.7	1758	2	T29350	hypothetical prote	527	74.5	5.4	931	2	S13580	collagen alpha 1(I
455	79	5.7	1759	2	T29351	collagen alpha 2(I	528	74.5	5.4	1496	1	CGH02V	collagen alpha 2(I
456	78.5	5.7	294	2	T22639	hypothetical prote	529	74.5	5.4	1690	1	CGH1B	collagen alpha 4(I
457	78.5	5.7	310	2	T22641	hypothetical prote	530	74.5	5.4	1763	2	S16366	collagen alpha 2(I
458	78.5	5.7	504	2	T34995	probable integral	531	74	5.4	246	2	S29328	complement subcomp
459	78.5	5.7	1315	2	A56101	collagen alpha 1(X	532	74	5.4	248	1	LNRTPS	pulmonary surfacta
460	78.5	5.7	1774	2	B56101	collagen alpha 1(X	533	74	5.4	273	2	AS0682	probable secreted
461	78.5	5.7	2115	2	S38480	nonstructural prot	534	74	5.4	302	2	A1921	collagen dpy-13 pr
462	78.5	5.7	2214	2	T16305	hypothetical prote	535	74	5.4	325	2	T18594	hypothetical prote
463	78.5	5.7	4135	2	A42629	tenascin-X - bovin	536	74	5.4	457	2	T04226	hypothetical prote
464	78.5	5.7	4545	1	S25111	alpha-2-macroglobu	537	74	5.4	470	2	D41977	retinoid receptor
465	78	5.7	300	2	T36768	secreted serine pr	538	74	5.4	513	2	S11439	cellulose 1,4-beta
466	78	5.7	359	2	E83312	hypothetical prote	539	74	5.4	566	2	S69887	hemagglutinin prec
467	78	5.7	394	2	T33641	hypothetical prote	540	74	5.4	614	2	T33149	hypothetical prote

541	74	5.4	886	2	I50694	collagen alpha 1(I	614	71.5	5.2	895	2	T49010	hypothetical prote
542	74	5.4	1124	1	I58388	protein-tyrosine k	615	71.5	5.2	918	2	JC4361	scavenger receptor
543	74	5.4	1413	2	T26467	hypothetical prote	616	71	5.2	181	2	S56532	hypothetical 20K p
544	74	5.4	1670	1	CGH3B	collagen alpha 3(I	617	71	5.2	316	2	S25264	virK protein - Shi
545	74	5.4	1677	2	T14267	xin protein, stage	618	71	5.2	359	2	E70606	probable regulator
546	73.5	5.3	246	2	T16403	hypothetical prote	619	71	5.2	407	2	AI0595	imidazolonepropion
547	73.5	5.3	294	2	T29838	hypothetical prote	620	71	5.2	458	2	T31631	hypothetical prote
548	73.5	5.3	305	2	B84413	hypothetical prote	621	71	5.2	490	2	T37884	transcription fact
549	73.5	5.3	321	2	T28760	hypothetical prote	622	71	5.2	497	2	B42827	interleukin enhanc
550	73.5	5.3	346	2	JA0159	cysteine proteinas	623	71	5.2	575	2	A97635	adenine deaminase
551	73.5	5.3	411	2	A65184	arylsulfatase acti	624	71	5.2	575	2	AC2858	adenine deaminase
552	73.5	5.3	482	2	AE0839	succinate-semialde	625	71	5.2	639	2	D70931	hypothetical glyci
553	73.5	5.3	483	2	D83613	succinate-semialde	626	71	5.2	818	2	B75606	hypothetical prote
554	73.5	5.3	525	1	SC8794	cellulose 1,4-beta	627	71	5.2	883	2	TS1221	hypothetical prote
555	73.5	5.3	680	1	CGHUID	collagen alpha 1(X	628	71	5.2	1230	2	E64664	outer membrane pro
556	73.5	5.3	724	2	A48569	antigen Em100 - B1	629	71	5.2	1391	2	T20406	hypothetical prote
557	73.5	5.3	791	2	D64629	iron-regulated out	630	71	5.2	1691	1	S22917	collagen alpha 5(I
558	73.5	5.3	1806	1	CGHUIE	collagen alpha 1(X	631	71	5.2	1717	1	A45558	epidermal growth f
559	73	5.3	50	2	S55674	cerastocytin (EC 3	632	71	5.2	2164	1	GNNY89	genome polypeptid
560	73	5.3	295	2	T22833	hypothetical prote	633	71	5.2	2531	2	S18188	notch protein homo
561	73	5.3	360	2	T36763	probable secreted	634	71	5.2	2531	2	T16743	hypothetical prote
562	73	5.3	508	2	B70865	probable transmemb	635	71	5.2	3512	2	T17121	CPY protein - midg
563	73	5.3	597	2	S71352	metalloproteinase	636	70.5	5.1	238	2	S28001	osmotin-like prote
564	73	5.3	662	2	I38400	melanoma-associate	637	70.5	5.1	284	2	T29528	hypothetical prote
565	73	5.3	707	1	TSBYAB	tryptophan synthas	638	70.5	5.1	290	2	AE1176	fructokinases homo
566	73	5.3	728	2	S43768	transcription acti	639	70.5	5.1	325	2	T06784	probable GTP-bind
567	73	5.3	767	2	T05662	hypothetical prote	640	70.5	5.1	325	2	T09613	hypothetical prote
568	73	5.3	881	2	S25445	nitrate reductase	641	70.5	5.1	339	2	T22607	cysteine proteinas
569	73	5.3	997	2	A60776	230k bullous pemph	642	70.5	5.1	356	2	S66348	hypothetical prote
570	73	5.3	1339	2	JC4387	epidermal growth f	643	70.5	5.1	366	2	S11449	collagen short cha
571	73	5.3	1744	2	S40991	collagen alpha 1(I	644	70.5	5.1	396	1	TRYXB4	alpha-lytic protei
572	73	5.3	2207	1	GNNY5P	genome polypeptid	645	70.5	5.1	400	2	T35106	probable secreted
573	73	5.3	2555	2	A40043	notch protein homo	646	70.5	5.1	423	2	A41207	collagen 13, nonfi
574	73	5.3	3061	1	JN0545	genome polypeptid	647	70.5	5.1	585	2	T37526	probable transcrip
575	73	5.3	3623	2	T08618	intrinsic factor-B	648	70.5	5.1	627	2	T35608	polyketide hydroxy
576	72.5	5.3	135	1	TI2M1	trypsin/factor XII	649	70.5	5.1	630	2	T43460	hypothetical prote
577	72.5	5.3	230	2	D85553	probable chaperone	650	70.5	5.1	860	1	EAMS	elastin precursor
578	72.5	5.3	230	2	A90703	probable chaperone	651	70.5	5.1	920	2	A45748	collagen alpha 1(V
579	72.5	5.3	230	2	B64785	molecular chaperon	652	70.5	5.1	1342	2	A36223	kinase-related tra
580	72.5	5.3	286	2	C81681	dihydrodipicolinat	653	70.5	5.1	1414	1	S23809	collagen alpha 2(I
581	72.5	5.3	302	2	T32872	hypothetical prote	654	70.5	5.1	1486	1	B40333	collagen alpha 1(I
582	72.5	5.3	328	2	JC5350	2-nitrotoluene red	655	70.5	5.1	1747	2	A54121	collagen alpha-4 c
583	72.5	5.3	362	2	T35287	probable secreted	656	70.5	5.1	3198	2	A43426	collagen alpha 2 f
584	72.5	5.3	488	2	T47697	Regulator of chrom	657	70	5.1	261	2	S40210	chlorophyll a/b-bi
585	72.5	5.3	606	2	T08180	PF20 protein, micr	658	70	5.1	283	2	JS0170	collagen col-19 -
586	72.5	5.3	1132	2	T03844	telomerase catalyt	659	70	5.1	285	2	S60598	collagen alpha cha
587	72.5	5.3	1497	2	I49607	procollagen type V	660	70	5.1	300	2	T19829	hypothetical prote
588	72.5	5.3	1514	2	T34869	glutamate synthase	661	70	5.1	304	2	T26185	hypothetical prote
589	72	5.2	207	2	T46415	hypothetical prote	662	70	5.1	304	2	T26184	hypothetical prote
590	72	5.2	220	2	T18553	probable O-methylt	663	70	5.1	313	2	T26465	hypothetical prote
591	72	5.2	229	2	D95398	hypothetical prote	664	70	5.1	315	2	C95941	probable transcrip
592	72	5.2	258	2	A29259	Ubx protein - frui	665	70	5.1	343	2	JQ2370	hemagglutinin - in
593	72	5.2	392	2	A56123	streptogrisin D (E	666	70	5.1	389	2	I49263	potential oncogene
594	72	5.2	577	2	B37057	integrin beta-6 ch	667	70	5.1	389	2	AS9392	Wnt10b protein pre
595	72	5.2	673	2	F89101	protein F25E5.7 (I	668	70	5.1	395	1	T45547	arylsulfatase acti
596	72	5.2	691	2	T44543	probable bacteriop	669	70	5.1	402	2	H82228	imidazolonepropion
597	72	5.2	814	2	T49207	receptor kinase-11	670	70	5.1	485	2	F97228	glu-tRNAgln amidot
598	72	5.2	957	2	T15976	hypothetical prote	671	70	5.1	548	2	H82432	sucrose-6-phosphat
599	72	5.2	1220	2	A56136	jagged protein pre	672	70	5.1	560	2	D84205	hypothetical prote
600	72	5.2	2150	1	GNNYH2	genome polypeptid	673	70	5.1	561	2	T75543	6-aminohexanoate-c
601	72	5.2	2194	1	GNNYE7	genome polypeptid	674	70	5.1	671	1	CGRT1S	collagen alpha 1(I
602	72	5.2	2205	1	GNNY2W	genome polypeptid	675	70	5.1	674	2	S23297	collagen alpha 1(X
603	71.5	5.2	58	2	A45526	collagen homolog A	676	70	5.1	798	2	T28906	hypothetical prote
604	71.5	5.2	236	2	T24799	hypothetical prote	677	70	5.1	863	2	A53034	gag polypeptid -
605	71.5	5.2	283	2	JC5579	chymotrypsin-like	678	70	5.1	877	2	S43197	envelope protein p
606	71.5	5.2	284	2	T07732	probable thiolisufa	679	70	5.1	938	2	C84480	hypothetical prote
607	71.5	5.2	297	2	T18638	hypothetical prote	680	70	5.1	1188	2	D86236	protein F14N23.5 l
608	71.5	5.2	305	2	T20906	hypothetical prote	681	70	5.1	1366	2	T35985	probable large pro
609	71.5	5.2	466	2	I39707	probable indoleace	682	70	5.1	2043	2	T18524	scavenger receptor
610	71.5	5.2	524	2	T04623	cruciferin F2009.2	683	70	5.1	2206	1	GNNY4P	genome polypeptid
611	71.5	5.2	547	2	T29717	hypothetical prote	684	70	5.1	2206	1	GNNY27	genome polypeptid
612	71.5	5.2	665	1	VCMWKA	env polypeptid pr	685	70	5.1	2206	2	S03822	genome polypeptid
613	71.5	5.2	793	2	AH2126	hypothetical prote	686	70	5.1	4391	2	A38096	perlecan precursor

687	69.5	5.1	126	2	S47010	Ig heavy chain V4.	760	68.5	5.0	337	2	H8582	CT 368 hypothetica
688	69.5	5.1	184	2	E82345	probable galactosy	761	68.5	5.0	357	2	H8919	conserved hypothet
689	69.5	5.1	244	1	LN5M5C	mannose-binding le	762	68.5	5.0	372	2	S60207	fomF protein - Str
690	69.5	5.1	248	1	LN5G5S	pulmonary surfacta	763	68.5	5.0	412	2	G86003	probable transport
691	69.5	5.1	250	2	S30157	osmotin precursor	764	68.5	5.0	412	2	A91158	protein transport
692	69.5	5.1	275	2	E84179	endonuclease IV (I	765	68.5	5.0	412	2	B65134	cysteine proteinase
693	69.5	5.1	303	2	T19289	hypothetical prote	766	68.5	5.0	427	2	S57776	MFS permease (impo
694	69.5	5.1	337	2	T23794	hypothetical prote	767	68.5	5.0	487	2	AF2692	hypothetical prote
695	69.5	5.1	353	2	S16785	hemagglutinin - in	768	68.5	5.0	528	2	B97474	spore coat protein
696	69.5	5.1	356	2	S16907	collagen alpha 1(I	769	68.5	5.0	537	2	B33485	conserved hypothet
697	69.5	5.1	382	2	S20375	collagen alpha 3(V	770	68.5	5.0	544	2	G87330	collagen alpha cha
698	69.5	5.1	432	2	F96919	ABC transporter (p	771	68.5	5.0	547	2	A36046	4-alpha-D-((1->4)-
699	69.5	5.1	466	2	T06416	cysteine proteinas	772	68.5	5.0	575	2	JC7727	MPJ-K protein prec
700	69.5	5.1	482	2	S76475	hypothetical prote	773	68.5	5.0	579	2	B45266	nitrous-oxide redu
701	69.5	5.1	545	2	C82617	NH3-dependent NAD	774	68.5	5.0	634	1	S24384	MPJ-P protein prec
702	69.5	5.1	556	2	JC2005	integrin beta-5 ch	775	68.5	5.0	635	2	A45266	collagen alpha 1(I
703	69.5	5.1	739	2	C87559	phosphoribosylform	776	68.5	5.0	673	1	C8B06C	collagen alpha 1(X
704	69.5	5.1	749	2	I38488	trophinin - huma	777	68.5	5.0	674	2	S13301	probable membrane-
705	69.5	5.1	1024	2	S18251	collagen alpha 1(X	778	68.5	5.0	677	2	F95910	collagen alpha 1(V
706	69.5	5.1	1181	2	C97851	DNA-directed DNA p	779	68.5	5.0	744	1	A34246	collagen alpha 1(V
707	69.5	5.1	1418	2	T45467	collagen alpha 1(I	780	68.5	5.0	744	1	S23298	collagen alpha 1(V
708	69.5	5.1	1464	2	S59856	collagen alpha 1(I	781	68.5	5.0	744	2	S15435	collagen alpha 1(X
709	69.5	5.1	1487	1	C8H06C	collagen alpha 1(I	782	68.5	5.0	888	2	S28791	collagen alpha 1(X
710	69.5	5.1	1603	2	S23810	collagen alpha 1(X	783	68.5	5.0	915	2	T21772	hypothetical prote
711	69.5	5.1	1986	2	S28353	probable polyketid	784	68.5	5.0	927	2	T21772	hypothetical prote
712	69.5	5.1	2019	1	JQ1322	tenascin precursor	785	68.5	5.0	937	2	I53282	gene PACE4 protein
713	69.5	5.1	2201	2	A32160	tenascin-C - huma	786	68.5	5.0	1049	1	C8B07S	collagen alpha 1(I
714	69	5.0	38	2	T01677	pseudo-kallikrein	787	68.5	5.0	1419	2	A41182	collagen alpha 1(I
715	69	5.0	224	2	S06545	finger protein (cl	788	68.5	5.0	1487	2	B41182	collagen alpha 1(I
716	69	5.0	239	1	LN5M5A	mannose-binding le	789	68.5	5.0	2206	1	GNNY21	genome polyprotein
717	69	5.0	290	2	T24586	hypothetical prote	790	68.5	5.0	2403	2	A59386	sanko - human
718	69	5.0	290	2	T24590	hypothetical prote	791	68.5	5.0	2482	2	I48922	cation-independent
719	69	5.0	294	2	T21668	hypothetical prote	792	68.5	5.0	2483	1	A49617	insulin-like growt
720	69	5.0	297	1	PR5WAG	streptogrisin A (S	793	68.5	5.0	2560	1	I40457	peptide synthetase
721	69	5.0	327	2	S48839	guanine nucleotide	794	68.5	5.0	2715	2	T13049	eyelid - fruit fly
722	69	5.0	329	2	B83162	molybdopterin bios	795	68.5	5.0	3106	1	S53868	laminin alpha-2 ch
723	69	5.0	334	1	S74957	cytochrome c-type	796	68.5	5.0	4544	1	S02392	alpha-2-macroglobu
724	69	5.0	395	2	S41035	hypothetical prote	797	68.5	5.0	4660	2	T42737	gp330 protein prec
725	69	5.0	399	2	H84717	hypothetical prote	798	68.5	5.0	175	1	A60010	early E1A 20K prot
726	69	5.0	406	2	A47696	acetamidase - Myco	799	68	4.9	177	2	S37749	collagen alpha 2(X
727	69	5.0	435	2	T50991	beta transducin -	800	68	4.9	229	1	S54799	nitrite hydratase
728	69	5.0	438	2	T50991	hypothetical prote	801	68	4.9	237	2	A88640	protein C34H4.4 [i
729	69	5.0	441	2	A45565	cysteine proteinas	802	68	4.9	248	1	LNHUMC	mannose-binding le
730	69	5.0	469	2	A24450	collagen alpha 2(V	803	68	4.9	272	2	H87075	probable conserved
731	69	5.0	523	2	B95922	hypothetical nucle	804	68	4.9	289	2	T37708	hypothetical prote
732	69	5.0	532	2	F70580	hypothetical glyci	805	68	4.9	297	2	T46864	nicotinate-nucleot
733	69	5.0	567	1	C55516	hydrogenase (EC 1.	806	68	4.9	330	2	T26004	hypothetical prote
734	69	5.0	567	2	G85958	probable large sub	807	68	4.9	343	1	HMIVTA	hemagglutinin HA1
735	69	5.0	567	2	G91113	hydrogenase-2 larg	808	68	4.9	349	2	D72175	G2R protein - vari
736	69	5.0	613	2	T11464	NADH2 dehydrogenas	809	68	4.9	354	2	A35788	hemagglutinin - in
737	69	5.0	635	2	A57131	collagen alpha 2(V	810	68	4.9	358	2	T26281	hypothetical prote
738	69	5.0	682	2	D84579	probable Tail-like	811	68	4.9	384	2	S46110	hypothetical prote
739	69	5.0	950	2	S27473	URRS1 protein - sm	812	68	4.9	387	2	B49175	Moich A protein -
740	69	5.0	1366	1	C8H02S	collagen alpha 2(I	813	68	4.9	404	2	A54871	gal beta-1, 3galNA
741	69	5.0	1669	1	C8H04B	collagen alpha 1(I	814	68	4.9	412	2	JC6317	glutamate dehydrog
742	69	5.0	1749	2	S75071	hypothetical prote	815	68	4.9	447	2	F82862	conjugal transfer
743	69	5.0	1786	1	MMHUB1	laminin beta-1 cha	816	68	4.9	453	2	S49168	beta tubulin 1 - r
744	69	5.0	2207	2	S09553	genome polyprotein	817	68	4.9	460	2	A39938	phosphotransferase
745	69	5.0	2209	1	GNNY2P	protein-tyrosine-p	818	68	4.9	484	2	F98208	succinate-semialde
746	69	5.0	2450	2	T071625	protein-tyrosine-p	819	68	4.9	484	2	AC3078	succinate-semialde
747	69	5.0	4957	2	T03455	ALR protein - huma	820	68	4.9	490	2	B95316	interleukin enhanc
748	69	5.0	5262	2	T03454	ALR protein - huma	821	68	4.9	543	2	A41285	hemagglutinin prec
749	68.5	5.0	127	2	F82617	ferredoxin XF1964	822	68	4.9	566	1	HMIV	hemagglutinin prec
750	68.5	5.0	155	2	B32669	vasotocin 2 / neur	823	68	4.9	566	1	HMIV17	hemagglutinin phos
751	68.5	5.0	233	2	S31829	pathogenesis-relat	824	68	4.9	605	2	T15291	spingomyelin phos
752	68.5	5.0	250	2	S25114	osmotin-like prote	825	68	4.9	631	2	JC2345	xekin-like protein
753	68.5	5.0	252	2	A55047	collagen alpha 1(V	826	68	4.9	656	2	G85731	Rhs element associ
754	68.5	5.0	285	2	T18814	hypothetical prote	827	68	4.9	680	2	S31216	collagen alpha 1(X
755	68.5	5.0	290	2	A11533	fructokinases homo	828	68	4.9	724	2	T37858	probable peroxidas
756	68.5	5.0	323	2	T19142	hypothetical prote	829	68	4.9	726	2	T35865	probable cyclase -
757	68.5	5.0	329	2	T32783	hypothetical prote	830	68	4.9	743	1	S23779	collagen alpha 1(V
758	68.5	5.0	336	1	S76928	probable aryl alco	831	68	4.9	754	2	A55267	collagen alpha 5(I
759	68.5	5.0	337	2	A72042	conserved hypothet	832	68	4.9	756	2	S67433	hypothetical prote





979	66	4.8	238	1	LNRMTA	mannose-binding le	1052	65.5	4.8	1629	2	C84839	ferredoxin-depende
980	66	4.8	239	2	D82727	6-phosphogluconola	1053	65.5	4.8	2518	2	A12140	polyketide synthas
981	66	4.8	256	2	AE0997	probable biotin bi	1054	65.5	4.8	2823	2	F87908	protein T22A3.8 [i
982	66	4.8	306	2	T21938	hypothetical prote	1055	65.5	4.8	2823	2	T23064	hypothetical prote
983	66	4.8	307	2	T18846	hypothetical prote	1056	65.5	4.8	3102	2	T43291	laminin alpha chai
984	66	4.8	311	2	S48400	carrier protein FL	1057	65.5	4.8	3871	2	T22812	hypothetical prote
985	66	4.8	313	2	A35122	metalloproteinase	1058	65.5	4.8	4848	2	T30289	pristinamycin I sy
986	66	4.8	326	2	JQ1437	hemagglutinin - in	1059	65	4.7	111	2	B82830	hypothetical prote
987	66	4.8	336	2	S41643	svrM protein - Rhi	1060	65	4.7	162	2	T49957	ribosomal protein
988	66	4.8	344	2	PQ0319	hemagglutinin - in	1061	65	4.7	181	2	T07661	maturating protein
989	66	4.8	348	2	T25288	hypothetical prote	1062	65	4.7	188	2	A54270	insulin-like growt
990	66	4.8	353	2	D96596	hypothetical prote	1063	65	4.7	229	1	S19713	insulin-like growt
991	66	4.8	355	1	S37460	glutamyl endopepti	1064	65	4.7	229	1	S19713	insulin-like growt
992	66	4.8	435	2	T15143	hypothetical prote	1065	65	4.7	232	2	F70789	probable protease -
993	66	4.8	553	2	T52362	hypothetical prote	1066	65	4.7	249	2	F70925	hypothetical prote
994	66	4.8	614	2	T05741	hypothetical prote	1067	65	4.7	287	2	D70625	probable transposa
995	66	4.8	687	2	T02459	probable beta-amyl	1068	65	4.7	299	2	T20605	hypothetical prote
996	66	4.8	753	2	S35371	finger protein neu	1069	65	4.7	303	2	S45461	hypothetical prote
997	66	4.8	787	2	T05617	hypothetical prote	1070	65	4.7	311	2	F75366	hypothetical prote
998	66	4.8	854	2	A96574	protein F12M16.30	1071	65	4.7	313	2	H89865	hypothetical prote
999	66	4.8	864	2	T30441	probable capsid-as	1072	65	4.7	313	2	T22828	hypothetical prote
1000	66	4.8	1194	2	C59436	KIAA1391 protein [	1073	65	4.7	342	2	A46396	ets-related protei
1001	66	4.8	1364	2	T05059	notch4 - mouse	1074	65	4.7	349	2	T43457	hypothetical prote
1002	66	4.8	2114	2	E96505	hypothetical prote	1075	65	4.7	356	2	T22827	hypothetical prote
1003	66	4.8	2193	2	S52919	polyprotein (1A, 1	1076	65	4.7	358	2	T36415	probable iron-side
1004	66	4.8	3442	2	E82589	hemagglutinin-like	1077	65	4.7	359	1	S28043	cinnamyl-alcohol d
1005	66	4.8	3455	2	B82519	hemagglutinin-like	1078	65	4.7	370	2	T22510	hypothetical prote
1006	66	4.8	3507	2	T34513	hypothetical prote	1079	65	4.7	406	2	S73592	glycine hydroxymet
1007	65.5	4.8	37	2	S03570	trypsin (EC 3.4.21	1080	65	4.7	416	2	H82968	sarcosine oxidase
1008	65.5	4.8	97	2	S26898	Ig heavy chain V r	1081	65	4.7	418	2	H82968	probable fumarylac
1009	65.5	4.8	97	2	JH0428	Ig gamma chain V r	1082	65	4.7	428	2	D33861	hypothetical prote
1010	65.5	4.8	114	2	I72667	cold agglutinin FS	1083	65	4.7	446	2	T10711	anthranilate N-ben
1011	65.5	4.8	117	2	T35913	hypothetical prote	1084	65	4.7	469	2	T36362	probable DNA repai
1012	65.5	4.8	140	2	S78052	Ig heavy chain pre	1085	65	4.7	476	2	T29054	probable transmemb
1013	65.5	4.8	147	2	A84546	50S ribosomal prot	1086	65	4.7	619	2	T08613	hypothetical prote
1014	65.5	4.8	202	2	T35703	hypothetical prote	1087	65	4.7	711	2	D86296	hypothetical prote
1015	65.5	4.8	228	2	T49891	glycine-rich prote	1088	65	4.7	715	2	S05381	probable membrane
1016	65.5	4.8	245	1	C1HU24	complement subcomp	1089	65	4.7	737	2	S22675	hypothetical prote
1017	65.5	4.8	286	2	F71524	dihydrodipicolinat	1090	65	4.7	759	2	T44142	DR1 protein (impor
1018	65.5	4.8	298	2	T27644	hypothetical prote	1091	65	4.7	783	2	T35389	probable serine-th
1019	65.5	4.8	304	2	JC5845	chitinase (EC 3.2.	1092	65	4.7	784	2	JQ0317	hypothetical 82K p
1020	65.5	4.8	311	2	E85867	hypothetical prote	1093	65	4.7	826	2	A60385	monocyte surface a
1021	65.5	4.8	311	2	D91023	hypothetical prote	1094	65	4.7	837	2	E70835	hypothetical glyci
1022	65.5	4.8	327	2	AG3367	alcohol dehydrogen	1095	65	4.7	866	2	S57936	CotC protein precu
1023	65.5	4.8	350	2	S63248	hypothetical prote	1096	65	4.7	881	2	T49279	hypothetical prote
1024	65.5	4.8	360	2	T37285	collagen dpy-2 - C	1097	65	4.7	984	2	T00326	hypothetical prote
1025	65.5	4.8	363	2	T16831	hypothetical prote	1098	65	4.7	1112	2	S49432	replicase 126K - o
1026	65.5	4.8	371	2	B72461	hypothetical prote	1099	65	4.7	1196	1	DNBER5	DNA-binding protei
1027	65.5	4.8	396	2	T29773	hypothetical prote	1100	65	4.7	1374	2	T16129	hypothetical prote
1028	65.5	4.8	397	2	S28274	collagen alpha 2(I	1101	65	4.7	1439	2	T02087	gag/pol polyprotei
1029	65.5	4.8	402	1	CG802S	collagen alpha 2(I	1102	65	4.7	1489	2	D70807	hypothetical glyci
1030	65.5	4.8	452	2	T30082	hypothetical prote	1103	65	4.7	1522	2	T00028	brain-specific ang
1031	65.5	4.8	467	1	WZBE61	gene 61 protein -	1104	65	4.7	1603	1	BVASA1	3-dehydroquinatase
1032	65.5	4.8	479	2	CQ0457	cytochrome b558/56	1105	65	4.7	1707	2	F33526	collagen alpha 2(I
1033	65.5	4.8	486	2	A27353	collagen alpha 1(I	1106	65	4.7	1901	2	F70806	hypothetical glyci
1034	65.5	4.8	578	2	S33327	catalase (EC 1.11.	1107	65	4.7	2083	2	T42721	CRP-ductin-alpha p
1035	65.5	4.8	615	2	A05269	collagen alpha 1(I	1108	65	4.7	2166	2	S11339	calcium channel pr
1036	65.5	4.8	691	2	A54741	erythrocyte membra	1109	65	4.7	2244	2	S05054	calcium channel al
1037	65.5	4.8	730	2	A36226	collagen alpha 1 c	1110	65	4.7	2252	2	T08212	RNA-directed RNA p
1038	65.5	4.8	741	2	G69514	hypothetical prote	1111	65	4.7	2294	2	I67630	protein-tyrosine-p
1039	65.5	4.8	775	2	A61228	collagen alpha 2(I	1112	65	4.7	2395	1	S050820	surface protein ty
1040	65.5	4.8	782	2	B83966	formate dehydrogen	1113	65	4.7	2466	2	I67629	protein-tyrosine-p
1041	65.5	4.8	877	2	T03098	p97 protein - Toxo	1114	65	4.7	2490	1	A54971	protein-tyrosine-p
1042	65.5	4.8	947	2	T23107	hypothetical prote	1115	65	4.7	2509	2	G01880	fatty-acid synthas
1043	65.5	4.8	966	1	P1BVB8	RNA 1a protein - b	1116	65	4.7	159	2	I49618	gamma-P-crystallin
1044	65.5	4.8	969	2	B87083	excinuclease ABC s	1117	64.5	4.7	171	2	A34493	collagen alpha 1(I
1045	65.5	4.8	1137	2	T02097	glutamate synthase	1118	64.5	4.7	191	2	D90712	lipote biosynthes
1046	65.5	4.8	1210	1	GQHUE	epidermal growth f	1119	64.5	4.7	191	2	H85562	lipote biosynthes
1047	65.5	4.8	1395	2	A32901	gip1 protein precu	1120	64.5	4.7	191	2	D64797	lipote-protein li
1048	65.5	4.8	1353	1	JQ2168	E2 glycoprotein pr	1121	64.5	4.7	210	2	T20973	hypothetical prote
1049	65.5	4.8	1360	2	T33922	hypothetical prote	1122	64.5	4.7	222	2	A88102	protein W09G10.1 [
1050	65.5	4.8	1376	1	JQ1534	E2 glycoprotein pr	1123	64.5	4.7	232	2	E90834	minor tail protein
1051	65.5	4.8	1492	2	A40333	collagen alpha 1(I	1124	64.5	4.7				

1125	64.5	4.7	242	2	S60143	cellulase (EC 3.2.1)	1198	64	4.7	426	2	D88103	protein W10G11.6 [
1126	64.5	4.7	262	2	A54889	IgE-binding protei	1199	64	4.7	465	1	S47738	cytochrome-c perox
1127	64.5	4.7	266	2	T22706	hypothetical prote	1200	64	4.7	465	1	F91178	cytochrome-c perox
1128	64.5	4.7	277	1	Q0BEC2	HKRFx protein - hu	1201	64	4.7	465	2	G86024	cytochrome-c perox
1129	64.5	4.7	297	2	T27525	hypothetical prote	1202	64	4.7	487	2	T45923	hypothetical prote
1130	64.5	4.7	301	2	B31219	collagen 2 - Caeno	1203	64	4.7	502	2	S36526	L1 protein - human
1131	64.5	4.7	317	2	T29960	hypothetical prote	1204	64	4.7	504	2	S58745	cellulase (clone pGM31
1132	64.5	4.7	318	2	S27977	cuticle collagen d	1205	64	4.7	516	2	S42093	cellulose 1,4-beta
1133	64.5	4.7	323	2	AD1916	alcohol dehydrogen	1206	64	4.7	566	1	HMIVUR	hemagglutinin prec
1134	64.5	4.7	328	2	T15867	hypothetical prote	1207	64	4.7	566	2	S69888	hemagglutinin prec
1135	64.5	4.7	354	2	B75400	phosphoribosylform	1208	64	4.7	595	2	P95379	probable adenine d
1136	64.5	4.7	356	2	T05119	leucoanthocyanidin	1209	64	4.7	563	1	S18572	tetracycline resis
1137	64.5	4.7	387	2	E95933	probable calcium-b	1210	64	4.7	669	2	A35103	cell surface recep
1138	64.5	4.7	398	2	B71284	probable periplasm	1211	64	4.7	697	2	T37946	tryptophan synthas
1139	64.5	4.7	411	2	B91220	probable arylsulfa	1212	64	4.7	717	2	T49238	hypothetical prote
1140	64.5	4.7	411	2	D86066	probable arylsulfa	1213	64	4.7	719	2	A87292	prinosomal protein
1141	64.5	4.7	411	2	S58105	Cu metalloregulato	1214	64	4.7	721	2	F70649	probable Acyl-CoA
1142	64.5	4.7	416	2	T41665	probable dipeptida	1215	64	4.7	728	2	I50719	C-Delta-1 - chicke
1143	64.5	4.7	445	2	D86620	phosphoshikimate v	1216	64	4.7	753	2	AH0097	probable biotin su
1144	64.5	4.7	445	2	C72004	hemopexin precurs	1217	64	4.7	823	2	T21104	hypothetical prote
1145	64.5	4.7	460	1	Q0RT	L1 protein - human	1218	64	4.7	843	2	T13334	probable tail-host
1146	64.5	4.7	529	2	S36578	DnaK-type molecula	1219	64	4.7	861	2	B49847	nitrate reductase
1147	64.5	4.7	532	2	AE1964	60K cysteine-rich	1220	64	4.7	963	2	AD0541	outer membrane fim
1148	64.5	4.7	547	1	A32244	60K cysteine-rich	1221	64	4.7	963	2	T19140	hypothetical prote
1149	64.5	4.7	553	2	D71515	choline dehydrogen	1222	64	4.7	998	2	T35745	probable ATP-bindi
1150	64.5	4.7	562	2	A85524	choline dehydrogen	1223	64	4.7	1000	2	A83467	sarcosine oxidase
1151	64.5	4.7	562	2	E90673	proline transport	1224	64	4.7	1083	2	H86921	probable arabinosy
1152	64.5	4.7	570	2	S42708	proline transport	1225	64	4.7	1955	1	AGCH	agrin precursor -
1153	64.5	4.7	570	2	S04547	alpha-glucosidase	1226	64	4.7	2042	2	T18399	variant-specific s
1154	64.5	4.7	597	2	JC7615	hypothetical prote	1227	64	4.7	2321	2	S78549	notch3 protein - h
1155	64.5	4.7	599	2	T25835	collagen alpha 2(I	1228	64	4.7	3137	2	A37797	reelin precursor -
1156	64.5	4.7	618	2	S32436	hypothetical prote	1229	64	4.7	3461	2	S58870	collagen alpha 3(V
1157	64.5	4.7	626	2	T27035	succinate dehydrog	1230	64	4.7	3635	2	T10053	laminin alpha 5 ch
1158	64.5	4.7	626	2	C86589	succinate dehydrog	1231	64	4.7	7463	2	T36248	CDA peptide synthe
1159	64.5	4.7	644	2	JC2346	kexin-like protein	1232	63.5	4.6	97	2	G34964	ig heavy chain V-I
1160	64.5	4.7	646	2	H96665	protein P2C12.10	1233	63.5	4.6	144	2	S24805	hypothetical prote
1161	64.5	4.7	653	1	S23667	cytochrome c-type	1234	63.5	4.6	152	2	T24064	hypothetical prote
1162	64.5	4.7	653	2	T02080	probable carbonate	1235	63.5	4.6	184	2	D83234	hypothetical prote
1163	64.5	4.7	666	2	F71310	probable periplasm	1236	63.5	4.6	191	2	I46412	keratin KAP5.4 - s
1164	64.5	4.7	678	2	B84856	hypothetical prote	1237	63.5	4.6	191	2	AF0580	lipotein-protein li
1165	64.5	4.7	715	2	S70397	zona pellucida gly	1238	63.5	4.6	215	2	AD0455	thiamine-phosphate
1166	64.5	4.7	721	2	C84732	probable homeodoma	1239	63.5	4.6	220	2	S35789	US2 protein - bovi
1167	64.5	4.7	724	2	T71274	hypothetical prote	1240	63.5	4.6	232	1	T18753	minor tail protein
1168	64.5	4.7	730	2	H86295	hypothetical prote	1241	63.5	4.6	234	2	T31753	hypothetical prote
1169	64.5	4.7	884	2	S61569	hypothetical prote	1242	63.5	4.6	253	1	CIHUQB	complement subcomp
1170	64.5	4.7	1374	1	GNVYEC	genome polyprotein	1243	63.5	4.6	256	2	T28853	hypothetical prote
1171	64.5	4.7	1376	1	VG1HJ72	E2 glycoprotein pr	1244	63.5	4.6	269	2	C83516	hypothetical prote
1172	64.5	4.7	1388	2	A53317	collagen alpha 1(X	1245	63.5	4.6	281	2	T32765	hypothetical prote
1173	64.5	4.7	1408	2	S16148	gene serrate prote	1246	63.5	4.6	281	2	C88638	protein F50F6.1 [i
1174	64.5	4.7	1487	2	T02850	hypothetical prote	1247	63.5	4.6	289	2	T34241	hypothetical prote
1175	64.5	4.7	1546	1	CGHU2E	collagen alpha 2(I	1248	63.5	4.6	289	2	T26812	hypothetical prote
1176	64.5	4.7	1712	1	CGHU2B	collagen alpha 2(I	1249	63.5	4.6	290	2	A32249	collagen - sea urc
1177	64.5	4.7	2139	2	A35672	crumbs protein - f	1250	63.5	4.6	291	2	T34494	hypothetical prote
1178	64.5	4.7	3623	2	T03456	intrinsic factor-B	1251	63.5	4.6	294	2	T23916	hypothetical prote
1179	64	4.7	104	2	JH0345	T-cell receptor al	1252	63.5	4.6	308	2	H90452	conserved hypotet
1180	64	4.7	118	1	A31429	hisactophilin [val	1253	63.5	4.6	311	2	B64998	hypothetical prote
1181	64	4.7	128	2	JQ1002	keratin, claw - ch	1254	63.5	4.6	316	2	T20497	hypothetical prote
1182	64	4.7	133	2	B38911	ig heavy chain v r	1255	63.5	4.6	320	2	C81029	3-oxoacyl-(acyl-ca
1183	64	4.7	218	2	T03287	osmotin protein ho	1256	63.5	4.6	320	2	T39110	probable gpase ac
1184	64	4.7	238	2	B75266	phosphoribosylform	1257	63.5	4.6	326	2	T02340	GTP-binding regula
1185	64	4.7	248	1	LNHPU6	pulmonary surfacta	1258	63.5	4.6	328	2	T16970	GTP-binding protei
1186	64	4.7	278	2	A43670	integral membrane	1259	63.5	4.6	335	2	A40038	MHC class I histoc
1187	64	4.7	304	2	T23801	hypothetical prote	1260	63.5	4.6	338	2	T49182	probable chloropla
1188	64	4.7	310	2	T29731	hypothetical prote	1261	63.5	4.6	357	2	H75541	probable oxidoredu
1189	64	4.7	333	2	T50630	hypothetical prote	1262	63.5	4.6	371	2	E88633	protein F56B3.1 [i
1190	64	4.7	346	2	T45069	8-hydroxy-guanine	1263	63.5	4.6	375	2	A95867	probable pyrroloqu
1191	64	4.7	394	1	VGBE17	glycoprotein D pre	1264	63.5	4.6	378	2	AB0894	conserved hypotet
1192	64	4.7	394	1	VGBED1	glycoprotein D - h	1265	63.5	4.6	381	2	T27806	hypothetical prote
1193	64	4.7	401	2	C89102	protein F25E5.10 [	1266	63.5	4.6	388	2	T22553	hypothetical prote
1194	64	4.7	411	2	T16982	glutamate dehydrog	1267	63.5	4.6	404	2	T40553	Trp-Asp repeat pro
1195	64	4.7	411	2	T04342	glutamate dehydrog	1268	63.5	4.6	418	2	S31124	hypothetical prote
1196	64	4.7	411	2	T03294	glutamate dehydrog	1269	63.5	4.6	435	2	B87412	conserved hypotet
1197	64	4.7	426	2	AH2144	hypothetical prote	1270	63.5	4.6	445	2	C72695	probable amidase A

1271	63.5	4.6	481	2	A33712	metalloproteinase	1344	63	4.6	437	2	JC7138	alpha-amylase (EC
1272	63.5	4.6	498	2	B84789	probable protein w	1345	63	4.6	437	2	JT0946	alpha-amylase 3E -
1273	63.5	4.6	504	1	L1ML31	l1 protein - human	1346	63	4.6	438	2	D88206	protein nhr-21.a [
1274	63.5	4.6	538	2	S65764	chitinase (EC 3.2.	1347	63	4.6	453	2	A71891	glu-tRNA amidotran
1275	63.5	4.6	556	1	S10901	choline dehydrogen	1348	63	4.6	453	2	AE2955	glutamyl-tRNA amid
1276	63.5	4.6	564	2	A34734	transcription fact	1349	63	4.6	471	2	A39024	collagen alpha 3(I
1277	63.5	4.6	680	2	T29343	conserved hypotet	1350	63	4.6	475	2	AE0855	conserved hypotet
1278	63.5	4.6	680	2	C25832	hypothetical prote	1351	63	4.6	475	2	H91077	probable 4-hydroxy
1279	63.5	4.6	690	2	T08604	hypothetical prote	1352	63	4.6	475	2	T44997	probable 4-hydroxy
1280	63.5	4.6	700	2	T41401	spore outgrowth fa	1353	63	4.6	475	2	AE5923	probable 4-hydroxy
1281	63.5	4.6	724	2	D87530	isoquinoline l-oxi	1354	63	4.6	480	2	F70785	hypothetical prote
1282	63.5	4.6	728	2	S26427	70K structural pro	1355	63	4.6	487	2	T21384	hypothetical prote
1283	63.5	4.6	742	4	C34734	transcription fact	1356	63	4.6	513	1	EUTQ1	cellulose 1,4-beta
1284	63.5	4.6	768	2	A42755	p-selectin precurs	1357	63	4.6	513	2	S45380	cellulose 1,4-beta
1285	63.5	4.6	803	2	C83561	probable type II s	1358	63	4.6	545	2	H82282	viobactin-speci
1286	63.5	4.6	825	4	B34734	transcription fact	1359	63	4.6	545	2	T02079	probable carbonate
1287	63.5	4.6	872	2	A49538	CoC protein precu	1360	63	4.6	582	2	S10099	transcription fact
1288	63.5	4.6	883	2	T07651	potassium channel	1361	63	4.6	611	2	T27013	hypothetical prote
1289	63.5	4.6	901	2	T04108	receptor kinase ho	1362	63	4.6	622	2	T27155	hypothetical prote
1290	63.5	4.6	907	2	T15792	hypothetical prote	1363	63	4.6	633	2	B40983	collagen alpha 1(X
1291	63.5	4.6	932	2	I52527	PACF4A - mouse (fr	1364	63	4.6	638	2	I53169	cytokerin 2 - hu
1292	63.5	4.6	1042	2	T26644	hypothetical prote	1365	63	4.6	658	2	AB3253	glucose inhibited
1293	63.5	4.6	1345	2	S46817	hypothetical prote	1366	63	4.6	684	2	F83375	hypothetical prote
1294	63.5	4.6	1381	2	E70806	hypothetical glyci	1367	63	4.6	692	2	B96628	translation elonga
1295	63.5	4.6	1549	2	I49103	hypothetical glyci	1368	63	4.6	692	2	C83666	translation elonga
1296	63.5	4.6	1573	2	S01845	type VII collagen	1369	63	4.6	692	2	T44380	translation elonga
1297	63.5	4.6	1649	2	C86822	DNA (cytosine-5-)-	1370	63	4.6	695	2	AE1406	translation elonga
1298	63.5	4.6	1693	2	S76086	hypothetical prote	1371	63	4.6	695	2	AE1782	translation elonga
1299	63.5	4.6	1959	1	AGRT	beta transducin-li	1372	63	4.6	695	2	GB7316	nuclease, probable
1300	63.5	4.6	2185	1	GNNYBT	agrin - rat	1373	63	4.6	705	2	C84406	hypothetical prote
1301	63.5	4.6	2185	1	JQ2021	genome polyprotein	1374	63	4.6	760	2	A45174	hypothetical prote
1302	63.5	4.6	2195	2	T34264	genome polyprotein	1375	63	4.6	946	2	T16297	eye cell developme
1303	63.5	4.6	2352	2	T30201	hypothetical prote	1376	63	4.6	1125	1	S57846	hypothetical prote
1304	63.5	4.6	2533	2	T28675	Notch homolog prot	1377	63	4.6	1170	2	AS3612	protein-tyrosine k
1305	63.5	4.6	2533	2	T28675	alpha-5iD immobili	1378	63	4.6	1203	2	A49175	laminin B1k chain
1306	63.5	4.6	3063	2	S55505	alpha-5iD-immobili	1379	63	4.6	1331	2	T18310	Motch B protein -
1307	63.5	4.6	3429	2	T13853	fatty-acid synthas	1380	63	4.6	1345	2	S55669	receptor-adenylate
1308	63	4.6	40	2	A49081	hypothetical prote	1381	63	4.6	1367	2	T33819	tegument protein 7
1309	63	4.6	99	2	S26801	capillary permeabi	1382	63	4.6	1820	2	A55494	hypothetical prote
1310	63	4.6	119	2	B45937	Ig heavy chain v r	1383	63	4.6	2157	1	GNNY1B	latent transformin
1311	63	4.6	119	2	S24937	early chorion prot	1384	63	4.6	2437	2	S42612	genome polyprotein
1312	63	4.6	198	2	A83153	chorion protein -	1385	63	4.6	2647	2	A37098	transmembrane prot
1313	63	4.6	212	2	E86179	hypothetical prote	1386	63	4.6	3176	2	CGH3A	gelatin factor A8
1314	63	4.6	228	2	A44982	collagen UCOL1 - p	1387	62.5	4.5	97	2	S14474	collagen alpha 3(V
1315	63	4.6	240	2	F70631	probable sodC prot	1388	62.5	4.5	118	2	S29653	Ig heavy chain V r
1316	63	4.6	242	1	F75433	probable phosphos	1389	62.5	4.5	144	2	S01391	textilotoxin chain
1317	63	4.6	245	1	CLHQQC	complement subcomp	1390	62.5	4.5	155	2	C44012	phospholipase A2 (
1318	63	4.6	248	1	LNHUPS	pulmonary surfacta	1391	62.5	4.5	165	2	S72776	insulin-like growt
1319	63	4.6	257	2	T28946	hypothetical prote	1392	62.5	4.5	181	2	A70627	Bl496_F141 protei
1320	63	4.6	265	2	AG0814	cob(I) alamin adeno	1393	62.5	4.5	198	2	I49558	hypothetical prote
1321	63	4.6	269	2	S36166	paired box transcr	1394	62.5	4.5	214	2	T18539	collagen alpha 1(I
1322	63	4.6	285	2	T29982	hypothetical prote	1395	62.5	4.5	222	2	S19931	phosphoglycerate m
1323	63	4.6	299	2	T24833	hypothetical prote	1396	62.5	4.5	231	2	B3746	glycine-rich prote
1324	63	4.6	302	2	T15936	hypothetical prote	1397	62.5	4.5	247	2	S33197	Ig Fab region IV-J
1325	63	4.6	303	2	E86591	hypothetical prote	1398	62.5	4.5	299	2	T29956	osmotin-like prote
1326	63	4.6	303	2	T27031	CT580 hypothetical	1399	62.5	4.5	306	2	H81036	hypothetical prote
1327	63	4.6	308	2	S32172	neurosporene hydro	1400	62.5	4.5	313	2	T33010	riboflavin kinase/
1328	63	4.6	309	2	H69995	hypothetical prote	1401	62.5	4.5	316	2	T19288	hypothetical prote
1329	63	4.6	320	2	C81972	probable 3-oxoacyl	1402	62.5	4.5	341	2	F70625	hypothetical prote
1330	63	4.6	326	2	JS0169	collagen col-14 -	1403	62.5	4.5	352	2	JE0296	thyrotropin releas
1331	63	4.6	346	2	T28623	hypothetical prote	1404	62.5	4.5	356	2	S61061	hypothetical prote
1332	63	4.6	349	2	C36858	gene G4R protein -	1405	62.5	4.5	359	2	T22774	hypothetical prote
1333	63	4.6	357	1	S33321	glutamyl endopepti	1406	62.5	4.5	391	2	F87258	acyl-CoA dehydrog
1334	63	4.6	369	2	S33603	surfactant protein	1407	62.5	4.5	398	2	AG0128	1-deoxy-D-xylulose
1335	63	4.6	383	2	C83518	hypothetical prote	1408	62.5	4.5	398	2	T35255	probable racemase
1336	63	4.6	400	2	A75336	hypothetical prote	1409	62.5	4.5	402	2	S37789	hypothetical prote
1337	63	4.6	403	2	H98327	serine proteinase,	1410	62.5	4.5	411	2	S71217	glutamate dehydrog
1338	63	4.6	418	2	T15142	enantiomers-selecti	1411	62.5	4.5	427	2	S75210	glycine hydroxymet
1339	63	4.6	422	1	A56674	hypothetical prote	1412	62.5	4.5	450	2	E70681	probable trpE - My
1340	63	4.6	424	2	C86247	paired box transcr	1413	62.5	4.5	466	2	A87638	glutamate-1-semial
1341	63	4.6	428	2	T27544	hypothetical prote	1414	62.5	4.5	473	2	AS6175	Glutamate-1-semial
1342	63	4.6	434	2	D96760	zinc resistance pr	1415	62.5	4.5	478	2	S31906	adhesive plaque pr
1343	63	4.6	436	1	S42234	hypothetical prote	1416	62.5	4.5	482	2	S76376	beta-1,3-glucanase
1344	63	4.6	436	1	S42234	paired box transcr	1416	62.5	4.5	482	2	S76376	hypothetical prote

1417 62.5 4.5 498 2 A72725 probable beta-lact  
1418 62.5 4.5 532 2 T49824 hypothetical prote  
1419 62.5 4.5 560 2 T16833 hypothetical prote  
1420 62.5 4.5 561 2 A84287 hypothetical prote  
1421 62.5 4.5 577 2 A60501 thrombomodulin pre  
1422 62.5 4.5 589 2 T23299 hypothetical prote  
1423 62.5 4.5 612 2 S53714 probable dinitrifi  
1424 62.5 4.5 678 2 B40809 growth arrest-spec  
1425 62.5 4.5 684 2 A53019 collagen alpha 1(X  
1426 62.5 4.5 695 2 E71463 probable polyribon  
1427 62.5 4.5 709 2 S33907 glycercol kinase [E  
1428 62.5 4.5 722 2 I43824 DELTA-like 1 - mou  
1429 62.5 4.5 731 2 JC7701 ARGA9 protein -  
1430 62.5 4.5 784 2 A26601 elastin precursor  
1431 62.5 4.5 799 2 A38308 integrin beta-5 ch  
1432 62.5 4.5 810 2 C84845 probable salt-indu  
1433 62.5 4.5 979 2 D96574 hypothetical prote  
1434 62.5 4.5 1030 2 H98568 unknown protein, 2  
1435 62.5 4.5 1039 2 A41131 lymphocyte-Peyer's  
1436 62.5 4.5 1107 2 T15884 hypothetical prote  
1437 62.5 4.5 1160 2 F88369 protein unc-52 [im  
1438 62.5 4.5 1257 2 S28764 neurocan precursor  
1439 62.5 4.5 1308 2 A47253 epidermal growth f  
1440 62.5 4.5 1610 2 A48227 voltage-dependent  
1441 62.5 4.5 1846 2 JH0422 voltage-dependent  
1442 62.5 4.5 2203 2 C88369 protein unc-52 [im  
1443 62.5 4.5 2295 2 C88369 insulin-like growt  
1444 62.5 4.5 2491 1 A28372 pristinamycin I sy  
1445 62.5 4.5 2591 2 T30288 hypothetical prote  
1446 62.5 4.5 3375 2 T19821 cocoonase (EC 3.4.  
1447 62 4.5 43 2 A61168 nosr protein - Par  
1448 62 4.5 98 2 S39410 Ig heavy chain V r  
1449 62 4.5 99 2 S26800 Ig heavy chain V r  
1450 62 4.5 99 2 S26800 hypothetical prote  
1451 62 4.5 137 2 B72679 vasotocin - Pacifi  
1452 62 4.5 161 2 A46189 general secretory  
1453 62 4.5 208 2 E82670 hibernation-relate  
1454 62 4.5 215 2 C48150 hypothetical prote  
1455 62 4.5 237 2 T16265 hypothetical prote  
1456 62 4.5 240 2 S30406 probable transposa  
1457 62 4.5 247 2 T35602 hypothetical prote  
1458 62 4.5 283 2 T19731 hypothetical prote  
1459 62 4.5 283 2 T29980 hypothetical prote  
1460 62 4.5 283 2 T29980 hypothetical prote  
1461 62 4.5 286 2 C87380 conserved hypothet  
1462 62 4.5 298 2 AH0289 probable aldo/keto  
1463 62 4.5 299 2 A96665 protein F2C12.24  
1464 62 4.5 299 2 S68198 probable transcrip  
1465 62 4.5 302 2 T21257 hypothetical prote  
1466 62 4.5 308 2 T19846 hypothetical prote  
1467 62 4.5 317 2 T19143 hypothetical prote  
1468 62 4.5 327 2 T34203 hypothetical prote  
1469 62 4.5 328 2 G64901 ABC-type transport  
1470 62 4.5 330 2 S08500 QUTG protein - Eme  
1471 62 4.5 336 2 F81849 probable CDP-6-deo  
1472 62 4.5 336 2 A35160 repressor protein  
1473 62 4.5 336 2 T20348 hypothetical prote  
1474 62 4.5 342 2 A46529 Ig gamma chain (5.  
1475 62 4.5 387 2 AC1813 IMP dehydrogenase  
1476 62 4.5 393 1 F9BEDZ glycoprotein D pre  
1477 62 4.5 399 2 F82657 beta-ketoacyl-[ACP  
1478 62 4.5 401 2 B64598 tetrahydroadipicoli  
1479 62 4.5 401 2 E82951 probable MFS trans  
1480 62 4.5 416 2 S48957 hypothetical prote  
1481 62 4.5 426 2 H84349 peroxidase / catal  
1482 62 4.5 446 2 D70597 probable signal-pe  
1483 62 4.5 456 2 C96684 F12P19.15 [impor  
1484 62 4.5 462 2 T42565 capsid protein 22  
1485 62 4.5 468 2 A69468 ammonium transport  
1486 62 4.5 483 2 A12868 phosphomannomutase  
1487 62 4.5 502 2 JE0295 Ll protein - human  
1488 62 4.5 506 2 C97645 phosphomannomutase  
1489 62 4.5 508 2 G84339 phosphoglycerate m

1490 62 4.5 552 2 C86171 hypothetical prote  
1491 62 4.5 566 2 S69889 hemagglutinin prec  
1492 62 4.5 567 2 AC0885 hydrogenase-2 larg  
1493 62 4.5 589 2 B38128 epichelin/granulin  
1494 62 4.5 591 2 B70523 hypothetical glyci  
1495 62 4.5 592 2 JN0877 protein kinase C (  
1496 62 4.5 606 2 T51880 hypothetical prote  
1497 62 4.5 628 2 AB0548 PrP<sup>Sc</sup> protein limpo  
1498 62 4.5 651 2 J27705 death receptor-6 -  
1499 62 4.5 670 2 S22293 zinc finger protei  
1500 62 4.5 693 2 E89822 translational elon

## ALIGNMENTS

## RESULT 1

I56559

neuropsin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I56559

R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishim

J. Neurosci. 15: 5088-5097, 1995

A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gen

A:Reference number: I56559; PMID:95348817; PMID:7623137

A:Accession: I56559

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-260 &lt;RES&gt;

A:Cross-references: UNIPROT:Q61955; GB:D30785; NID:gl648847; PID:BAA06451.1; PID:gl0200;

C:Superfamily: trypsin; trypsin homology

F:33-252/Domain: trypsin homology &lt;TRY&gt;

Query Match 45.3%; Score 622.5; DB 2; Length 260;

Best Local Similarity 49.0%; Pred. No. 3.2e-43;

Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTAA 61

Db 13 ILLLLFMGAWAGLTRAQSKILLEGRECIPIHSPQWQAALFQGERLTCGGVLVGDRLWLTAA 72

QY 62 HCSGRYWRVLRGEHSLDQDWTQEQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLRLPVRV 120

Db 73 HCKKQKYSVRLGDHSLQSRDQEQEIQVAQSIQHPCYNNSPEDSHDMLRLQNSANL 132

QY 121 TSSVQPLPLPNDCAATAGTECHVSGNGITNHPNPEDLLQCLNLSVSHATGHVYVPGI 180

Db 133 GDKVPVQLANLCPKVQKCIISGWGTVTSPQENFNTLNCAEVKIYSQNKCEAYPGKI 192

QY 181 TSNMYCAGVPQDACCQDSGGPLVCGGVLOGLVSWGSGVPCGQDGPVGVYVYICKYVDW 240

Db 193 TEGMVCASSNGADTCQDSGGPLVCDGMLQITSWGSDPCGKPEKPGVYTKICRYTTW 251

QY 241 IRMIMRN 247

Db 252 IKKTMND 258

## RESULT 2

S55066

trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken

N:Alternate names: trypsinogen II

C:Species: Gallus gallus (chicken)

C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: S55066; S72347

R:Wang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken trypsinogen gene family.

A:Reference number: S55065; PMID:95251611; PMID:7733885

A:Accession: S55066

A:Molecule type: mRNA

A:Residues: 1-248 &lt;WAN1&gt;

A;Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603904  
A;Experimental source: clone 2-P29  
A;Accession: S72347  
A;Molecule type: DNA  
A;Residues: 1-248 <WAN2>  
A;Cross-references: EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603907  
A;Experimental source: clone 2-P29  
A;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;17-25/Domain: activation peptide #status predicted <APT>  
F;26-248/Product: trypsin II #status predicted <MAT>  
F;26-241/Domain: trypsin homology <TRY>  
F;65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.4%; Score 569.5; DB 2; Length 248;  
Best Local Similarity 47.5%; Pred. No. 68-39;  
Matches 116; Conservative 39; Mismatches 78; Indels 11; Gaps 6;

QY 5 IFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIIDHRWLT 59  
Db LFLILSLCLGAFAVPGGADDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLSINQWVLUS 62  
QY 60 AAHCSSGRYVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVYLGASTSHEHDLRLRLPVR 119  
Db 63 AAHCYKSRIQVRLGEYNIDVQEDSEVRSVIRHPKY--SSITLNNDIMLIKASAVE 120  
QY 120 VTSSVQPLPNDCATAGTCHEVSGWGIITNHPNFPDILQCLNLSIVSHATCHGVY 179  
Db 121 YSADIQPIALPSSCAKAGTECLISGNGTSLNGYNYPELLQCLNAPILSDQCEAYPGD 180  
QY 180 ITSNNMVCAGVP-GQDACQSGGGLVCGVGLQGLVSGVSGVPCGQDGPVGVYTVICKV 238  
Db 181 ITSNNMVCGLFEGGKDCQSGGPGVPCVNGELQGLVSWG-IG-CALKGYPGVYTKVCNV 238  
QY 239 DWIR 242  
Db 239 DWIQ 242

RESULT 3  
S55067  
trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken  
N;Alternate names: trypsinogen I  
C;Species: Gallus gallus (chicken)  
C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text\_change 09-Jul-2004  
A;Accession: S55067; S72345; S55065; S72346; S71155  
Biochem. J. 307, 471-479, 1995  
A;Title: Isolation and characterization of the chicken trypsinogen gene family.  
A;Reference number: S55065; MUID:95251611; PMID:7733885  
A;Accession: S55067  
A;Molecule type: mRNA  
A;Residues: 1-248 <WAN1>  
A;Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:G603904  
A;Experimental source: clone 1-P38  
A;Accession: S72345  
A;Molecule type: DNA  
A;Residues: 1-248 <WAN2>  
A;Experimental source: clone 1-P38  
A;Accession: S55065  
A;Molecule type: mRNA  
A;Residues: 1-9, 'V', 11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 <WAN3>  
A;Cross-references: EMBL:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903  
A;Experimental source: clone P1  
A;Accession: S72346  
A;Molecule type: DNA  
A;Residues: 1-9, 'V', 11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 <WAN4>  
A;Cross-references: GB:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903  
A;Experimental source: clone P1  
R;Wang, K.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S71155

A;Accession: S71155  
A;Molecule type: mRNA  
A;Residues: 1-102, 'A', 104-248 <WAN5>  
A;Cross-references: EMBL:U15156; NID:G603904; PIDN:AAA79913.1; PID:G603905  
A;Experimental source: clone 1-P38  
A;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-25/Domain: activation peptide #status predicted <APT>  
F;26-248/Product: trypsin I #status predicted <MAT>  
F;26-241/Domain: trypsin homology <TRY>  
F;65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.3%; Score 567; DB 2; Length 248;  
Best Local Similarity 45.5%; Pred. No. 9, 68-39;  
Matches 115; Conservative 38; Mismatches 88; Indels 12; Gaps 6;

QY 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIIDHRW 56  
Db 1 MKFLVLVAFLGVAVAFPISEDDDDKIVGGYSCARSAAPVQVSLNSGYHF-CGGSLSISSQW 59  
QY 57 ULTAHCSSGRYVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVYLGASTSHEHDLRLRL 116  
Db 60 VLSSAAHCYKSRIQVRLGEYNLAADQSGEQTSSSKVIRHSGY--NSNTLNNDIMLIKUSK 117  
QY 117 PVRTSSVQPLPNDCATAGTCHEVSGWGIITNHPNFPDILQCLNLSIVSHATCHGVY 176  
Db 118 AATLSYNTVPLPFTSCVTAGTCLISGNGTSLSGSLYPPDVLOCLNAPVLSSQCSNAY 177  
QY 177 PGRITSNMVCAGVP-GQDACQSGGGLVCGVGLQGLVSGVSGVPCGQDGPVGVYTVICK 235  
Db 178 PGRITSNMICIYGLNGKDKSCQSGGPGVPCVNGQLQGFVSWG-IG-CAQKGYGVYTKVC 235  
QY 236 KYDWMIRMNN 248  
Db 236 NYVSWIKTTMSN 248

RESULT 4  
TRPGTR  
trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)  
N;Contains: trypsinogen  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text\_change 09-Jul-2004  
A;Accession: A90641; A90368; A00947  
R;Charles, M.; Rovey, M.; Guidoni, A.; Desmuelle, P.  
Biochim. Biophys. Acta 69, 115-129, 1963  
A;Title: Su le trypsinogene et la trypsine de porc.  
A;Reference number: A90641  
A;Accession: A90641  
A;Molecule type: protein  
A;Residues: 1-10 <CHA>  
A;Cross-references: UNIPROT:P00761  
R;Hermodson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.  
Biochemistry 12, 3146-3153, 1973  
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator analysis  
A;Reference number: A90368; MUID:73258692; PMID:4738933  
A;Accession: A90368  
A;Molecule type: protein  
A;Residues: 9-231 <HER>  
A;Note: at position 20, Ile and Val occur alternatively  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zymogen  
F;1-231/Product: trypsinogen #status experimental <ZYM>  
F;9-231/Product: activation peptide #status experimental <APT>  
F;9-224/Domain: trypsin #status experimental <MAR>  
F;9-224/Domain: trypsin homology <TRY>  
F;15-145, 33-49, 117-218, 124-191, 156-170, 181-205/Disulfide bonds: #status predicted  
F;48, 92, 185/Active site: His, Asp, Ser #status predicted  
F;60, 62, 65, 70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.8%; Score 561; DB 1; Length 231;  
Best Local Similarity 46.7%; Pred. No. 2, 78-38;

Matches	107	Conservative	39	Mismatches	77	Indels	6	Gaps	4
Qy	21	KIFNGTECGNSOPQWGLFEGTSLRCGGVLIDHRWVLTAAHCGSGSYRWRLGHSLSQL	80						
Db	8	KIVGGYTCAANSIPYQVSLNSGGHF-CCGSLINSQWVSAAHCKYSRIQVRLGSHNDIVL	66						
Qy	81	DWTEQIRHSGFSVTHPCYLCASSTSHRHDLRLRLRPVRTSSVQPLPLPNDCTATGEC	140						
Db	67	EGNEQFINAKIITHPNFNG--NFLDNDIMLIKLSSPATINSRVATVSLSPRCAAATGEC	124						
Qy	141	HVSGGKITNHRNPPFDLLQLCLNLSIVSHATGHGVPRGRTSNNMVCAGGVP-GQDACQGD	199						
Db	125	LISGWGNTKSSGSSYPQLLQCLAPVLSDSCKSSYPQGITGNMICVGFLEGGKDSQGD	184						
Qy	200	SGGPLVCGGLVGLVSGSVPCQDGI PGVYTWICKYVDWIRMENN	248						
Db	185	SGSPVVCNGQLGVISWGY--GCAQKNKPGYITKVCNVIWNIQOTIAAN	231						

RESULT 5  
A35871  
trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 09-Jul-2004  
C:Accession: A35871; S12117  
R:Shi, Y.B.; Brown, D.D.  
Genes Dev. 4, 1107-1113, 1990  
A:Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in *Xenopus laevis*  
A:Reference number: A35871; MUID:91007255; PMID:2210372  
A:Accession: A35871  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-243 <SHI>  
A:Cross-references: UNIPROT:P19799; EMBL:X53458; NID:g65162; PIDN:CAA37538.1; PID:g65163  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-20/Domain: activation peptide #status predicted <API>  
F:21-236/Domain: trypsin homology <TRY>  
F:26-243/Product: trypsin I #status predicted <MAT>  
F:27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted  
F:60,104,197/Active site: His, Asp, Ser #status predicted

Query Match	40.4%;	Score 555;	DB 2;	Length 243;
Best Local Similarity	45.7%;	Pred. No. 8.8e-38;		
Matches 113;	Conservative 42;	Mismatches 82;	Indels 10;	Gaps 6;
QY	6	FLLLCVLGLSQAAT---	PKIPNGTECGRNSQPMQVGLFEGTSRLCGVGLDHRWLTAAH	62
DB	3	FLLLCVL-LGAAAAFDDDKIIGGCATCAKSSVPYIVTSLNSGYHF-CGGSLLITNQWVSSAAH	60	
QY	63	CSGSRYVRLGEHLSQLDWTQEIQRHSGFSVTHPGYLGASTSHSDHLRLRLRLRPVTVS	122	
DB	61	CYKASTQVRLGEHNIALSEGTQFISSKVRHSGY--NSVTLDDIMLTKLSSPASINA	118	
QY	123	SVQPLPLPNDCAATGTECHVSGWGITNHPNRPFDLLQCLNLSIVSHATGCHVVPGRITS	182	
DB	119	AVNTVPLPSCSAACTSLISGHGNTLSGNTSPDILLQCLNAPILTNACNSAYPGEITA	178	
QY	183	NMVCAAGVP-GODACQGDSSGPLYCGGVLAGLVSWGSGVPGQDGFPGVYTYICKYVDWI	241	
DB	179	NMLCVGMEGGKDCQGDSSGPPVVCNQLQGVVSWGY--GCAMENYFGVYTKVCYNNAWI	236	
QY	242	RMIMRN	248	
DB	237	ONTIAAN	243	

RESULT 6  
A53968  
serine proteinase SCCE precursor - human  
N;Alternate names: stratum corneum chymotryptic enzyme  
C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: A53968  
R;Hansson, L.; Stroomqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.  
J; Biol. Chem. 269, 19420-19426, 1994  
A;Title: Cloning, expression, and characterization of stratum corneum chymo-  
A;Reference number: A53968; MUID:94308225; PMID:8034709  
A;Accession: A53968  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-253 <HAN>  
A;Cross-references: UNIPROT:P49862; GB:L33404; NID:G521214; PIDN:AAC37551.1  
C;Genetics:  
A;Gene: GDB:PRS86; SCCE  
A;Cross-references: GDB:377730  
A;Map position: 7q35-7q35  
C;Superfamily: trypsin homology  
F:30-245/Domain: trypsin homology <TRY>

Query Match	40.4%;	Score 555;	DB 2;	Length 253;
Best Local Similarity	44.6%;	Pred. No. 9.2e-38;		
Matches 115;	Conservative 37;	Mismatches 90;	Indels 16;	Gaps 6
Qy	1	MGLSIFLLLCVLGLS-----QAATPKIFNGTECGRNSOPVOGLPEGTSLRCGGVLI	52	
Db	1	MARSLLLPLQLLLSLALETAGEEAOGDKIDGAPCARGSHPWQALLSGNQLHCGGVLV	60	
Qy	53	DHRWLVTAAHCSSRYVRLGEHLSQLDWTQEIRHSGFSVTHPGYLGASTSHEHDLRL	112	
Db	61	NERWLVTAAHCXKMEYTVHLGSDTLG--DRRAQRIKAKSKSPRHGY--STQTHWNDMLV	116	
Qy	113	RLRLPVRTVTSVQPLPLPNCATAGTCSHVGWGITNHPNRPFPDLQLCLMSIVSHATC	172	
Db	117	KLSAQRLSSWKKVRLPSRCEPPIGTTCTVSGWGTITSPDVTFFSDLMCVDVKLISPDCC	176	
Qy	173	HGVYPGRITSNWCAGVPG--QDACGGDSGLPLVCGGVTLQGLVSWGSVPGCGDGIPIGV	230	
Db	177	TKVYKDLLENSMLCA-GIPDSKKACNGDSGGLVCRGTLQGLVSWGTF-PCGQPNDPGV	234	
Qy	231	YTYICKYVDWIRIMRNIN	248	
Db	235	YTVQCKFTKWINDTMKKH	252	

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RESULT 7
B25528
  trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse
A:Reference number: A93645; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>
A:Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIDN:CAA28243.1;
A:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-246/Product: trypsin #status predicted <MAT>
F:24-239/Domain: trypsin homology <TRY>
F:P30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
  Query Match 40.2%; Score 553; DB 2; Length 246;
  Best Local Similarity 44.7%; Pred. No. 1.3e-37;
  Matches 113; Conservative 45; Mismatches 81; Indels 14; Gaps

Qy 3 LSIFLLLCVLGSQA-----ATPKIFNGTEGRNSQPMQVGLFEQTSRCGGVLIDHRHWIL
Db 1 MSALITLALGAAPFVDDDDKTVGGYTCRESSVPYQVSLNAGYHF-CGGSLLINDQWVY

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Qy	59	TAHCSGSYWRVLRGHSLSQLDWTEQTRHSGFSVTHPGYLGASTSHEHDLRLRLP	118
Db	60	SAACHCYKRIQVRLGEHNIINVLGNEQFVDSAKIIRHPNY--NSWTILDNDIMIKLASPV	117
Qy	119	RVTSVVQPLPLNDCATAGTECHVSGWG--ITNHPRPFPDLLOCLNLSIVSHATCHGVY	176
Db	118	TLNARVASVPLPSSCAPAGTQCLISGWGNTLSNGVN--PDLQCVDPAPVLPOADCEASY	175
Qy	177	PGRITSNMYCAGVP--GODACGGDSGGPLVCGGVLOGLVSMGSPCGQDGIPGVYTYIC	235
Db	176	PGDITNNMICVGFLEGGKDSQCGDSGGPVVNCBGLQIVSWEY--GCAQPDAPGVYTKVC	233
Qy	236	KYVDWIRMTIMRNN	248
Db	234	NYVDWINTIADN	246

RESULT 8

TRBOTR

trypsin (EC 3.4.21.4) precursor - bovine

N;Contains: trypsinogen

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence revision 28-Feb-1986 #text\_change 18-Jul-1997

C;Accession: A90164; A09946; S08774

R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.

Biochem. Biophys. Res. Commun. 24, 346-352, 1966

A;Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.

A;Reference number: A90164; MUID:67168848; PMID:5967094

A;Accession: A90164

A;Molecule type: protein

A;Residues: 1-57, 'Q', 59-67, 'Q', 69-150, 'N', 152-176, 'N', 178-229 <MKT>

R;Hartley, B.S.

Philos. Trans. R. Soc. Lond. B257, 77-87, 1970

A;Reference number: A93755

A;Contents: annotation; revisions

R;Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 14, 1358-1366, 1975

A;Title: Amino acid sequence of dogfish trypsin.

A;Reference number: A00950; MUID:75146445; PMID:1092332

A;Contents: annotation; revisions

A;Note: the sequence agrees with that shown

R;Bode, W.; Schwager, P.

J. Mol. Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution

A;Reference number: A92954; MUID:76072097; PMID:512

A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal

s pseudotrypsin. A cleavage may also occur after Arg-105.

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F;1-229/Product: trypsinogen #status experimental <ZYM>

F;1-6/Domain: activation peptide #status experimental <APT>

F;7-222/Domain: trypsin homology <TRY>

F;7-131,132-229/Product: alpha-trypsin #status experimental <MPT>

F;6-7/Cleavage site: Lys-116 (enteropeptidase) #status experimental

F;13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental

F;46,90,183/Active site: His, Asp, Ser #status experimental

F;58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental

F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental

		Query Match	40.2%	Score 552;	DB 1;	Length 229;
		Best Local Similarity	46.3%;	Pred. No. 1.4e-37;		
		Matches 106;	Conservative 40;	Mismatches 77;	Indels 6;	Gaps 4
Qy	21	KIPNGTEGRNSQPQWGLFEGTSLRCCGVLDIHRVLTAAHCSGSSYWRVLGEHLSQL	80			
		:     :				
Db	6	KIVGGYTGCANTVPYQVSLNSCYHF-CGGSLLNSQWVVSAACRYKSGIQVRLGEDNINV	64			
		:     :				
Qy	81	DWTEQTRHGSPFTHPGYLGASTSHEHDILRLRLPLRVRTSSVQPIPLPNDCAATAGTC	140			
		:     :				
Db	65	EGNEOFISAKSVIHPSY--NSNTLNNDIMLIKLSAASLNSRVASISLPSTCASACTOC	122			
		:     :				

Qy	141	HVSGWGI TNHPNPPDLLQCLNLSIVSHATCHGVYGRITSTNNVCAGVGP-CODACQGD	199
Db	123	LISGWNKTSSTGYDPDLVKCLKAPILSSSSKSAIPGQITSTNMFCAGYLEGGKDSQGD	182
Qy	200	SGGPLVCGGVILQGLVSVGSVGPCQGDIPGVYTYICKYVDIMIRNN	248
Db	183	SGGPVCSGKLGQIVSWGS--GCAQKNKPGVYTKCVNVSVMIKQTASN	229

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RESULT 9
trypsin (EC 3.4.21.4) - bovine
SI3813
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: SI3813
R:le Huerou, I.; Wicker, C.; Guilleateau, P.; Toullec, R.; Puigserver, A.
Eur. J. Biochem. 193, 767-773, 1990
A:Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic
A:Reference number: SI3813; MUID:91065383; PMID:1701147
A:Accession: SI3813
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-247 <HUE>
A:Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PI
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:24-233/Domain: trypsin homology <TRY>
F:63,107,200/Active site: His, Asp, Ser
#status predicted

```

Query March	40.0%;	Score 550;	DB 2;	Length 247;
Best Local Similarity	45.7%;	Fred. No. 2.3e-37;		
Matches 113;	Conservative 40;	Mismatches 84;	Indels 10;	Gaps 5
Qy	7	LLLCVGLISQA----	ATPKIEFGTECGRNSQFQVQLFEFTSLRCGGVLIDHRWLVTAAH	62
Db	5	LILAFVGAAVAPSPDDDDKIVGGYTCAENSVYPQVSLNAGYHF--CGGSLINDQWVVVSAAH	63	
Qy	63	CSGSRYVRVLRGEHLSOLDWTETQIRHSGFSTHPGYLGASTSHEHLRLRLRLRPVRTS	122	
Db	64	CYQTHIQVRLGEYNIDVLEGGEOIFDASKIIRHPKY--SSWTLDNLDLILIKLSTPAVINA	121	
Qy	123	SVQPLPLPNDCATAGTECHVSGWGITNNPRNPFPDLLOCLNLNISVSHATCHGVYPGRIITS	182	
Db	122	RVSTLLLPASACASAGTECLIISGWNTLISSGVNYPDLLQCLNAPLLSHADCEASYPGQITN	181	
Qy	183	NMVCAGGVP--GDACCGSGGPLCVGGVQLGVLSWGSVGPCQGDIIPGYVTYTVICKVDVI	241	
Db	182	NMI CAGFLGGKDSQQGDSGFVACNGQIQIVSWGYY--GCAQKPKPYTTCVNCVDMI	239	
Qy	242	RMIMRN	248	
Db	240	QETIAA	246	

```

RESULT 10
TRDG
  trypsin (EC 3.4.21.4) precursor, anionic - dog
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26273
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: A26273
A:Molecule type: mRNA
A:Residues: 1-247 <PIN>
A:Cross-references: UNIPROT:P06872; GB:M11589; NTD:g164094; PIDN:AAA30899.1; P
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>

```



F:16-23/Domain: activation peptide #status predicted <APT>  
F:24-247/Product: trypsin, anionic #status predicted <ENZ>  
F:24-239/Domain: trypsin, anionic #status predicted <TRY>  
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted  
F:63,107,200/Active site: His, Asp, Ser #status predicted  
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.7%; Score 546; DB 1; Length 247;  
Best Local Similarity 45.6%; Pred. No. 4.8e-37;  
Matches 113; Conservative 38; Mismatches 85; Indels 12; Gaps 6;

QY 7 LLLCVGLSQATP-----KIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWLTAA 61  
DB 5 LILAFGL-AAVATPTDDDDKIIVGGYTCENSPYQVSLNAGYHF-CGGLSLISDQWVWSAA 62  
QY 62 HCGSGRYVRLGHEHSLQSDWTEQIRHSGFVTHPCYLGASTSHEHDLRLRLRPVRYT 121  
DB 63 HCYSRIQVRLGEYINIDVLENGEQFINSKAVIRHPNY--NSWILDNDIMLIKLSFAVLN 120  
QY 122 SSVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATCHGVYPRIT 181  
DB 121 ARVATISLPRAAAPGTQCLISGWGNTLSSGTNYPELLQCLDAPILTQAQCEASYPGQIT 180  
QY 182 SNWVCAGVP-QQDACQDSCGGLVCGVLOGLVSGSVGPGCGDIPGVYTYICKYVDW 240  
DB 181 ENMICAGFLEGKDCQDSCGSGPVVCGSLQGLVSWGY--GCAQKNKPGVYTKVCFVDM 238  
QY 241 IRMIRNN 248  
DB 239 IQSTTAA 246

RESULT 11  
TRDGC  
trypsin (EC 3.4.21.4) precursor, cationic - dog  
N:Alternate names: cationic trypsinogen  
C:Species: Canis lupus familiaris (dog)  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
C:Accession: B26273  
R:Pinsky, S.D.; LaForge, K.S.; Scheele, G.  
Mol. Cell. Biol. 5, 2669-2676, 1985  
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequence  
A:Reference number: A26273; MUID:86284628; PMID:3841794  
A:Accession: B26273  
A:Molecule type: mRNA  
A:Residues: 1-246 <PIN>  
A:Cross-references: UNIPROT:P06871; GB:M11590; NID:gl64096; PIDN:AAA30900.1; PID:gl64097  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: pancreas; protein digestion; serine proteinase; zymogen  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-23/Domain: activation peptide #status predicted <APT>  
F:24-246/Product: trypsin, cationic #status predicted <ENZ>  
F:24-239/Domain: trypsin homology <TRY>  
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted  
F:63,107,200/Active site: His, Asp, Ser #status predicted  
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.7%; Score 545; DB 1; Length 246;  
Best Local Similarity 44.2%; Pred. No. 5.8e-37;  
Matches 111; Conservative 43; Mismatches 87; Indels 10; Gaps 6;

QY 3 LSIFLLCVGLSQAA-----ATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWL 58  
DB 1 MKTFIFALLGATVAFIDDDDKIVGGYTCRNSVPYQVSLNAGYHF-CGGLSLINSQWV 59  
QY 59 TAAHCSGRYVRLGHEHSLQSDWTEQIRHSGFVTHPCYLGASTSHEHDLRLRLRPV 118  
DB 60 SAACHYKSRIOVRLGEYINIDVLENGEQFINSKAVIRHPY-NANTIDNDIMLIKLSPPA 117  
QY 119 RVTSVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATCHGVY 178  
DB 118 TLNSRVSAIALPKSCPAAGTQCLISGWGNTSIGONYPDVLQCLKAPILSDVCRNAYPG 177

F:16-23/Domain: activation peptide #status predicted <APT>  
F:24-247/Product: trypsin, anionic #status predicted <ENZ>  
F:24-239/Domain: trypsin, anionic #status predicted <TRY>  
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted  
F:63,107,200/Active site: His, Asp, Ser #status predicted  
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.6%; Score 544.5; DB 2; Length 247;  
Best Local Similarity 43.3%; Pred. No. 6.3e-37;  
Matches 109; Conservative 43; Mismatches 89; Indels 11; Gaps 5;

QY 3 LSIFLLCVGLSQAA-----TPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWV 57  
DB 1 MKALIFLAFGLAAVALPLDDDDDKIVGGYTCQKSLPYQVSLNAGYHF-CGGLSLINSQW 59  
QY 58 LTAACHCSGRYVRLGHEHSLQSDWTEQIRHSGFVTHPCYLGASTSHEHDLRLRLRP 117  
DB 60 VSAACHYKSRIOVRLGEYINIDVLENGEQFIDAAKIRHPY--NANTPNDIMLIKLSNP 117  
QY 118 RVTSVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATCHGVY 177  
DB 118 ATLNSRVSTVSLPRSCGSGGTCLVSGWNTLSSGTNYPELLQCLDAPVLSDDSCSKSY 177  
QY 178 GRITSNWVCAGVP-QQDACQDSCGGLVCGVLOGLVSGSVGPGCGDIPGVYTYICK 236  
DB 178 GKITSNMFLCLFLEGKDCQDSCGSGPVVCGVLOGLVSWGY--GCAQKGRPGVYTKVCN 235  
QY 237 YVDWIRMIIRNN 248  
DB 236 YVNWIQQTVAAN 247

RESULT 13  
TRRT1  
trypsin (EC 3.4.21.4) I precursor - rat  
N:Alternate names: trypsinogen I  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004  
C:Accession: B22657; A00948  
R:Craik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.  
J. Biol. Chem. 259, 14255-14264, 1984  
A:Title: Structure of two related rat pancreatic trypsin genes.  
A:Reference number: A22657; MUID:85054880; PMID:6094547  
A:Accession: B22657  
A:Molecule type: DNA  
A:Residues: 1-246 <CRA>  
A:Cross-references: UNIPROT:P00762; GB:J00778; NID:9206507; PIDN:AAA98518.1; PID:g206508  
A>Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17  
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.  
J. Biol. Chem. 257, 9724-9732, 1982

A>Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of  
A:Reference number: A00948; MUID:82265624; PMID:6896710  
A:Accession: A00948  
A:Molecule type: mRNA  
A:Residues: 1-246 <MAC>  
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
C:Genetics:  
A:Introns: 14/1; 67/2; 152/1; 197/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-23/Domain: activation peptide #status predicted <APT>  
F:24-246/Product: trypsin I #status predicted <ENZ>  
F:24-239/Domain: trypsin homology <TRY>  
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted  
F:63,107,200/Active site: His, Asp, Ser #status predicted  
F:75,77,80,95/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.5%; Score 543; DB 1; Length 246;  
Best Local Similarity 44.5%; Pred. No. 8.4e-37;  
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;

QY 3 LSIFILLCVLGSQA----ATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWL 58  
DB 1 MSALLILALVGAFAFLEDDDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGLINDQWV 59  
QY 59 TAAHCSGRYVRLGHELSQLDWTETQIRHSGFVTHPGYLGASTSHEHDLRLRLRPV 118  
DB 60 SAACHYKSRQVRLGHEHNVLEGEQFINAKIKHPNY--SSWTLNNDIMLKLSGPV 117  
QY 119 RVTSSVQPLPNDCATAGTECHVSGWG--ITNPRNPPDLLQCLNLSIVSHATCHGVY 176  
DB 118 KLNARVAPVALPSACAPAGTQCLISGWNLSGNN--PDLQCVDPAPVLSQADCEAAY 175  
QY 177 PGRITSNMVACGVP-GQDACGDSGGLVCGVQLGVLVSGVSGPCGQDGPVYTYIC 235  
DB 176 PGEITSSMICVFLGEGKDCQDGGPVVCGQLQGVWSGY--GCALPDNPGVYTKVC 233  
QY 236 KYVDWIR 242  
DB 234 NFVGHQ 240

RESULT 14  
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S66657; S31779  
R:Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.  
A>Title: Molecular cloning and characterization of anionic and cationic variants of tryp  
A:Reference number: S66657; MUID:96035908; PMID:7556223  
A:Accession: S66657  
A:Molecule type: mRNA  
A:Residues: 1-238 <MAL>  
A:Cross-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>  
F:8-15/Domain: activation peptide #status predicted <APT>  
F:16-238/Product: trypsin III #status predicted <MAT>  
F:16-231/Domain: trypsin homology <TRY>  
F:22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted  
F:55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.3%; Score 540; DB 2; Length 238;  
Best Local Similarity 47.2%; Pred. No. 1.4e-36;  
Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 21 KIFNGTECGRNSQPVQVGLFEGTSLRCGGVLIDHRWLTAHCSGRYVRLGHELSQL 80  
DB 15 KIVGVECKNSASYQASLQSYHF-CGGLISSTWVWSAAHCYKSRQVRLGHEHNV 73

QY 81 DWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVVTSSVQPLPLPNDCATAGTEC 140  
DB 74 EGTEQFIDSVKVIHPSY--NSRNLNDNDIMLKSPASLNSYSTVALPSSCASSGTRC 131  
QY 141 HVSCHGINTNPRNPPDLLQCLNLSIVSHATCHGVYPCGRTITSNMVCAGVP-GQDACG 199  
DB 132 LVSGWNLSSSSNYPDTLRCLDLPILSSSCNSNAYPGQITSNMFCACGFMGGKDCQGD 191  
QY 200 SGGPLVCGGVQLGVLVSGVSGPCGQDGPVYTYICKYVDWIRIMRN 248  
DB 192 SGGPVVCGQLQGVWSGY--GCAQRNKPQVYTKVCTRSMISSTMSN 238

## RESULT 15

S05494  
trypsin (EC 3.4.21.4) IV precursor - rat  
N:Alternate names: 23K protein; trypsinogen IV precursor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: S05494  
R:Luetteke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.  
A:Nucleic Acids Res. 17, 6736, 1989  
A>Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.  
A:Reference number: S05494; MUID:89386010; PMID:2780302  
A:Accession: S05494  
A:Molecule type: mRNA  
A:Residues: 1-247 <LUB>  
A:Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-23/Domain: activation peptide #status predicted <APT>  
F:24-247/Product: trypsin IV #status predicted <MAT>  
F:24-240/Domain: trypsin homology <TRY>  
F:30-161,49-65,133-233,140-207,172-186/Disulfide bonds: #status predicted  
F:64,108,201/Active site: His, Asp, Ser #status predicted  
F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 38.8%; Score 533.5; DB 2; Length 247;  
Best Local Similarity 43.4%; Pred. No. 4.9e-36;  
Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;

QY 1 MGLSIF--LLLCVLGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWL 58  
DB 1 MKISIFFAPLGAVALPVNDDDKIVGGYTCPKHLPYQVSLHDGISHQCGSLISDQWVL 60  
QY 59 TAAHCSGRYVRLGHELSQLDWTETQIRHSGFVTHPGYLGASTSHEHDLRLRLPV 118  
DB 61 SAACHYKSRQVRLGHEHNVLEGEQFIDAEKIRHPEY--NKDTLNDNDIMLKSGPA 118  
QY 119 RVTSSVQPLPNDCATAGTECHVSGWGTNHPNPPDLLQCLNLSIVSHATCHGVYPG 178  
DB 119 VNSQVSVSLPRSCASTDAQCLVSGWNTVSGIKYFALLQCLEAPVLSSCKSKSYPG 178  
QY 179 RITSNMVACGVP-GQDACGDSGGLVCGVQLGVLVSGVSGPCGQDGPVYTYICKY 237  
DB 179 QITSNMFCGLFLEGKDCDGDGGPVVCGBIQGVWSGV--CAMRKPQVYTKVCNY 236  
QY 238 VDWIRIMRN 248  
DB 237 LSWIOETMANN 247

Search completed: March 5, 2005, 20:46:44  
Job time : 56 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 5, 2005, 20:42:30 ; Search time 174 Seconds

(without alignments)  
729.860 Million cell updates/sec

Title: US-10-015-385A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVYTYCKYVDWIRMERN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1374	100.0	248	1	KLK8	HUMAN	Q9ukr0 homo sapien
2	952.5	69.3	234	2	Q9CV76		Q9cv76 mus musculus
3	630.5	45.9	260	1	KLK8	HUMAN	Q60259 homo sapien
4	627.5	45.7	260	2	Q81W69		Q81w69 homo sapien
5	622.5	45.3	260	1	NRPN	MOUSE	Q61955 mus musculus
6	621.5	45.2	260	1	NRPN	RAT	Q88780 rattus norv
7	618.5	45.0	250	1	KLK8	HUMAN	Q9ubx7 homo sapien
8	611	44.5	255	2	Q7JIG6		Q7jig6 saguinus oe
9	610	44.4	250	2	Q63ZF2		Q63zf2 rattus norv
10	608	44.3	254	2	Q8CGR4		Q8cgr4 mus musculus
11	601	43.7	275	2	Q81XD7		Q81xd7 homo sapien
12	599	43.6	255	2	Q6IS10		Q6isi0 homo sapien
13	599	43.6	256	1	KLK8	HUMAN	Q9h2r5 homo sapien
14	597.5	43.5	249	2	Q9QYN4		Q9qyn4 mus musculus
15	597.5	43.5	276	2	Q9QYN3		Q9qyn3 m hippostas
16	595	43.3	255	2	Q96RQ0		Q96rq0 homo sapien
17	588.5	42.8	293	2	Q9D140		Q9d140 mus musculus
18	588	42.8	276	2	Q8CGR6		Q8cgr6 mus musculus
19	586	42.6	250	2	Q8CGR5		Q8cgr5 mus musculus
20	578	42.1	242	2	Q8OV54		Q8ovs4 mus musculus
21	576	41.9	246	2	Q6P3Z0		Q6p3z0 mus musculus
22	569.5	41.4	248	1	TRY3	CHICK	Q90629 gallus gall
23	569.5	41.4	251	1	KLK8	HUMAN	Q9p0g3 homo sapien
24	569.5	41.4	251	2	Q6B089		Q6b089 homo sapien
25	568.5	41.4	250	1	KLK9	HUMAN	Q9ukq9 homo sapien
26	567	41.3	277	1	KLK9	HUMAN	Q9ukr3 homo sapien
27	566	41.2	248	1	TRY2	CHICK	Q90628 gallus gall
28	565	41.1	248	1	TRY1	CHICK	Q90627 gallus gall
29	564.5	41.1	293	1	KLK5	HUMAN	Q9Y337 homo sapien
30	564	41.0	276	1	KLKA	HUMAN	Q43240 homo sapien
31	563	41.0	244	1	TRY2	XENLA	P70059 xenopus lae

32	563	41.0	248	2	Q7SZT1		Q7sztl xenopus lae
33	562	40.9	255	2	Q6GNU2		Q6gnu2 xenopus lae
34	561	40.8	231	1	TRY1_PIG		P00761 sus scrofa
35	561	40.8	243	1	TRY1_BOVIN		P00760 bos taurus
36	561	40.8	244	1	KLK6_HUMAN		Q92876 homo sapien
37	557	40.5	237	2	Q6GYJ5		Q6gyj5 struthio ca
38	555	40.4	243	1	TRY1_XENLA		P19799 xenopus lae
39	555	40.4	243	2	Q7SZ06		Q7sz06 xenopus lae
40	555	40.4	253	1	KLK7_HUMAN		P49862 homo sapien
41	553.5	40.3	246	2	Q88301		Q88301 mus musculus
42	553.5	40.3	253	2	Q91Y82		Q91y82 mus musculus
43	553	40.2	246	1	TRY2_MOUSE		P07146 mus musculus
44	550.5	40.1	247	2	Q9D7V7		Q9d7v7 mus musculus
45	550	40.0	247	1	TRY2_BOVIN		Q29463 bos taurus
46	549.5	40.0	247	2	Q9CPN9		Q9cpn9 m mus muscu
47	548	39.9	246	2	Q6IE66		Q6ie66 rattus norv
48	546.5	39.8	251	2	Q54854		Q54854 rattus norv
49	546	39.7	247	1	TRY2_CANFA		P06872 canis fami
50	545	39.7	246	1	TRY1_CANFA		P06871 canis fami
51	544.5	39.6	247	1	TRY3_RAT		P08426 rattus norv
52	544	39.6	253	2	Q8N5N9		Q8n5n9 homo sapien
53	543	39.5	246	1	TRY1_RAT		P00762 rattus norv
54	543	39.5	246	2	Q792Z1		Q792z1 mus musculus
55	541.5	39.4	247	2	Q9CPN7		Q9cpn7 mus musculus
56	540	39.3	238	1	TRY3_SALSA		P35033 salmo salar
57	540	39.3	246	2	Q792Y8		Q792y8 mus musculus
58	538.5	39.2	249	2	Q91VE3		Q91ve3 m thymopsin
59	536	39.0	246	2	Q7TT42		Q7tt42 mus musculus
60	536	39.0	246	2	Q9ROT7		Q9rot7 m pancreati
61	535.5	39.0	245	2	Q6R670		Q6r670 oreochromis
62	535.5	39.0	261	2	Q6H320		Q6h320 bos taurus
63	534.5	38.9	245	2	Q6R671		Q6r671 oreochromis
64	533.5	38.8	245	2	Q792Y9		Q792y9 mus musculus
65	533.5	38.8	247	1	TRY4_RAT		P12788 rattus norv
66	533	38.8	246	1	TRY2_RAT		P00763 rattus norv
67	533	38.8	246	2	Q9Z1R9		Q9z1r9 mus musculus
68	532	38.7	246	2	Q9OUK9		Q9ouk9 mus musculus
69	528	38.4	246	2	Q792Z0		Q792z0 mus musculus
70	528	38.4	263	2	Q6H319		Q6h319 sus scrofa
71	527.5	38.4	261	1	KLK7_RAT		P36373 rattus norv
72	525	38.2	240	2	Q98TH0		Q98th0 engraulis j
73	523.5	38.1	246	2	Q7M754		Q7m754 mus musculus
74	522	38.0	244	2	Q6QGW3		Q6qgw3 anguilla ja
75	521.5	38.0	246	1	KLK_PIG		P00752 sus scrofa
76	521.5	38.0	261	1	KLK6_MOUSE		P15947 mus musculus
77	520.5	37.9	258	2	Q63ZF4		Q63zf4 rattus norv
78	519	37.8	246	1	TRYA_RAT		P32821 rattus norv
79	518	37.7	246	1	TRYB_RAT		P32822 rattus norv
80	518	37.7	261	1	KLK8_RAT		P36374 rattus norv
81	514.5	37.4	242	2	Q7TIR8		Q7tir8 pangasius h
82	514	37.4	239	2	Q63275		Q63275 rattus norv
83	513.5	37.4	231	1	TRY2_SALSA		P35032 salmo salar
84	513.5	37.4	239	1	KLK2_CAVPO		P12323 cavia porce
85	513.5	37.4	243	2	Q8AV83		Q8av83 brachydanio
86	513.5	37.4	261	2	Q9NIQ1		Q9nli1 saguinus oe
87	513.5	37.4	278	2	Q99M20		Q99m20 mus musculus
88	512	37.3	279	2	Q6IE55		Q6ie55 rattus norv
89	511.5	37.2	261	2	Q29474		Q29474 canis fami
90	510.5	37.2	238	2	Q9W706		Q9w7q6 paralichthy
91	510.5	37.2	261	1	KLK3_MOUSE		P00756 mus musculus
92	509.5	37.1	222	2	Q8AV11		Q8av11 oncorhynch
93	509.5	37.1	235	2	Q63274		Q63274 rattus norv
94	508	37.0	242	1	TRY1_SALSA		P35031 salmo salar
95	508	37.0	242	2	Q9W7Q7		Q9w7q7 paralichthy
96	507	36.9	244	2	Q42159		Q42159 petromyzon
97	507	36.9	259	2	Q63ZP5		Q63zfp5 rattus norv
98	506	36.8	245	2	Q42160		Q42160 petromyzon
99	505	36.8	242	2	Q7SX90		Q7sx90 brachydanio
100	505	36.8	249	2	Q92046		Q92046 disostichu
101	505	36.8	260	1	ESTA_CANFA		P09582 canis fami
102	505	36.8	282	2	Q76B45		Q76b45 blarina bre
103	504.5	36.7	269	2	Q8IU55		Q8iu55 homo sapien
104	503	36.6	241	2	Q98TG9		Q98tg9 engraulis j

105	503	36.6	263	1	KLKR_PRANA	P32824	pracmys nat	178	458.5	33.4	261	1	KLK2_HUMAN	P20151	homo sapien
106	502	36.5	249	2	Q9W6K0	Q9W6K0	notothenia	179	452	32.9	260	2	Q71QJ4	Q71QJ4	trimeresuru
107	501	36.5	259	1	KLKC_RAT	P63376	rattus norv	180	451	32.8	260	2	Q7T229	Q7T229	bothrops ja
108	501.5	36.5	237	2	Q915I5	Q91515	fugu rubrip	181	450	32.8	260	2	Q8UVX1	Q8UVX1	agkistrodon
109	501	36.5	242	2	Q93266	Q93266	pseudopleur	182	449	32.7	258	1	VSP1_TRIST	Q91516	trimeresuru
110	501	36.5	247	1	TR12_HUMAN	P07478	homo sapien	183	448	32.6	258	2	Q8AY78	Q8AY78	trimeresuru
111	501	36.5	247	2	Q9W7Q5	Q9W7Q5	paralichthy	184	446.5	32.5	257	2	Q71QI5	Q71QI5	trimeresuru
112	499.5	36.4	241	1	TRXK_GADMO	Q91041	gadus morhu	185	445.5	32.4	257	1	VSP3_TRIMU	Q91509	trimeresuru
113	499	36.3	239	2	Q8N1C9	Q8N1C9	homo sapien	186	444.5	32.4	249	2	Q8JFQ7	Q8JFQ7	gadus morhu
114	498	36.2	249	2	Q788V0	Q788V0	disostichu	187	443	32.2	258	1	VSP2_AKAC	Q818X1	agkistrodon
115	498	36.2	254	1	KLK4_HUMAN	Q9Y5K2	homo sapien	188	443	32.2	258	1	VSP3_BOTJA	Q9Btu8	bothrops ja
116	497	36.2	257	2	Q61E61	Q61E61	rattus norv	189	439.5	32.0	257	2	VSP7_TRIMU	Q90G84	trimeresuru
117	497	36.2	258	1	KLK1_PAPHA	Q28773	papio hamad	190	439	32.0	279	2	VSPGJ8	Q9YgJ8	agkistrodon
118	497	36.2	261	2	Q725F4	P725F4	homo sapien	191	438	31.9	259	1	VSP1_VIPLE	Q9Pt41	vipera lebe
119	496.5	36.1	261	1	KLX5_MOUSE	P15945	mus musculus	192	437.5	31.8	257	1	VSP2_TRIMU	Q91508	trimeresuru
120	496	36.1	242	2	Q92059	Q92059	paranotothe	193	437.5	31.8	257	1	VSP4_TRIMU	Q91510	trimeresuru
121	496	36.1	247	2	Q42158	Q42158	petromyzon	194	436.5	31.8	233	2	Q9PT51	Q9PT51	agkistrodon
122	496	36.1	247	2	Q42608	Q42608	petromyzon	195	436.5	31.8	250	2	Q93955	Q93955	pracmys nat
123	496	36.1	262	2	Q86U61	Q86U61	homo sapien	196	436.5	31.8	257	1	VSP1_TRIMU	Q91507	trimeresuru
124	495.5	36.1	257	1	KLK1_MACFA	Q07276	macaca fasc	197	436.5	31.8	257	1	VSP5_TRIMU	Q91511	trimeresuru
125	495.5	36.1	261	1	KLXB_MOUSE	P15946	mus musculus	198	435.5	31.7	257	2	Q71QI7	Q71QI7	trimeresuru
126	495	36.0	261	2	Q725F3	P725F3	homo sapien	199	435	31.7	257	2	VSP2_TRIBE	Q9df67	trimeresuru
127	495	36.0	261	2	Q6H322	Q6H322	equus cabal	200	434	31.6	258	1	VSP3_TRIBE	Q9df66	trimeresuru
128	494.5	36.0	247	1	TRV1_HUMAN	P07477	homo sapien	201	434	31.6	260	1	VSPB_TRIGA	Q13061	trimeresuru
129	493.5	35.9	248	2	Q66L05	Q66L05	xenopus lae	202	434	31.6	260	2	Q71QI9	Q71QI9	trimeresuru
130	493	35.9	262	1	KLK1_HUMAN	P06870	homo sapien	203	433.5	31.6	257	2	Q71QJ0	Q71QJ0	trimeresuru
131	492	35.8	262	2	Q66U59	Q66U59	homo sapien	204	433	31.5	260	1	VSP1_AKHP	Q9YgJ2	agkistrodon
132	491.5	35.8	241	1	TRV1_GADMO	P16049	gadus morhu	205	432	31.4	236	1	VSPA_DABRU	P18964	daboia rusa
133	491	35.7	256	1	KLK4_MOUSE	P00757	mus musculus	206	432	31.4	257	2	Q9PTL3	Q9PTL3	agkistrodon
134	490.5	35.7	229	1	TRYP_SOUAC	P00764	squalus aca	207	432	31.4	260	1	VSP2_AKHP	Q9YgI6	agkistrodon
135	490.5	35.7	261	1	KLKD_MOUSE	P36368	mus musculus	208	432	31.4	260	2	Q73800	Q73800	agkistrodon
136	489.5	35.6	261	1	KLKL_MOUSE	P61759	mus musculus	209	431.5	31.4	205	2	Q96JEO	Q96JEO	homo sapien
137	489	35.6	244	1	KLKA_RAT	P63375	rattus norv	210	431.5	31.4	257	2	Q71QJ1	Q71QJ1	equus cabal
138	488	35.5	247	2	Q8NHM4	Q8NHM4	homo sapien	211	431.5	31.4	261	1	KLK2_HORSE	Q6h321	equus cabal
139	487.5	35.5	251	2	Q9DBQ8	Q9dbq8	mus musculus	212	431.5	31.4	261	1	KLKG_MOUSE	P04071	mus musculus
140	486	35.4	242	2	Q6R179	Q6r179	tautogolabr	213	431	31.4	260	1	VSPA_TRIGA	P01060	trimeresuru
141	485.5	35.3	234	2	Q9R048	Q9r048	mus musculus	214	431	31.4	260	2	Q8AY81	Q8AY81	trimeresuru
142	485.5	35.3	261	2	Q88309	Q88309	mus musculus	215	431	31.4	262	1	VSP1_AKCA	Q91053	agkistrodon
143	484.5	35.3	251	2	Q8N2U3	Q8N2U3	homo sapien	216	429.5	31.3	205	2	Q96JE2	Q96JE2	homo sapien
144	484.5	35.3	259	1	KLKM_MOUSE	P15948	mus musculus	217	429	31.2	176	2	Q8K5D7	Q8K5D7	mus musculus
145	484.5	35.3	304	1	TRV3_HUMAN	P35030	homo sapien	218	429	31.2	258	1	VSP3_TRIGA	Q13063	trimeresuru
146	484	35.2	255	2	Q9Z0M1	Q9Z0M1	mus musculus	219	429	31.2	260	2	Q71QI0	Q71QI0	trimeresuru
147	483.5	35.2	261	1	KLK1_RAT	P00758	rattus norv	220	428.5	31.2	262	2	Q9QHK3	Q9QHK3	crataleus ac
148	483.5	35.2	265	2	Q68G17	Q68G17	rattus norv	221	427	31.1	260	2	Q93502	Q93502	agkistrodon
149	482	35.1	255	2	Q9JIS2	Q9JIS2	mus musculus	222	426.5	31.0	257	1	VSPC_TRIGA	Q13062	trimeresuru
150	481.5	35.0	261	1	KLX9_MOUSE	P15949	mus musculus	223	425	30.9	260	1	VSP1_AKAC	Q918X2	agkistrodon
151	481	35.0	254	2	Q9XSN6	Q9Xsn6	sus scrofa	224	424.5	30.9	257	2	Q71QJ3	Q71QJ3	trimeresuru
152	480.5	35.0	263	1	KLXR_MOUSE	Q9Jm71	mus musculus	225	423	30.8	204	2	Q96JEL	Q96JEL	homo sapien
153	479	34.9	261	1	KLK3_MACMU	P33619	macaca mula	226	423	30.8	238	1	VSP1_AKHA	P81176	agkistrodon
154	479	34.9	261	2	Q6DT45	Q6dt45	macaca fasc	227	422.5	30.7	234	2	Q9YGS1	Q9YGS1	agkistrodon
155	478.5	34.8	248	2	Q6GPX7	Q6gpX7	xenopus lae	228	422.5	30.7	259	2	Q8UUK2	Q8UUK2	crataleus ad
156	478.5	34.8	250	2	Q93265	Q93265	pseudopleur	229	422	30.7	256	2	Q7SYF1	Q7SYF1	cerastes ce
157	477.5	34.8	256	2	Q61E12	Q61e12	rattus norv	230	421.5	30.7	163	2	Q66H01	Q66H01	xenopus lae
158	477.5	34.8	261	1	KLK1_MOUSE	P00755	mus musculus	231	420.5	30.6	257	2	Q71QI8	Q71QI8	trimeresuru
159	477.5	34.8	263	1	KLKO_MOUSE	Q61754	mus musculus	232	419.5	30.5	234	2	Q8UUU1	Q8UUU1	agkistrodon
160	477	34.7	247	2	Q66PG9	Q66PG9	fugu rubrip	233	419	30.5	258	2	Q8QHK2	Q8QHK2	crataleus at
161	476.5	34.7	344	2	Q9W6J9	Q9W6J9	disostichu	234	418.5	30.5	257	2	Q71QI6	Q71QI6	trimeresuru
162	476.5	34.7	675	2	Q9W6J8	Q9W6J8	disostichu	235	418	30.4	260	2	Q8AY82	Q8AY82	trimeresuru
163	475.5	34.6	219	2	Q91036	Q91036	gadus morhu	236	417	30.3	236	1	VSPG_DABRU	P18965	daboia rusa
164	472.5	34.4	235	2	Q6FPG8	Q6Fpg8	fugu rubrip	237	415.5	30.2	178	2	Q93594	Q93594	dicentrarch
165	471	34.3	249	2	Q6DIW2	Q6diw2	xenopus tro	238	415.5	30.2	257	2	Q71QH8	Q71QH8	trimeresuru
166	470.5	34.2	257	2	Q6LDS3	Q6lds3	homo sapien	239	414	30.1	237	2	Q8UUU2	Q8UUU2	agkistrodon
167	470.5	34.2	261	1	KLK3_HUMAN	P07288	homo sapien	240	413	30.1	258	1	VSP1_TRIGA	Q13059	trimeresuru
168	470	34.2	258	2	Q71QI1	Q71q11	trimeresuru	241	413	30.1	258	2	Q7SZE1	Q7sze1	gloydius sa
169	469.5	34.2	261	1	KLX8_MOUSE	P07628	mus musculus	242	413	30.1	260	1	VSP1_TRIFL	P05620	trimeresuru
170	469.5	34.2	261	2	Q8C232	Q8c232	mus musculus	243	411.5	29.9	228	1	VSPA_LACMU	P33589	lachesis mu
171	468	34.1	259	1	KLK2_RAT	P00759	rattus norv	244	411	29.9	239	2	Q6T5L0	Q6T5L0	gloydius sh
172	467.5	34.0	261	1	KLKQ_MOUSE	P36369	mus musculus	245	411	29.9	258	2	Q71QH7	Q71QH7	trimeresuru
173	467	34.0	258	2	Q71QH6	P71qh6	trimeresuru	246	411	29.9	260	2	Q7SZC3	Q7szc3	gallus gall
174	462.5	33.7	261	2	Q8K0C6	Q8K0C6	mus musculus	247	409	29.8	260	1	VSP2_VIPLE	Q9Pt40	vipera lebe
175	461.5	33.6	259	1	KLX9_RAT	P07647	rattus norv	248	408.5	29.7	257	2	Q8JH62	Q8Jh62	vipera lebe
176	461	33.6	258	2	Q8AY80	P08480	trimeresuru	249	408	29.7	235	1	VSP2_AKBI	Q9pan3	agkistrodon
177	458.5	33.4	250	1	TRYP_PLEPL	P35034	pleuronecte	250	407	29.6	237	2	Q93421	Q93421	agkistrodon

251	407	29.6	258	1	VSP2 AGKCA	042207 agkistrodon	324	361.5	26.3	267	2	Q7SZ51	Q7sz51 brachydania
252	407	29.6	258	2	Q8AY79	Q8ay79 trimeresuru	325	361	26.3	255	2	Q6WGR1	Q6wgr1 ictalurus p
253	407	29.6	260	1	VSP2 TRIFL	Q13057 trimeresuru	326	361	26.3	267	2	Q640E1	Q640e1 xenopus lae
254	406.5	29.6	231	1	VSP1 AGKCO	P09872 agkistrodon	327	359.5	26.2	259	2	Q6AZC2	Q6azc2 brachydania
255	406.5	29.6	257	2	Q71QH5	P09872 trimeresuru	328	359.5	26.2	269	2	Q6ISU5	Q6iaus5 homo sapien
256	405.5	29.5	257	2	Q71QI3	Q71q13 trimeresuru	329	359.5	26.2	277	1	TRY2 ANOGA	P35036 anopheles g
257	405	29.5	234	2	Q7SZE2	Q7sze2 agkistrodon	330	359.5	26.2	342	1	PS88 MOUSE	Q9esd1 mus musculus
258	403.5	29.4	233	2	Q6IWF1	Q6iwf1 bothrops al	331	359	26.1	265	2	Q6P326	Q6p326 xenopus tro
259	402.5	29.3	232	1	VSP1 BOTJA	P81824 bothrops ja	332	359	26.1	311	2	Q8OXZ3	Q804x0 rattus norv
260	402.5	29.3	257	2	Q9YGVJ9	Q9ygvj9 agkistrodon	333	359	26.1	430	2	Q804X0	Q804x0 fagu rubrip
261	402	29.3	255	1	VSPA BOTAT	P04371 bothrops at	334	358.5	26.1	245	1	MCT1 SHEEP	P80931 ovis aries
262	402	29.3	260	1	VSP1 TRIJE	Q9df68 trimeresuru	335	358.5	26.1	444	1	FA7_RABIT	P80931 ovis aries
263	402	29.3	260	1	VSP6 TRIMU	Q9df68 trimeresuru	336	358	26.1	812	1	PLMN_BOVIN	P06868 bos taurus
264	400	29.1	234	1	VSP2 AGKCO	P82981 agkistrodon	337	357.5	26.0	232	2	Q9XY45	Q9xy45 ctenoscephal
265	400	29.1	258	2	Q802F0	Q802f0 agkistrodon	338	357.5	26.0	371	2	Q8MS52	Q8ms52 drosophila
266	399.5	29.1	257	2	Q8QG86	Q8qg86 bothrops in	339	357.5	26.0	643	2	O97506	Q97506 sus scrofa
267	399	29.0	260	2	Q71QJ2	Q71qj2 trimeresuru	340	357	26.0	262	1	GRAA HUMAN	P12544 homo sapien
268	397	28.9	235	2	Q90Z47	Q90z47 agkistrodon	341	357	26.0	263	1	CTRB_HUMAN	P17538 homo sapien
269	397	28.9	260	2	Q71QI4	Q71q14 trimeresuru	342	357	26.0	271	1	CTRI_PENVA	Q00871 penaeus van
270	395.5	28.8	264	2	Q9ER05	Q9er05 mus musculus	343	357	26.0	806	1	PLMN_MACEU	O18783 macropus eu
271	395	28.7	260	2	Q71QH9	Q71qh9 trimeresuru	344	357	26.0	1019	1	LFC TACTR	P28175 tachypleus
272	394.5	28.7	257	1	VSP2 BOTJA	O13069 bothrops ja	345	357	26.0	1019	2	Q8T9S1	Q8t9s1 tachypleus
273	393.5	28.6	264	2	Q9D7P8	Q9d7p8 mus musculus	346	356.5	25.9	261	2	Q9W7Q4	Q9w7q4 paralichthy
274	393	28.6	260	1	VSPA AGKAC	Q9i8w9 agkistrodon	347	356.5	25.9	321	1	TRYG_HUMAN	Q9nr12 homo sapien
275	392	28.5	258	2	Q71QI2	Q71q12 trimeresuru	348	356.5	25.9	321	2	Q9GRZ8	Q9grz8 homo sapien
276	391.5	28.5	264	2	Q9BQZ8	Q9eqz8 rattus norv	349	355.5	25.9	260	2	Q9V7G4	P21845 mus musculus
277	391	28.5	253	2	Q8WZB4	Q8wzb4 homo sapien	350	355.5	25.9	276	1	MCT6 MOUSE	Q9v7g4 drosophila
278	389	28.3	258	1	CFAD HUMAN	P00746 homo sapien	351	355	25.8	342	1	PS88 RAT	Q9es87 rattus norv
279	389	28.3	253	2	Q8JH85	Q8jh85 vipera lebe	352	354.5	25.8	249	2	Q6QX59	Q6qx59 lepeophthei
280	388.5	28.3	257	1	VSP3 TRIFL	O13058 trimeresuru	353	354.5	25.8	311	2	Q8WZM5	Q8wzm5 trichoderma
281	388	28.2	189	1	EL2_PIG	P08419 sus scrofa	354	354.5	25.8	331	2	Q8XIA6	Q8ria6 mus musculus
282	387	28.2	261	2	Q8NFV7	Q8nfv7 homo sapien	355	354.5	25.8	331	2	Q8XIA6	Q8ria6 mus musculus
283	387	28.2	243	2	Q86VJ5	Q86vj5 homo sapien	356	354	25.8	260	2	Q9W7P9	P05208 mus musculus
284	387	28.2	258	2	Q98TT5	Q98tt5 agkistrodon	357	354	25.8	271	1	EL2 MOUSE	Q9w7p9 paralichthy
285	386.5	28.1	257	1	VSPA AGKAC	P018x0 agkistrodon	358	353.5	25.7	263	1	CTFA_GADMO	P47796 gadus norhu
286	386	28.1	232	1	VSPA BOTJA	P81661 bothrops ja	359	353.5	25.7	270	1	TRYT_MERUN	P50342 meriones un
287	386	28.1	258	2	Q91961	Q91961 agkistrodon	360	353.5	25.7	333	2	Q7Q5Z6	Q7q5z6 anopheles g
288	386	28.1	258	2	Q9W7S1	Q9w7s1 agkistrodon	361	353	25.7	274	1	MCT6 RAT	P50343 rattus norv
289	386	28.1	260	2	Q676S7	Q676s7 bitis gabon	362	353	25.7	314	1	TEST HUMAN	Q9y5m0 homo sapien
290	385.5	28.1	188	1	KLK3 RAT	P15950 rattus norv	363	353	25.7	456	1	PRTC_CANFA	Q28278 canis famil
291	385.5	28.1	264	1	CTRL_HUMAN	P40313 homo sapien	364	353	25.7	459	1	PRTC_PIG	Q9g1p2 sus scrofa
292	385.5	28.1	264	2	Q9D960	Q9d960 mus musculus	365	352.5	25.7	263	2	Q6PGS4	Q6pgs4 xenopus lae
293	385.5	28.1	269	2	Q8LIUW0	Q8liuw0 homo sapien	366	352.5	25.7	321	2	Q6GNK3	Q6gnk3 xenopus lae
294	384.5	28.0	195	2	Q07277	Q07277 homo sapien	367	352	25.6	111	2	Q6GNK2	Q6gnk2 homo sapien
295	382.5	27.8	1524	2	Q91674	Q91674 xenopus lae	368	352	25.6	260	1	GRAA MOUSE	P11032 mus musculus
296	381	27.7	263	1	CFAD RAT	P32038 rattus norv	369	352	25.6	277	2	Q7T0T6	Q7t0t6 xenopus lae
297	380.5	27.7	235	2	Q8NAE0	Q8nae0 homo sapien	370	352	25.6	304	1	DISP RAT	P83748 rattus norv
298	380	27.7	157	2	Q6B338	Q6b338 symphysodon	371	352	25.6	505	2	Q966V4	Q966v4 halocynthia
299	380	27.7	455	2	Q7SY86	Q7sy86 xenopus lae	372	351.5	25.6	460	1	PRTC MOUSE	P33587 mus musculus
300	379	27.6	220	2	Q8NCW4	Q8ncw4 homo sapien	373	351	25.5	310	1	DISP MOUSE	Q9gy29 mus musculus
301	378	27.5	261	2	Q6DHD9	Q6dhd9 brachydania	374	351	25.5	456	1	PRTC_BOVIN	P00745 bos taurus
302	374.5	27.3	259	1	CFAD MOUSE	P03953 mus musculus	375	350.5	25.5	265	2	O804G1	Q804g1 brachydania
303	372.5	27.1	228	2	Q6FHW3	Q6fhw3 homo sapien	376	350.5	25.5	274	2	O16133	Q16133 anopheles s
304	372.5	27.1	261	2	Q8CJF4	Q8cjf4 rattus norv	377	350.5	25.5	274	2	Q17086	Q17086 anopheles s
305	371	27.0	271	1	EL2 RAT	P00774 rattus norv	378	350.5	25.5	434	2	Q7T3B6	Q7t3b6 brachydania
306	370.5	27.0	204	2	Q86V17	Q86v17 homo sapien	379	350	25.5	263	2	Q6QPI1	Q6qp11 homo sapien
307	370.5	27.0	259	1	CFAD PIG	P51779 sus scrofa	380	350	25.5	268	2	Q6QGE9	Q6qge9 xenopus lae
308	370.5	27.0	263	1	CTR2_CANFA	P04813 canis famil	381	350	25.5	268	2	Q642S8	Q642s8 xenopus tro
309	370	26.9	234	1	VSP1_AGRH	P26324 agkistrodon	382	350	25.5	271	2	O18487	Q18487 penaeus van
310	370	26.9	270	2	Q819P2	Q819p2 apllysina fi	383	349.5	25.4	261	2	Q66HW9	Q66hw9 brachydania
311	369	26.9	330	2	Q6NVR7	Q6nvr7 xenopus tro	384	349.5	25.4	269	1	EL2A_HUMAN	P08217 homo sapien
312	368.5	26.8	343	1	PS88 HUMAN	P16651 homo sapien	385	349.5	25.4	269	2	Q6ICV2	Q6icv2 homo sapien
313	368	26.8	256	1	TRP3_PSEAM	Q93267 pseudopleur	386	349.5	25.4	277	2	O96899	Q96899 scolopendra
314	368	26.8	418	1	HATT_HUMAN	P06235 homo sapien	387	349.5	25.4	371	2	Q8CJ16	Q8cj16 rattus norv
315	367.5	26.7	638	1	KAL_HUMAN	P03952 homo sapien	388	349.5	25.4	445	2	Q8CJ17	Q8cj17 rattus norv
316	366	26.6	258	1	VSP2_AGRH	P47797 agkistrodon	389	349.5	25.4	558	2	Q6L711	Q6l711 rattus norv
317	366	26.6	260	2	Q9W7Q3	Q9w7q3 paralichthy	390	349.5	25.4	1130	2	Q7QIM7	Q7qim7 anopheles g
318	365.5	26.6	245	2	Q9XY60	Q9xy60 ctenoscephal	391	349	25.4	1019	1	LFC CARRO	Q26422 carinoscoc
319	365	26.6	263	2	Q7SX97	Q7sx97 brachydania	392	349	25.4	1083	2	Q26423	Q26423 carinoscoc
320	363.5	26.5	339	2	Q9144	Q9144 mus musculus	393	348.5	25.4	429	2	Q8AVB0	Q8avb0 brachydania
321	363	26.4	340	2	Q8B3V6	Q8b3v6 mus musculus	394	348.5	25.4	503	2	Q8AYE4	Q8aye4 brachydania
322	362.5	26.4	246	1	MCT1_MERUN	P50340 meriones un	395	348.5	25.4	799	2	Q6PF94	Q6pf94 mus musculus
323	362.5	26.4	387	2	Q9XY57	Q9xy57 ctenoscephal	396	348.5	25.4	811	1	TMS6_MOUSE	Q9dbi0 mus musculus

397	348.5	25.4	818	2	Q6PBA6	Q6pba6 brachydanio	470	339.5	24.7	258	1	GRAM RAT	Q03238 rattus norv
398	348	25.3	267	1	TRY7 ANOGA	P35041 anopheles g	471	339.5	24.7	271	2	Q803Z4	Q803z4 brachydanio
399	348	25.3	269	1	Q61SN8	Q61sn8 homo sapien	472	339.5	24.7	333	1	PLMN CANFA	P80009 canis famil
400	348	25.3	278	2	Q7ENF6	Q7pnf6 anopheles g	473	339	24.7	321	2	Q61E60	Q61e60 rattus norv
401	347.5	25.3	344	2	Q640F8	Q640f8 xenopus lae	474	339	24.7	335	2	Q8VIF2	Q8vif2 mus musculus
402	347	25.3	342	2	Q6FHB8	Q6fhb8 homo sapien	475	339	24.7	458	1	PRTC RABIT	Q28661 oryctolagus
403	347	25.3	342	2	Q6FHB8	Q6fhb8 homo sapien	476	339	24.7	461	1	FA9 HUMAN	P00740 homo sapien
404	346.5	25.2	267	1	PRTC HUMAN	P04070 homo sapien	477	339	24.7	461	1	FA9 PANTR	Q95nd7 pan troglod
405	346.5	25.2	269	1	EL2 BOVIN	Q9bk47 luidia foli	478	339	24.7	625	1	FALL HUMAN	P03951 homo sapien
406	346.5	25.2	334	2	Q650Y7	Q29461 bos taurus	479	339	24.7	812	1	PLMN RAT	Q01177 rattus norv
407	346.5	25.2	351	2	Q816K0	Q46507 papio hamad	480	338.5	24.6	256	2	Q18599	Q18599 drosophila
408	346.5	25.2	435	1	TMS4 MOUSE	Q816k0 holotrichia	481	338.5	24.6	258	1	EL1 HUMAN	Q9unil1 homo sapien
409	346.5	25.2	435	1	Q9NPF2	Q8vca5 mus musculus	482	338.5	24.6	258	2	Q867B0	Q867b0 canis famil
410	346.5	25.2	446	1	PA7 MOUSE	Q70375 mus musculus	483	338.5	24.6	307	2	O02569	Q02569 cullex quinq
411	346.5	25.2	456	1	Q7OC30	P70375 mus musculus	484	338.5	24.6	307	2	Q8ZND6	Q8znd6 homo sapien
412	346.5	25.2	461	1	PRTC RAT	P31394 rattus norv	485	338.5	24.6	455	2	Q8CDR0	Q8cdr0 mus musculus
413	346.5	25.2	612	2	Q68FY8	Q68fy8 rattus norv	486	338.5	24.6	562	2	Q7PN85	Q7pn85 anopheles g
414	346.5	25.2	612	2	Q804W7	Q804w7 fugu rubrip	487	338.5	24.6	704	1	CRAR MOUSE	P98064 mus musculus
415	346	25.2	311	1	TRYG MOUSE	Q9qu17 mus musculus	488	338.5	24.6	802	2	Q6UXD8	Q6uxd8 homo sapien
416	346	25.2	322	2	Q920S2	Q920s2 mus musculus	489	338	24.6	210	2	Q63Z11	Q63z11 xenopus lae
417	345.5	25.1	454	2	Q46506	Q46506 papio hamad	490	338	24.6	365	2	Q97366	Q97366 holotrichia
418	345.5	25.1	467	2	Q967X8	Q967x8 panulirus a	491	338	24.6	388	2	O44330	O44330 manduca sex
419	345	25.1	253	1	TRXD DROER	P54626 drosophila	492	338	24.6	418	2	Q7FGU3	Q7fgu3 anopheles g
420	344.5	25.1	117	2	Q9PUF3	Q9puf3 bothrops ja	493	338	24.6	625	1	THRB BOVIN	P00735 bos taurus
421	344.5	25.1	187	2	Q6PK75	Q6pk75 homo sapien	494	337.5	24.6	238	1	TRY5 AEDAE	P29787 aedes aegyp
422	344.5	25.1	275	2	Q6B051	Q6b051 homo sapien	495	337.5	24.6	261	2	Q6GX60	Q6gx60 lepeophthei
423	344.5	25.1	855	2	Q72410	Q7z410 homo sapien	496	337.5	24.6	264	1	GRAX HUMAN	P49863 homo sapien
424	344.5	25.1	1059	2	Q72411	Q7z411 homo sapien	497	337.5	24.6	282	2	Q9DA13	Q9da13 mus musculus
425	344	25.0	257	2	Q8BZ04	Q8bz04 mus musculus	498	337.5	24.6	317	2	Q9DGR3	Q9dgr3 xenopus lae
426	344	25.0	265	2	Q6QX61	Q6qx61 lepeophthei	499	337.5	24.6	328	2	Q80Z40	Q80z40 rattus norv
427	344	25.0	275	1	TRB2 HUMAN	P62231 homo sapien	500	337.5	24.6	432	2	Q6GNA2	Q6gna2 xenopus lae
428	344	25.0	282	2	Q6NZY1	Q6nzy1 homo sapien	501	337.5	24.6	471	2	Q8CFE0	Q8cfe0 mus musculus
429	344	25.0	417	2	Q8BZ10	Q8bz10 mus musculus	502	337	24.5	247	2	O17039	Q17039 anopheles g
430	343.5	25.0	266	2	O46644	O46644 macaca fasc	503	337	24.5	263	2	Q9D8X8	Q9d8x8 mus musculus
431	343.5	25.0	273	1	MCT7 MOUSE	Q02844 mus musculus	504	337	24.5	275	2	Q96RZ6	Q96rz6 homo sapien
432	343.5	25.0	273	2	Q921N4	Q921n4 mus musculus	505	337	24.5	432	2	Q6UX37	Q6ux37 homo sapien
433	343.5	25.0	457	1	TMS5 HUMAN	Q9h383 homo sapien	506	337	24.5	434	1	UROK CHICK	P15120 gallus gall
434	343	25.0	275	1	TRY7 CANFA	P15944 canis famil	507	337	24.5	437	1	TMS4 HUMAN	Q9nr84 homo sapien
435	343	25.0	284	2	Q8NF86	Q8nf86 homo sapien	508	336.5	24.5	247	1	MCT1 PAPHA	P52195 papio hamad
436	343	25.0	318	2	Q7RTY9	Q7rty9 homo sapien	509	336.5	24.5	251	1	MCT3 SHEEP	O46683 ovis aries
437	342.5	24.9	248	2	O16126	O16126 boltenia vi	510	336.5	24.5	260	2	Q8FV99	Q8fzv9 xenopus tro
438	342.5	24.9	248	2	Q9XY52	Q9xy52 ctenocephal	511	336.5	24.5	329	2	O42272	O42272 xenopus lae
439	342.5	24.9	271	1	Q8HYJ2	Q8hyj2 bos taurus	512	336.5	24.5	428	2	Q8WPM7	Q8wpm7 oikopleura
440	342.5	24.9	273	1	MCT7 RAT	P27435 rattus norv	513	336.5	24.5	638	1	KAL MOUSE	P26262 mus musculus
441	342.5	24.9	273	2	Q6P6W8	Q6p6w8 rattus norv	514	336	24.5	227	2	Q8IXI4	Q8ixi4 homo sapien
442	342.5	24.9	433	2	Q8JHD0	Q8jhd0 brachydanio	515	336	24.5	263	2	Q9CR35	Q9cr35 m muscu
443	342.5	24.9	433	2	Q90YK1	Q90yk1 brachydanio	516	336	24.5	263	2	Q9DC86	Q9dc86 mus musculus
444	342.5	24.9	517	2	Q8K0D2	Q8kod2 mus musculus	517	336	24.5	273	1	TRYT SHEEP	Q9xsm2 ovis aries
445	342.5	24.9	624	1	FALL MOUSE	Q91y47 mus musculus	518	336	24.5	280	2	Q64ID5	Q64id5 anthonomus
446	342.5	24.9	810	1	PLMN HUMAN	P00747 homo sapien	519	336	24.5	402	2	Q7QB73	Q7qb73 anopheles g
447	342.5	24.9	811	1	TMS6 HUMAN	Q8iu80 homo sapien	520	336	24.5	416	1	FA9 BOVIN	P00741 bos taurus
448	342	24.9	275	1	TRB1 HUMAN	Q15661 homo sapien	521	336	24.5	485	2	Q7PKX0	Q7pkk0 anopheles g
449	342	24.9	355	2	Q7PQR9	Q7pqr9 anopheles g	522	336	24.5	556	2	Q803D5	Q803d5 brachydanio
450	342	24.9	812	1	PLMN MOUSE	P20918 mus musculus	523	336	24.5	654	2	Q6QNF4	Q6qnf4 canis famil
451	341.5	24.9	258	1	GRAX RAT	P49864 rattus norv	524	336	24.5	790	1	PLMN PIG	P06867 sus scrofa
452	341.5	24.9	455	1	TMS5 MOUSE	Q9er04 mus musculus	525	335.5	24.4	258	2	Q6ISM6	Q6ism6 homo sapien
453	341.5	24.9	573	2	Q9V516	Q9v516 drosophila	526	335.5	24.4	266	1	EL1 BOVIN	Q28153 bos taurus
454	341.5	24.9	1134	2	Q7RTY7	Q7rty7 homo sapien	527	335.5	24.4	275	1	TRYT PIG	Q9n2d1 sus scrofa
455	341	24.8	251	2	Q9GLN2	Q9gln2 bos taurus	528	335.5	24.4	389	2	Q9PVX7	Q9pvx7 xenopus lae
456	341	24.8	328	2	Q63ZK0	Q63zk0 xenopus lae	529	335.5	24.4	558	2	Q8EYm4	Q8eym4 homo sapien
457	341	24.8	328	2	Q61RA4	Q61ra4 xenopus lae	530	335	24.4	216	2	Q9UD19	Q9ud19 homo sapien
458	341	24.8	719	2	Q6RTY8	Q6rty8 homo sapien	531	335	24.4	318	2	Q8MNY6	Q8my6 nilaparvata
459	341	24.8	572	2	Q6DJ90	Q6dj90 xenopus tro	532	335	24.4	433	2	Q804X5	Q804x5 gallus gall
460	340.5	24.8	246	1	MCT4 MOUSE	P21812 mus musculus	533	335	24.4	701	2	Q9JJS9	Q9jjs9 rattus norv
461	340.5	24.8	274	1	TRY1 ANOGA	P35035 anopheles g	534	335	24.4	703	2	Q8CHN8	Q8chn8 rattus norv
462	340.5	24.8	446	1	FAV RAT	Q8k3u6 rattus norv	535	334.5	24.3	247	2	Q70500	Q70500 rattus norv
463	340.5	24.8	624	2	Q9DAT3	Q9dat3 mus musculus	536	334.5	24.3	263	1	GRAX MOUSE	O35205 mus musculus
464	340	24.7	273	2	Q9XSM1	Q9xsm1 ovis aries	537	334.5	24.3	275	2	Q7YS62	Q7ys62 equus cabal
465	340	24.7	280	2	Q8N171	Q8n171 homo sapien	538	334.5	24.3	537	2	Q9BYE1	Q9bye1 homo sapien
466	340	24.7	297	2	O88781	Q88781 rattus ratt	539	334.5	24.3	581	2	Q9BYE2	Q9bye2 homo sapien
467	340	24.7	360	2	O17489	O17489 anopheles g	540	334	24.3	234	2	O15096	O15096 homo sapien
468	339.5	24.7	247	2	O08732	O08732 mesocricetu	541	334	24.3	264	2	Q08QF6	Q8qgf6 xenopus lae
469	339.5	24.7	253	1	TRYB DROER	P54625 drosophila	542	333.5	24.3	253	2	Q8MKZ1	Q8mkz1 drosophila

543	333.5	24.3	253	2	Q8SXZ4	Q8sxz4 drosophila	616	328.5	23.9	365	2	Q7Q1D1	Q7q1d1 anopheles g
544	333.5	24.3	275	2	Q7PNF7	Q7pnf7 anopheles g	617	328.5	23.9	524	2	Q7SXH8	Q7sxh8 brachydanio
545	333.5	24.3	290	1	PR27 HUMAN	Q9bqr3 homo sapien	618	328.5	23.9	615	2	Q6GNK4	Q6gnk4 xenopus lae
546	333.5	24.3	824	2	Q6ICC2	Q6icc2 homo sapien	619	328.5	23.9	681	2	Q7ZT70	Q7zt70 lampetra ja
547	333	24.2	245	1	CTRA_BOVIN	P00766 bos taurus	620	328.5	23.9	683	2	Q8MRH5	Q8mrh5 drosophila
548	333	24.2	256	2	Q9ROK0	Q9rok0 mus musculus	621	328.5	23.9	786	1	STUB_DROME	Q05319 drosophila
549	333	24.2	285	1	FA9_CAYPO	P16295 cavia porce	622	328.5	23.9	787	2	Q9VEY6	Q9vey6 drosophila
550	333	24.2	320	2	Q7TOX2	Q7tox2 xenopus lae	623	328	23.9	226	1	COGS_UCAPU	P00771 uca pugil lat
551	333	24.2	355	2	Q7PEW0	Q7pew0 anopheles g	624	328	23.9	328	2	Q6BEA2	Q6bea2 rattus norv
552	333	24.2	360	2	Q7PEV7	Q7pev7 anopheles g	625	328	23.9	452	1	FA9_CANFA	P19540 canis famil
553	332.5	24.2	247	2	Q35342	Q35342 mesocricetu	626	328	23.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
554	332.5	24.2	254	2	Q8TG37	Q8tg37 aedes aegyp	627	327.5	23.8	247	1	MCT1_MACFA	P56335 macaca fasc
555	332.5	24.2	260	2	Q8T4P6	Q8t4p6 lepeophthei	628	327.5	23.8	263	2	Q7TYI6	Q7tyi6 penaeus van
556	332.5	24.2	262	2	Q8T4P7	Q8t4p7 lepeophthei	629	327.5	23.8	266	2	Q27761	Q27761 penaeus van
557	332.5	24.2	263	2	Q7Z1D5	Q7z1d5 lepeophthei	630	327.5	23.8	269	2	Q96QV5	Q96qv5 homo sapien
558	332.5	24.2	264	2	Q7YSS9	Q7yss9 lepeophthei	631	327.5	23.8	269	2	Q6ISM5	Q6ism5 homo sapien
559	332.5	24.2	490	1	TMS2_MOUSE	Q9jiq8 mus musculus	632	327.5	23.8	269	2	Q6GN82	Q6gn82 xenopus lae
560	332.5	24.2	638	1	KAL_RAT	P14272 rattus norv	633	327	23.8	259	1	DEF3_DERFA	P49275 dermatophag
561	332.5	24.2	810	1	PLMN_ERIEU	Q29485 erinaceus e	634	327	23.8	263	2	Q7SY84	Q7sy84 xenopus lae
562	332.5	24.2	810	1	PLMN_MACMU	P12545 macaca mula	635	327	23.8	270	2	Q27824	Q27824 uca pugil lat
563	332	24.2	247	2	Q7OT74	Q7ot74 equus cabal	636	327	23.8	466	2	Q6SA95	Q6sa95 felis silve
564	332	24.2	251	2	Q7Q9W2	Q7q9w2 anopheles g	637	327	23.8	600	2	Q7ZTR2	Q7ztr2 xenopus lae
565	332	24.2	258	2	Q97399	Q97399 phaeton coc	638	326.5	23.8	248	1	GRAC_MOUSE	P08882 mus musculu
566	332	24.2	266	2	Q92077	Q92077 gadus morhu	639	326.5	23.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
567	332	24.2	277	2	Q8SQ44	Q8sq44 sus scrofa	640	326.5	23.8	266	1	ELI_PIG	P00772 sus scrofa
568	332	24.2	355	2	Q8NFU1	Q8nfu1 anopheles g	641	326.5	23.8	266	2	Q91X79	Q91x79 mus musculu
569	331.5	24.1	250	2	Q8T4P4	Q8t4p4 lepeophthei	642	326.5	23.8	369	2	Q7QKL1	Q7qkl1 anopheles g
570	331.5	24.1	254	2	Q8MMK9	Q8mmk9 aedes aegyp	643	326.5	23.8	490	2	Q7TN04	Q7tn04 mus musculu
571	331.5	24.1	256	1	TRYA_DROME	P04814 drosophila	644	326	23.7	248	1	GRZ1_RAT	Q06505 rattus norv
572	331.5	24.1	260	2	Q8T4P5	Q8t4p5 lepeophthei	645	326	23.7	271	1	CTR2_PENVA	P36178 penaeus van
573	331.5	24.1	263	2	Q9PWQ6	Q9pwq6 gadus morhu	646	326	23.7	329	2	Q7PEV8	Q7pev8 anopheles g
574	331.5	24.1	264	2	Q6PPY5	Q6ppy5 xenopus lae	647	326	23.7	432	2	Q7QKL4	Q7qkl4 anopheles g
575	331.5	24.1	275	1	TRY3_ANOGA	P35037 anopheles g	648	325.5	23.7	259	2	Q8IRE0	Q8ire0 drosophila
576	331	24.1	263	1	CTRB_RAT	P07338 rattus norv	649	325.5	23.7	261	1	DER3_DERPT	P39575 dermatophag
577	331	24.1	622	1	THRB_HUMAN	P00734 homo sapien	650	325.5	23.7	268	2	O46151	O46151 pacifastacu
578	331	24.1	622	2	Q7Z7P3	Q7z7p3 homo sapien	651	325.5	23.7	306	1	BSS4_MOUSE	Q9er10 mus musculu
579	331	24.1	722	2	Q8AW90	Q8aw90 lampetra ja	652	325.5	23.7	891	2	Q9VV38	Q9vv38 drosophila
580	330.5	24.1	722	2	Q9PSZ5	Q9psz5 lampetra ja	653	324.5	23.6	146	2	Q9DDE1	Q9dde1 brachydanio
581	330.5	24.1	247	1	MCT1_HUMAN	P23946 homo sapien	654	324.5	23.6	228	2	Q7Q153	Q7q153 anopheles g
582	330.5	24.1	256	1	TRYA_DROER	P54624 drosophila	655	324.5	23.6	263	2	Q7PUB9	Q7pub9 anopheles g
583	330.5	24.1	269	2	Q61SP9	Q6isp9 homo sapien	656	324.5	23.6	275	1	TRYA_HUMAN	P15157 homo sapien
584	330.5	24.1	560	2	Q14520	Q14520 homo sapien	657	324.5	23.6	391	2	Q9V3Z2	Q9v3z2 drosophila
585	330.5	24.1	638	2	Q8ROP5	Q8rop5 mus musculu	658	324	23.6	253	1	TRYB_HUMAN	P35004 drosophila
586	330	24.0	236	2	Q7SIG3	Q7sig3 salmo salar	659	324	23.6	257	1	GRAM_DROME	P51124 homo sapien
587	330	24.0	253	2	Q9V5Y3	Q9v5y3 drosophila	660	324	23.6	266	2	Q9W7Q0	Q9w7q0 paralichthy
588	330	24.0	266	2	Q81916	Q81916 blomia trop	661	324	23.6	459	1	FA9_MOUSE	P16294 mus musculu
589	330	24.0	282	1	FA9_RAT	P16296 rattus norv	662	324	23.6	1019	1	ENTK_HUMAN	P98073 homo sapien
590	330	24.0	4548	1	APOA_HUMAN	P08519 homo sapien	663	323.5	23.5	277	2	Q80WM7	Q80wm7 mus musculu
591	329.5	24.0	237	2	Q29464	Q29464 bos taurus	664	323.5	23.5	299	2	Q9VSR7	Q9vsa7 drosophila
592	329.5	24.0	248	2	Q8T4P2	Q8t4p2 lepeophthei	665	323.5	23.5	328	2	Q8BJR6	Q8bjr6 mus musculu
593	329.5	24.0	253	1	TRYD_DROME	P42276 drosophila	666	323.5	23.5	466	1	FA7_HUMAN	P08709 homo sapien
594	329.5	24.0	262	2	Q7Z1D6	Q7z1d6 lepeophthei	667	323.5	23.5	490	2	Q6P7D7	Q6p7d7 rattus norv
595	329.5	24.0	266	2	Q8WR10	Q8wr10 paralichthod	668	323.5	23.5	608	2	Q9FTW7	Q9ftw7 struthio ca
596	329.5	24.0	269	1	EL2B_HUMAN	P08218 homo sapien	669	323	23.5	875	1	NETR_HUMAN	P56730 homo sapien
597	329.5	24.0	320	2	Q7PEV6	Q7pev6 anopheles g	670	323	23.5	281	2	O46137	O46137 lumbricus r
598	329.5	24.0	578	2	Q60017	Q6q017 bos taurus	671	323	23.5	296	2	Q9VDV1	Q9vdv1 drosophila
599	329.5	24.0	1420	1	APOA_MACMU	P14417 macaca mula	672	323	23.5	540	2	Q800Y7	Q800y7 meleagris g
600	329	23.9	216	1	VSPB_LACMU	P84036 lachesis mu	673	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
601	329	23.9	264	2	O08643	O08643 mus musculu	674	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
602	329	23.9	279	2	Q9NMS4	Q9nms4 mus musculu	675	322.5	23.5	249	2	Q6QX62	Q6qx62 lepeophthei
603	329	23.9	307	2	Q7TML0	Q7tml0 mus musculu	676	322.5	23.5	258	2	Q9W5U8	Q9wsu8 drosophila
604	329	23.9	572	2	Q8BIK6	Q8bik6 mus musculu	677	322.5	23.5	324	1	TEST_MOUSE	Q9jhj7 mus musculu
605	329	23.9	575	2	Q7Q9W3	Q7q9w3 anopheles g	678	322.5	23.5	336	2	Q80YD8	Q80yd8 mus musculu
606	329	23.9	722	2	Q6NUP5	Q6nuf5 xenopus lae	679	322.5	23.5	372	2	Q9Y1K6	Q9y1k6 anopheles g
607	328.5	23.9	239	2	Q8T4P3	Q8t4p3 lepeophthei	680	322.5	23.5	581	2	Q9XZM7	Q9xzm7 strongyloce
608	328.5	23.9	245	1	CTRB_GADMO	P80646 gadus morhu	681	322	23.4	210	2	Q6BDS2	Q6bds2 homo sapien
609	328.5	23.9	253	1	TRYG_DROME	P42277 drosophila	682	322	23.4	699	1	CRAR_HUMAN	P48740 h complemen
610	328.5	23.9	260	1	MCT1_RAT	P09650 rattus norv	683	322	23.4	1303	2	Q6GS84	Q6gs84 oikopleura
611	328.5	23.9	261	2	Q8T4P1	Q8t4p1 lepeophthei	684	321.5	23.4	263	2	O62562	O62562 penaeus van
612	328.5	23.9	275	2	Q86TM8	Q86tm8 homo sapien	685	321.5	23.4	265	2	Q7SYI8	Q7syi8 xenopus lae
613	328.5	23.9	276	2	Q86UAS	Q86uas homo sapien	686	321.5	23.4	266	2	Q9D936	Q9d936 mus musculu
614	328.5	23.9	338	1	PLMN_HORSE	P80010 equus cabal	687	321.5	23.4	679	2	Q96PQ8	Q96pq8 homo sapien
615	328.5	23.9	364	2	Q9NA59	Q9nas9 anopheles g	688	321	23.4	226	1	DDN1_BOVIN	P80219 bos taurus

689	321	23.4	230	2	Q61E13	Q61e13 rattus norv	762	314	22.9	629	2	Q6AZS7	Q6azs7 xenopus lae
690	321	23.4	247	1	MCT2 MERUN	P50341 meriones un	763	314	22.9	855	1	ST14_HUMAN	Q9Y5y6 homo sapien
691	321	23.4	248	1	NKP1_RAT	P18291 rattus norv	764	313.5	22.8	261	1	EUM3_EURMA	Q9Y370 euroglyphus
692	321	23.4	269	1	TRYM_CANFA	P19236 canis famil	765	313.5	22.8	321	2	Q80Y38	Q80y38 mus musculus
693	321	23.4	411	2	Q9VUF0	Q9vuf0 drosophila	766	313.5	22.8	326	2	Q9D9M0	Q9d9m0 mus musculus
694	321	23.4	655	1	HGFA_HUMAN	Q04756 homo sapien	767	313.5	22.8	364	2	Q9I7V4	Q9i7v4 drosophila
695	320.5	23.3	247	1	GRAB_MOUSE	P04187 mus musculus	768	313.5	22.8	425	2	Q804X7	Q804x7 gallus gall
696	320.5	23.3	312	2	Q7M755	P07m755 mus musculus	769	313	22.8	241	2	Q9I7L2	Q9i7l2 drosophila
697	320	23.3	249	2	Q9W7Q1	Q9w7q1 paralichthy	770	313	22.8	336	2	Q8CIR9	Q8cjr9 mus musculus
698	320	23.3	489	2	Q7Q432	Q7q432 anopheles g	771	313	22.8	420	2	Q90504	Q90504 eptatretus
699	320	23.3	536	2	Q7PAX72	Q7px72 anopheles g	772	313	22.8	613	2	Q03711	Q03711 xenopus lae
700	319.5	23.3	265	2	Q6NGG0	Q6ngg0 xenopus lae	773	313	22.8	697	2	Q8CG43	Q8cg43 rattus norv
701	319.5	23.3	559	2	Q6P7U0	Q6p7u0 mus musculus	774	313	22.8	733	2	Q920S0	Q920s0 mus musculus
702	319.5	23.3	607	2	Q6DPJ5	Q6dfj5 xenopus lae	775	313	22.8	733	2	Q8CD27	Q8cd27 mus musculus
703	319	23.2	241	2	Q7PPF7	Q7ppf7 anopheles g	776	313	22.8	855	2	Q9UJI7	Q9uji7 rattus norv
704	319	23.2	264	2	Q8IPY7	Q8ipy7 drosophila	777	312.5	22.7	241	2	Q8IYP2	Q8iyp2 homo sapien
705	319	23.2	270	2	Q64ID1	Q64id1 anthonomus	778	312.5	22.7	271	2	Q8I9R6	Q8isr6 culex pipie
706	319	23.2	320	2	Q8CIR7	Q8cir7 rattus norv	779	312.5	22.7	274	1	TRY5_ANOGA	P35039 anopheles g
707	319	23.2	461	2	Q95ND6	Q95nd6 pan troglod	780	312.5	22.7	300	2	Q96EF3	Q96ef3 homo sapien
708	319	23.2	1034	1	ENTK_PIG	P98074 sus scrofa	781	312.5	22.7	390	2	Q9Y157	Q9y157 drosophila
709	318.5	23.2	343	1	PLMN_SHEEP	P81286 ovis aries	782	312.5	22.7	615	1	FA12_HUMAN	P00748 homo sapien
710	318.5	23.2	418	2	Q61E15	Q61e15 rattus norv	783	312.5	22.7	680	2	Q868H5	Q868h5 branchiosto
711	318.5	23.2	430	2	Q920K3	Q920k3 rattus norv	784	312.5	22.7	1234	2	Q7PIQ7	Q7piq7 anopheles g
712	318	23.1	232	2	Q94508	Q94508 dermatophag	785	312.5	22.7	1322	2	Q7PNR7	Q7pnr7 anopheles g
713	318	23.1	258	2	Q7YRZ7	Q7yrr7 bos taurus	786	312.5	22.7	1322	2	Q9NJS5	Q9njs5 anopheles g
714	318	23.1	261	2	Q962G7	Q962g7 culex pipie	787	312	22.7	295	2	Q8CIP7	Q8cip7 rattus norv
715	318	23.1	265	2	O18488	O18488 penaeus van	788	312	22.7	374	2	Q8I862	Q8i862 dermaceator
716	318	23.1	271	1	FA9_PIG	P16293 sus scrofa	789	312	22.7	597	2	Q35727	Q35727 mus musculus
717	318	23.1	274	1	FA9_SHEEP	P16291 ovis aries	790	312	22.7	597	2	Q6PER0	Q6per0 mus musculus
718	318	23.1	295	2	Q69E28	Q69e28 homo sapien	791	312	22.7	609	2	Q80YC5	Q80yc5 mus musculus
719	318	23.1	618	1	THRB_MOUSE	P19221 mus musculus	792	311.5	22.7	255	2	Q25227	Q25227 lucilia cup
720	317.5	23.1	245	1	CTRB_BOVIN	P00767 bos taurus	793	311.5	22.7	255	2	Q7TN10	Q7tni0 mus musculus
721	317.5	23.1	246	1	GRAH_HUMAN	P20718 homo sapien	794	311.5	22.7	293	2	Q23528	Q23528 caenorhabdi
722	317.5	23.1	248	2	Q9XYX9	Q9xyx9 rhyzopertha	795	311.5	22.7	566	1	TPA_BOVIN	Q28198 bos taurus
723	317.5	23.1	256	1	TRFE_DROER	P54627 drosophila	796	311.5	22.7	645	2	Q7PWE4	Q7pwe4 anopheles g
724	317.5	23.1	374	2	Q9VUG2	Q9vug2 drosophila	797	311.5	22.7	761	1	NETR_MOUSE	Q08762 mus musculus
725	317.5	23.1	559	1	TPA_MOUSE	P11214 mus musculus	798	311.5	22.7	1322	2	Q9NAT0	Q9nat0 anopheles g
726	317.5	23.1	604	1	CFAT_RAT	P11214 mus musculus	799	311	22.6	249	2	Q6IE11	Q6ie11 rattus norv
727	317.5	23.1	617	2	Q8JIS1	Q8jis1 triakis scy	800	311	22.6	250	2	Q9V514	Q9v514 drosophila
728	317	23.1	248	2	Q63636	Q63636 rattus norv	801	311	22.6	261	1	CATG_MOUSE	P28293 mus musculus
729	317	23.1	624	2	Q9SME7	Q9sme7 oryctolagus	802	311	22.6	431	1	ACRO_RABIT	P48038 oryctolagus
730	316.5	23.0	246	1	MCT1_MOUSE	P10334 mus musculus	803	311	22.6	433	1	UROK_BOVIN	Q05589 bos taurus
731	316.5	23.0	441	2	Q81917	Q81917 manduca sex	804	311	22.6	1035	1	ENTK_BOVIN	P98072 bos taurus
732	316.5	23.0	607	2	Q91001	Q91001 gallus gall	805	311	22.6	1042	1	CORI_HUMAN	P98075 homo sapien
733	316	23.0	246	2	Q9XY46	Q9xy46 ctenocephal	806	310.5	22.6	247	1	MCT2_RAT	P00770 rattus norv
734	316	23.0	259	2	Q69EZ7	Q69ez7 homo sapien	807	310.5	22.6	259	2	Q7PFI7	Q7pfi7 anopheles g
735	316	23.0	263	2	O02570	O02570 culex quinq	808	310.5	22.6	371	2	Q8MY3	Q8my3 drosophila
736	316	23.0	269	2	Q9CQ52	Q9cq52 m mus muscu	809	310.5	22.6	473	2	Q7PV63	Q7pv63 anopheles g
737	316	23.0	269	2	Q9D7T9	Q9d7t9 mus musculus	810	310.5	22.6	559	1	TPA_RAT	P19637 rattus norv
738	315.5	23.0	254	1	TRY3_ABDAAE	P29786 aedes aegypt	811	310.5	22.6	1374	2	Q9VSU0	Q9vsu0 drosophila
739	315.5	23.0	264	2	O62561	O62561 penaeus van	812	310.5	22.6	1449	2	Q9UI12	Q9uli2 drosophila
740	315.5	23.0	265	2	Q66KR6	Q66kr6 xenopus lae	813	310.5	22.6	1450	2	O8IQB8	Q8iqb8 drosophila
741	315.5	23.0	266	1	ELJ_RAT	P00773 rattus norv	814	310.5	22.6	1462	2	Q9UI13	Q9uli3 drosophila
742	315.5	23.0	314	2	Q9VR15	Q9vr15 drosophila	815	310.5	22.6	2382	2	Q9BI19	Q9bil9 drosophila
743	315.5	23.0	374	2	Q7QCS5	Q7qcs5 anopheles g	816	310.5	22.6	2409	2	Q960G6	Q960g6 drosophila
744	315.5	23.0	392	1	EAST_DROME	P13582 drosophila	817	310.5	22.6	2786	2	Q9VSU2	Q9vsu2 drosophila
745	315.5	23.0	453	2	Q812A6	Q812a6 mus musculus	818	310	22.6	275	1	FA9_RABIT	P16292 oryctolagus
746	315.5	23.0	492	1	FA10_BOVIN	P00743 bos taurus	819	310	22.6	327	2	Q7O530	Q7q530 anopheles g
747	315	22.9	248	2	Q63224	Q63224 rattus norv	820	310	22.6	483	2	Q8T8X4	Q8t8x4 anopheles g
748	315	22.9	280	2	Q66NX6	Q66nx6 canis famil	821	310	22.6	483	2	Q9VK10	Q9vkl0 drosophila
749	315	22.9	323	2	Q96QG4	Q96qg4 homo sapien	822	310	22.6	1111	2	Q80YN4	Q80yn4 rattus norv
750	315	22.9	617	1	THRS_RAT	P18292 rattus norv	823	309.5	22.5	246	2	Q9EPR0	Q9epo0 mus musculus
751	315	22.9	686	1	MAS2_HUMAN	O00187 homo sapien	824	309.5	22.5	255	2	Q9Y7A9	Q9y7a9 metarhizium
752	314.5	22.9	256	1	TRVE_DROME	P35005 drosophila	825	309.5	22.5	265	2	Q9VVT3	Q9vvt3 drosophila
753	314.5	22.9	261	2	Q6IDF4	Q6idf4 drosophila	826	309.5	22.5	284	2	Q7Q493	Q7q493 anopheles g
754	314.5	22.9	283	2	Q6UWY2	Q6uwy2 homo sapien	827	309.5	22.5	482	1	FA10_RAT	Q63207 rattus norv
755	314.5	22.9	453	1	TMS3_MOUSE	Q8kit0 mus musculus	828	309.5	22.5	868	2	Q9Y1V3	Q9y1v3 polyandroca
756	314.5	22.9	609	2	Q7M761	Q7m761 mus musculus	829	309	22.5	285	2	Q8CG42	Q8cg42 rattus norv
757	314.5	22.9	680	1	Q868H7	Q868h7 branchiosto	830	309	22.5	404	2	Q7QKL2	Q7qkl2 anopheles g
758	314	22.9	275	1	TRY4_ANOGA	P35038 anopheles g	831	308.5	22.5	240	2	Q6IE06	Q6ie06 rattus norv
759	314	22.9	280	2	Q7Q494	Q7q494 anopheles g	832	308.5	22.5	246	1	MCT9_MOUSE	Q35164 mus musculus
760	314	22.9	280	2	Q66NX5	Q66nx5 canis famil	833	308.5	22.5	260	2	Q6VPÜ6	Q6vpü6 sarcopes s
761	314	22.9	422	2	Q8WVC1	Q8wvc1 homo sapien	834	308	22.4	125	2	Q804G0	Q804g0 spherooides



835	308	22.4	300	2	Q819P4	Q819p4 aurelia aur	908	302	22.0	269	2	Q7PW17	Q7pw17 anopheles g
836	308	22.4	317	1	BSS4_HUMAN	Q9gnz4 homo sapien	909	302	22.0	321	2	Q6MZL2	Q6mz12 homo sapien
837	308	22.4	334	2	Q6UXE0	Q6uxe0 homo sapien	910	302	22.0	394	1	URTG_DESRO	P49150 desmodus ro
838	308	22.4	335	2	Q86PB3	Q86pb3 drosophila	911	302	22.0	477	1	URF2_DESRO	P15638 desmodus ro
839	308	22.4	377	2	Q9VB68	Q9vb68 drosophila	912	301.5	21.9	241	2	Q8BW11	Q8bw11 m mus muscu
840	308	22.4	408	2	Q8MR95	Q8mr95 drosophila	913	301.5	21.9	394	2	P91817	P91817 tachypleus
841	308	22.4	498	2	Q6GPF9	Q6gpf9 xenopus lae	914	301.5	21.9	505	2	Q7QCV2	Q7qcv2 anopheles g
842	307.5	22.4	255	2	Q7PFI6	Q7pfi6 anopheles g	915	301	21.9	255	1	CATG_HUMAN	P08311 homo sapien
843	307.5	22.4	471	2	Q804X6	Q804x6 gallus gall	916	301	21.9	255	2	O34289	O34289 salvelinus
844	307.5	22.4	676	2	Q6DUJ6	Q6duj6 cyprinus ca	917	301	21.9	268	2	Q17030	Q17030 anopheles g
845	307	22.3	135	2	Q62284	Q62284 mus muscu	918	301	21.9	279	2	Q7PX39	Q7px39 anopheles g
846	307	22.3	250	2	Q62284	Q62284 mus muscu	919	301	21.9	279	2	Q7TNX3	Q7tnx3 mus muscu
847	307	22.3	259	1	CTR1_ANOGA	Q17036 anopheles g	920	301	21.9	283	2	Q95V22	Q95v22 lumbricus b
848	307	22.3	318	2	Q7Q9W4	Q27289 anopheles g	921	301	21.9	417	2	Q8VHK8	Q8vkh8 mus muscu
849	307	22.3	417	1	HEFS_HUMAN	P05981 homo sapien	922	301	21.9	417	2	Q8VDV1	Q8vdrv1 mus muscu
850	307	22.3	726	2	Q7QBP4	Q7qbp4 anopheles g	923	301	21.9	431	1	URTB_DESRO	P98121 desmodus ro
851	306.5	22.3	308	2	Q9W454	Q9w454 drosophila	924	301	21.9	728	2	Q96RS4	Q96rs4 homo sapien
852	306.5	22.3	365	2	Q7QGL1	Q7qgl1 anopheles g	925	300.5	21.9	239	2	Q7T2H1	Q7t2h1 xenopus lae
853	306.5	22.3	375	1	PCB_TACTR	P21902 tachypleus	926	300.5	21.9	276	2	P91894	P91894 arenicola m
854	306.5	22.3	418	2	Q8SZK2	Q8szk2 drosophila	927	300.5	21.9	278	2	Q68FN6	Q68fn6 brachydanio
855	306.5	22.3	468	2	Q9U0G3	Q9u0g3 pacifastacu	928	300.5	21.9	386	2	Q8I924	Q8i924 bombyx mori
856	306.5	22.3	162	2	Q6UBM2	Q6ubm2 homo sapien	929	300.5	21.9	424	2	Q9VA88	Q9va88 drosophila
857	306	22.3	247	2	Q8N1D2	Q8nid2 homo sapien	930	300.5	21.9	433	2	Q8MHY7	Q8mhy7 oryctolagus
858	306	22.3	266	2	Q6AZC0	Q6azc0 brachydanio	931	300.5	21.9	433	2	Q8MIL0	Q8milo oryctolagus
859	306	22.3	362	2	Q9W453	Q9w453 drosophila	932	300.5	21.9	442	1	UROK_PIG	P04185 sus scrofa
860	306	22.3	685	2	Q91WP0	Q91wp0 mus muscu	933	300.5	21.9	562	2	Q8SQ23	Q8sq23 sus scrofa
861	305.5	22.2	228	2	Q9XY49	Q9xy49 ctenocephal	934	300	21.8	245	1	GILX_HELHO	P43685 heloderma h
862	305.5	22.2	246	2	Q91VB1	Q91vb1 mus muscu	935	300	21.8	270	2	Q8WR11	Q8wr11 paralithode
863	305.5	22.2	256	1	HYPA_HYPLI	P35587 hypoderma l	936	300	21.8	291	2	Q8IQ89	Q8iq89 drosophila
864	305.5	22.2	274	2	Q6GNF0	Q6gnf0 xenopus lae	937	300	21.8	417	2	Q8VHJ4	Q8vhj4 rattus norv
865	305.5	22.2	383	2	Q77102	Q77102 manduca sex	938	300	21.8	698	2	Q9PU71	Q9pu71 xenopus lae
866	305.5	22.2	418	2	Q9VA87	Q9va87 drosophila	939	299.5	21.8	241	2	Q63637	Q63637 rattus norv
867	305.5	22.2	441	2	Q804X2	Q804x2 fugu rubrip	940	299.5	21.8	246	1	MCTX_MOUSE	Q00356 mus muscu
868	305	22.2	247	1	GRAB_HUMAN	P10144 h granzyme	941	299.5	21.8	254	2	Q6DBS8	Q6db88 brachydanio
869	305	22.2	281	2	Q67BC3	Q67bc3 homo sapien	942	299.5	21.8	257	2	O19023	O19023 macaca mula
870	305	22.2	307	2	Q641D2	Q641d2 anthonomus	943	299.5	21.8	258	1	CTR2_ANOGA	Q17025 anopheles g
871	305	22.2	391	2	Q7PXJ5	Q7pxj5 anopheles g	944	299.5	21.8	272	2	Q7Q9W5	Q7q9w5 anopheles g
872	305	22.2	395	2	Q9BZW1	Q9bzw1 homo sapien	945	299.5	21.8	282	2	Q7PT16	Q7pt16 anopheles g
873	305	22.2	532	2	Q7PX73	Q7px73 anopheles g	946	299.5	21.8	325	2	O15944	O15944 sarcophaga
874	304.5	22.2	258	2	Q9XY53	Q9xy53 ctenocephal	947	299.5	21.8	372	2	Q9W2C8	Q9w2c8 drosophila
875	304.5	22.2	271	2	Q7Q820	Q7q820 anopheles g	948	299.5	21.8	430	2	Q6RUJ3	Q6ruj3 trichinella
876	304.5	22.2	384	2	Q9XY63	Q9xy63 ctenocephal	949	299.5	21.8	436	1	ACRO_MOUSE	P23378 mus muscu
877	304.5	22.2	492	1	TMS2_HUMAN	O15393 homo sapien	950	299.5	21.8	465	2	Q9BJL7	Q9bjl7 trichinella
878	304.5	22.2	492	2	Q6CT73	Q6ct73 homo sapien	951	299.5	21.8	615	2	Q8I2Z5	Q8i2z5 homo sapien
879	304	22.1	268	1	CLCR_HUMAN	Q99895 homo sapien	952	299.5	21.8	974	2	Q90WD8	Q90wd8 bufo japoni
880	304	22.1	272	2	Q9XYV6	Q9xyv6 rhizopertha	953	299.5	21.8	1069	1	ENTK_MOUSE	P97435 mus muscu
881	304	22.1	375	2	Q817W8	Q817w8 dermatocent	954	299	21.8	256	2	Q6V1Q1	Q6v1q1 verticilliu
882	304	22.1	393	2	Q6RX66	Q6rx66 armigeres s	955	299	21.8	437	1	ACRO_RAT	P29293 rattus norv
883	304	22.1	400	2	Q9VCJ8	Q9vcj8 drosophila	956	298.5	21.7	235	2	Q91004	Q91004 gecko gecko
884	304	22.1	423	2	Q8BM10	Q8bm10 mus muscu	957	298.5	21.7	248	2	Q9VQ98	Q9vq98 drosophila
885	304	22.1	543	2	Q9BU99	Q9bu99 homo sapien	958	298.5	21.7	249	1	MCT1_CANFA	P21842 canis fami
886	304	22.1	562	1	TPA_HUMAN	P00750 homo sapien	959	298.5	21.7	350	2	Q7QKX0	Q7qky0 anopheles g
887	304	22.1	589	2	Q6PFA5	Q6pfa5 homo sapien	960	298.5	21.7	407	1	FAT_BOVIN	P22457 bos taurus
888	304	22.1	685	2	Q9Z338	Q9z338 mus muscu	961	298.5	21.7	433	2	Q8T3A2	Q8t3a2 ciona intes
889	304	22.1	1379	2	Q9V4N6	Q9v4n6 drosophila	962	298.5	21.7	733	2	Q9VTX9	Q9vtx9 drosophila
890	304	22.1	1397	2	Q7XQO9	Q7xqg9 drosophila	963	298	21.7	235	2	Q28731	Q28731 oryctolagus
891	303.5	22.1	240	2	Q7SYQ8	Q7syq8 xenopus lae	964	298	21.7	255	2	O18435	O18435 helicoverpa
892	303.5	22.1	244	1	MCT2_MOUSE	P15119 mus muscu	965	298	21.7	268	2	Q8T4T4	Q8t4t4 aedes aegypt
893	303.5	22.1	246	1	MCT4_RAT	P97592 rattus norv	966	298	21.7	348	2	Q86WS5	Q86ws5 homo sapien
894	303.5	22.1	278	2	Q7Q492	Q7q492 anopheles g	967	297.5	21.7	254	2	Q76520	Q76520 stomoxys ca
895	303.5	22.1	309	2	Q27083	Q27083 tachypleus	968	297.5	21.7	256	2	Q6MJY6	Q6mly6 bdellovibri
896	303.5	22.1	603	1	CFAI_MOUSE	Q61129 mus muscu	969	297.5	21.7	269	2	Q6AZF9	Q6azf9 xenopus lae
897	303.5	22.1	761	2	Q99JC8	Q99jc8 rattus norv	970	297.5	21.7	277	2	Q8IQ10	Q8iq10 drosophila
898	303	22.1	246	1	MCT2_SHEEP	P79204 ovis aries	971	297.5	21.7	293	2	Q7Q8F9	Q7q8f9 anopheles g
899	303	22.1	259	2	Q6JP95	Q6jpf95 neodipron	972	297.5	21.7	408	2	Q9VW19	Q9vw19 drosophila
900	302.5	22.0	119	2	Q9NR68	Q9nr68 homo sapien	973	297.5	21.7	435	1	SNAK_DROME	P05049 drosophila
901	302.5	22.0	223	2	Q9VBY4	Q9vby4 drosophila	974	297.5	21.7	472	2	Q7QI82	Q7qi82 anopheles g
902	302.5	22.0	273	1	TRY6_ANOGA	P35040 anopheles g	975	297.5	21.7	486	2	Q7PX74	Q7px74 anopheles g
903	302.5	22.0	1004	2	P79953	P79953 xenopus lae	976	297.5	21.7	519	2	Q8T3A3	Q8t3a3 ciona intes
904	302.5	22.0	1113	1	COR1_MOUSE	Q92319 mus muscu	977	297.5	21.7	616	2	Q97507	Q97507 sus scrofa
905	302	22.0	247	2	Q6T376	Q6t376 eisenia foe	978	297	21.6	237	1	TRYP_ASTFL	P00765 astacus flu
906	302	22.0	255	1	TRY4_LUCCU	P35044 lucilia cup	979	297	21.6	247	1	MCT5_MOUSE	P21844 mus muscu
907	302	22.0	268	2	Q9W7Q2	Q9w7q2 paralichthy	980	297	21.6	256	2	Q9XY51	Q9xy51 ctenocephal

981	297	21.6	268	2	Q9BIG0	Q9bi90 aedes aegypt	1054	291.5	21.2	270	2	Q7Q5A6	Q7q5a6 anopheles g
982	297	21.6	352	2	Q8IRX5	Q8irx5 drosophila	1055	291	21.2	239	2	Q6LCU4	Q6lcu4 lumbricus r
983	297	21.6	384	2	Q6UWB4	Q6uwb4 homo sapien	1056	291	21.2	271	2	Q54213	Q54213 streptomyce
984	297	21.6	369	2	Q6AXZ6	Q6axz6 rattus norv	1057	291	21.2	436	1	HEPS_MOUSE	Q35453 mus musculu
985	297	21.6	454	1	TMS3_HUMAN	P57727 homo sapien	1058	291	21.2	678	2	Q9JJS8	Q9jjs8 rattus norv
986	297	21.6	477	1	UR11_DESRO	P98119 desmodus ro	1059	290.5	21.1	483	2	Q7PKJ7	Q7pkj7 anopheles g
987	296.5	21.6	248	1	GRAB_MOUSE	P08863 mus musculu	1060	290.5	21.1	681	2	Q7Q554	Q7q554 anopheles g
988	296.5	21.6	270	1	EL3B_HUMAN	P08861 homo sapien	1061	290	21.1	149	2	Q6DTY8	Q6dty8 hypophthalm
989	296.5	21.6	272	2	Q7VJN3	Q7vxn3 drosophila	1062	290	21.1	256	1	HYPB_HYPLI	P35588 hypoderma l
990	296.5	21.6	273	2	Q7VJN3	Q7jyn3 drosophila	1063	290	21.1	257	2	Q27440	Q27440 aedes aegypt
991	296.5	21.6	581	2	Q960I5	Q960i5 drosophila	1064	290	21.1	390	2	Q8I927	Q8i927 hyphantria
992	296.5	21.6	1047	2	Q9VZH2	Q9vzh2 drosophila	1065	289.5	21.1	246	2	Q9BLI7	Q9bli7 lumbricus r
993	296	21.5	265	2	Q74696	Q74696 phaesophaer	1066	289.5	21.1	248	1	GRAG_MOUSE	P13366 mus musculu
994	296	21.5	279	2	Q9QZ74	Q9qz74 rattus norv	1067	289.5	21.1	257	2	Q6R560	Q6r560 ostrinia nu
995	296	21.5	281	2	Q76898	Q76898 drosophila	1068	289.5	21.1	317	2	Q8K417	Q8k417 mus musculu
996	296	21.5	314	2	Q6RUT2	Q6rut2 mus musculu	1069	289	21.0	260	2	Q7RTY3	Q7rty3 homo sapien
997	296	21.5	318	2	Q8OUR4	Q8our4 mus musculu	1070	289	21.0	278	2	Q7QHS0	Q7qhs0 anopheles g
998	295.5	21.5	239	2	Q9GME0	Q9gme0 ornithorhyn	1071	289	21.0	339	2	Q9QX91	Q9qx91 rattus norv
999	295.5	21.5	239	2	Q9I218	Q9i218 oncorhynch	1072	289	21.0	366	2	Q9QX85	Q9qx85 rattus norv
1000	295.5	21.5	270	2	Q9VRS4	Q9vrs4 drosophila	1073	289	21.0	376	1	FA10_TROCA	P81428 tropidochis
1001	295.5	21.5	433	1	UROK_MOUSE	P06869 mus musculu	1074	289	21.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1002	295.5	21.5	449	2	Q9VDU8	Q9vdu8 drosophila	1075	289	21.0	541	2	Q9QX90	Q9qx90 rattus norv
1003	295.5	21.5	453	2	Q6ZMC3	Q6zmc3 homo sapien	1076	289	21.0	583	1	CFAL_HUMAN	P05156 homo sapien
1004	295	21.5	260	2	Q9V6P6	Q9v6p6 drosophila	1077	289	21.0	623	2	Q9JJP3	Q9jjp3 rattus norv
1005	295	21.5	267	2	Q6DGM4	Q6dgm4 brachydanio	1078	289	21.0	643	2	Q9QX84	Q9qx84 rattus norv
1006	295	21.5	268	2	Q8T4T5	Q8t4t5 aedes aegypt	1079	288.5	21.0	255	2	Q9XY62	Q9xy62 ctenocephal
1007	295	21.5	269	2	Q95KW7	Q95kw7 bos taurus	1080	288.5	21.0	264	2	Q7Q290	Q7q290 anopheles g
1008	295	21.5	358	2	Q45029	Q45029 drosophila	1081	288.5	21.0	315	2	Q8IRR3	Q8irr3 drosophila
1009	295	21.5	553	2	Q6P7I9	Q6p7i9 xenopus lae	1082	288.5	21.0	317	2	Q8K4D1	Q8k4d1 mus musculu
1010	294.5	21.4	244	2	Q816N3	Q816n3 eisenia foe	1083	288.5	21.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1011	294.5	21.4	575	2	Q6IE57	Q6ie57 rattus norv	1084	288.5	21.0	442	2	Q804X1	Q804x1 fugu rubrip
1012	294	21.4	247	2	Q81E88	Q81e88 drosophila	1085	288.5	21.0	1047	2	Q24019	Q24019 drosophila
1013	294	21.4	259	2	Q9XY61	Q9xy61 ctenocephal	1086	288	21.0	257	2	Q9NB49	Q9nb49 aedes aegypt
1014	294	21.4	265	2	Q9VHF8	Q9vhf8 drosophila	1087	288	21.0	261	2	Q8IRE1	Q8ire1 drosophila
1015	294	21.4	271	2	Q9CTK2	Q9ctk2 culex quinq	1088	288	21.0	405	2	Q8MZM7	Q8mzm7 anopheles g
1016	294	21.4	283	2	Q25394	Q25394 lumbricus r	1089	288	21.0	405	2	Q7PGY0	Q7pgy0 anopheles g
1017	294	21.4	283	2	Q8ITU7	Q8itu7 lumbricus r	1090	288	21.0	421	2	Q60491	Q60491 cavia porce
1018	294	21.4	293	2	Q725A4	Q725a4 homo sapien	1091	288	21.0	730	2	Q6Q1Q8	Q6qlq8 gallus gall
1019	294	21.4	303	2	Q76900	Q76900 drosophila	1092	287.5	20.9	234	2	Q90244	Q90244 acipenser t
1020	293.5	21.4	246	2	Q6IE10	Q6ie10 rattus norv	1093	287.5	20.9	244	2	Q6T375	Q6t375 eisenia foe
1021	293.5	21.4	256	2	Q9XY11	Q9xy11 rhyzopertha	1094	287.5	20.9	249	2	Q7KR00	Q7krd0 drosophila
1022	293.5	21.4	257	2	Q7Z0G1	Q7z0g1 phlebotomus	1095	287.5	20.9	472	2	Q6IGB2	Q6igb2 drosophila
1023	293.5	21.4	302	2	Q8SYZ7	Q8syz7 drosophila	1096	287.5	20.9	603	1	FA12_CAVPO	Q63962 cavia porce
1024	293.5	21.4	302	2	Q9W586	Q9w586 drosophila	1097	287.5	20.9	845	2	Q63ZQ6	Q63zq6 xenopus lae
1025	293.5	21.4	431	1	UROK_HUMAN	P00749 homo sapien	1098	287	20.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1026	293.5	21.4	845	2	Q6GR54	Q6gr54 xenopus lae	1099	287	20.9	244	2	Q6LAW0	Q6lam0 homo sapien
1027	293	21.3	246	2	Q9R2C8	Q9r2c8 rattus norv	1100	287	20.9	256	2	Q25081	Q25081 hypoderma l
1028	293	21.3	247	1	MCT3_RAT	P50339 rattus norv	1101	287	20.9	268	2	Q8T4T3	Q8t4t3 aedes aegypt
1029	293	21.3	265	1	SER1_DROME	P17205 drosophila	1102	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1030	293	21.3	268	2	Q16900	Q16900 aedes aegypt	1103	287	20.9	416	2	Q86T26	Q86t26 homo sapien
1031	293	21.3	268	2	Q8N0R8	Q8n0r8 aedes aegypt	1104	287	20.9	422	1	DES1_HUMAN	Q9ul52 homo sapien
1032	293	21.3	277	2	Q9VPN8	Q9vpn8 drosophila	1105	287	20.9	423	2	Q6UW31	Q6uw31 homo sapien
1033	293	21.3	278	2	Q8WQ02	Q8wq02 drosophila	1106	287	20.9	481	1	FA10_MOUSE	Q88947 mus musculu
1034	293	21.3	301	2	Q7Q6U2	Q7q6u2 anopheles g	1107	287	20.9	581	2	FA10_MOUSE	Q81925 hyphantria
1035	293	21.3	427	2	Q6Y2X4	Q6y2x4 manduca sex	1108	286.5	20.9	220	2	CTR2_VESCR	P00769 vespa crabr
1036	293	21.3	433	1	UROK_PAPCY	P16227 papio cynoc	1109	286.5	20.9	220	2	Q7QM61	Q7qm61 anopheles g
1037	293	21.3	777	2	Q8CAN9	Q8can9 mus musculu	1110	286.5	20.9	376	2	Q7PTP7	Q7ptp7 anopheles g
1038	293	21.3	855	1	ST14_MOUSE	P56677 mus musculu	1111	286.5	20.9	425	2	Q7PZ85	Q7pzb5 anopheles g
1039	292.5	21.3	235	2	Q90387	Q90387 cynops pyrr	1112	286	20.8	235	2	Q6XGZ4	Q6xgz4 homo sapien
1040	292.5	21.3	236	2	Q9Z1H1	Q9z1h1 mus musculu	1113	286	20.8	254	1	CTRL_HALRU	P35003 haliois ru
1041	292.5	21.3	390	2	Q8MP08	Q8mp08 bombyx mori	1114	286	20.8	272	2	Q7Q483	Q7q483 anopheles g
1042	292.5	21.3	469	2	Q9GMD9	Q9gmd9 ornithorhyn	1115	286	20.8	416	2	Q8BZ13	Q8bz13 mus musculu
1043	292	21.3	257	2	Q8T639	Q8t639 aedes aegypt	1116	286	20.8	416	2	Q8BZ30	Q8bz30 mus musculu
1044	292	21.3	268	1	CLCR_RAT	P55091 rattus norv	1117	286	20.8	443	2	Q8JHC9	Q8jhc9 brachydanio
1045	292	21.3	270	2	Q8T4A8	Q8t4a8 drosophila	1118	286	20.8	667	2	Q9BJM1	Q9bjm1 trichinella
1046	292	21.3	276	2	Q97398	Q97398 phaeden coc	1119	285.5	20.8	175	2	Q6PLJ9	Q6plj9 squilla ora
1047	292	21.3	332	2	Q8SYS8	Q8sys8 drosophila	1120	285.5	20.8	248	1	MCT8_RAT	P97594 rattus norv
1048	292	21.3	413	2	Q8T9T2	Q8t9t2 aedes aegypt	1121	285.5	20.8	270	1	EL3A_HUMAN	P09093 homo sapien
1049	292	21.3	475	2	Q804W9	Q804w9 fugu rubrip	1122	285.5	20.8	270	2	Q96QL8	Q96ql8 homo sapien
1050	292	21.3	688	2	Q868H6	Q868h6 branchiosco	1123	285.5	20.8	270	2	Q91039	Q91039 gadus morhu
1051	291.5	21.2	216	1	CTR2_VESOR	P00768 vespa orien	1124	285.5	20.8	289	2	Q8MR67	Q8mr67 drosophila
1052	291.5	21.2	235	2	Q9Z1D3	Q9z1d3 rattus norv	1125	285.5	20.8	290	2	Q9VRT2	Q9vrt2 drosophila
1053	291.5	21.2	258	2	Q9NBC9	Q9nbc9 glossina mo	1126	285	20.7	470	2	Q8T3A1	Q8t3a1 ciona intes

1127	284.5	20.7	172	2	Q6T776	Q6t776 homo sapien	1200	277	20.2	273	2	Q9VKA8	Q9vka8 drosophila
1128	284.5	20.7	245	2	Q6DKQ3	P6dkq3 eisenia foe	1201	277	20.2	398	2	Q8Mkp4	Q8mkp4 drosophila
1129	284.5	20.7	253	1	CAC3_BOVIN	P5805 bos taurus	1202	277	20.2	1629	2	Q9V513	Q9v513 drosophila
1130	284.5	20.7	564	2	Q7RTZ1	Q7rtz1 homo sapien	1203	277	20.2	1674	2	Q8SY35	Q8sy35 drosophila
1131	284	20.7	235	2	Q6BAR4	Q6bar4 bos taurus	1204	276.5	20.1	257	2	Q97099	Q97099 anopheles d
1132	284	20.7	243	2	Q01309	Q01309 botryllus s	1205	276.5	20.1	262	2	Q9V5J2	Q9va52 drosophila
1133	284	20.7	257	2	Q86PL8	Q86pl8 aedes aegypt	1206	276	20.1	254	1	PRN3_MOUSE	Q61096 mus musculus
1134	283.5	20.6	268	2	Q9XY56	Q9xy56 ctenocephal	1207	276	20.1	257	2	Q818E4	Q818e4 ochlerotatu
1135	283.5	20.6	707	2	Q8QGV0	Q8qgv0 cyprinus ca	1208	276	20.1	271	1	S24D_ANOGA	Q17004 anopheles g
1136	283	20.6	247	1	TRYP_SIMVI	P35048 simulum vi	1209	276	20.1	300	2	Q7Q6U1	Q7q6u1 anopheles g
1137	283	20.6	320	2	Q7OKL3	Q7okl3 anopheles g	1210	276	20.1	302	2	Q9VCJ0	Q9vcj0 drosophila
1138	283	20.6	382	2	Q76HL1	Q76hl1 mus musculu	1211	276	20.1	376	1	FA10_HOPST	P83370 hoplocephal
1139	282.5	20.6	245	2	Q7FPUQ	Q7fpq0 anopheles g	1212	276	20.1	488	1	FA10_HUMAN	P00742 homo sapien
1140	282.5	20.6	246	2	Q817P0	Q817p0 lumbricus b	1213	276	20.1	717	2	Q8AXR1	Q8axr1 xenopus lae
1141	282.5	20.6	267	2	Q9VLF5	Q9vlf5 drosophila	1214	275.5	20.1	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1142	282.5	20.6	269	2	Q9V929	Q9v929 drosophila	1215	275.5	20.1	249	2	Q8C1Q8	Q8clq8 mus musculus
1143	282.5	20.6	424	2	Q6R558	Q6r558 ostrinia nu	1216	275.5	20.1	256	2	Q818E5	Q818e5 ochlerotatu
1144	282.5	20.6	687	2	Q69DK8	Q69dk8 sus scrofa	1217	275.5	20.1	258	2	Q6NLM5	Q6nlm5 drosophila
1145	282	20.5	258	2	Q6JKF3	Q6jkf3 neodiprion	1218	275.5	20.1	262	2	Q9V5X9	Q9v5x9 drosophila
1146	282	20.5	259	2	Q186Q0	Q186q0 drosophila	1219	275.5	20.1	296	2	Q8R9U6	Q8r9u6 aedes aegypt
1147	282	20.5	263	2	Q9NB92	Q9nb92 agrotis ips	1220	275	20.0	237	2	Q17035	Q17035 anopheles g
1148	282	20.5	416	1	HEPS_RAT	Q05511 rattus norv	1221	275	20.0	256	2	Q25082	Q25082 hypodermat
1149	282	20.5	686	2	Q6O1Q9	Q6qlq9 gallus gall	1222	275	20.0	260	2	Q9VSJ1	Q9vsj1 drosophila
1150	282	20.5	688	2	Q858H4	Q858h4 branchiosteo	1223	275	20.0	262	2	Q7ZOG3	Q7z0g3 phlebotomus
1151	281.5	20.5	258	2	Q9NGY6	Q9ngy6 aedes aegypt	1224	275	20.0	284	2	Q8AXQ8	Q8axq8 xenopus lae
1152	281.5	20.5	291	2	Q8MLC5	Q8mlc5 drosophila	1225	275	20.0	317	2	Q7Q619	Q7q619 anopheles g
1153	281.5	20.5	388	2	Q7Z1F0	Q7z1f0 cotesia rub	1226	275	20.0	496	2	Q8CHP7	Q8chp7 cavia porce
1154	281.5	20.5	430	2	Q7PNQ4	Q7pnq4 anopheles g	1227	275	20.0	717	2	Q8AXR0	Q8axr0 xenopus lae
1155	281	20.5	262	2	Q7Z0G5	Q7z0g5 phlebotomus	1228	274.5	20.0	695	1	CASP_MESAU	P15156 mesocricetu
1156	281	20.5	267	2	Q9VA66	Q9va66 drosophila	1229	274	19.9	87	2	Q9CQ78	Q9cq78 m mus muscu
1157	281	20.5	329	2	Q7QB72	Q7qb72 anopheles g	1230	274	19.9	265	2	Q9VHF7	Q9vhf7 drosophila
1158	281	20.5	564	2	Q8MKB1	Q8mbk1 oryctolagus	1231	273	19.9	125	2	Q86V18	Q86v18 homo sapien
1159	280.5	20.4	227	2	Q7PHB4	Q7phb4 anopheles g	1232	273	19.9	247	1	MCT8_MOUSE	P43430 mus musculus
1160	280.5	20.4	255	2	Q97100	Q97100 anopheles d	1233	273	19.9	254	2	Q8K597	Q8k597 rattus norv
1161	280.5	20.4	370	2	Q7Q0N6	Q7q0n6 anopheles g	1234	273	19.9	257	2	Q818E3	Q818e3 aedes polyn
1162	280.5	20.4	365	2	Q9Y1K7	Q9y1k7 anopheles g	1235	273	19.9	258	1	TRYU_DROER	P54629 drosophila
1163	280.5	20.4	410	2	Q7QJ44	Q7qj44 anopheles g	1236	273	19.9	265	2	Q17800	Q17800 caenorhabdi
1164	280.5	20.4	424	2	Q6R559	Q6r559 ostrinia nu	1237	273	19.9	377	2	Q9VEM8	Q9vem8 drosophila
1165	280.5	20.4	439	2	Q8BHM9	Q8bhm9 m mus muscu	1238	273	19.9	388	2	P79343	P79343 bos taurus
1166	280	20.4	241	1	TRYP_PQB3	P7pqb3 anopheles g	1239	272.5	19.8	258	2	Q9GME1	Q9gme1 ornithorhyn
1167	280	20.4	254	1	TRYP_SARBU	P51588 sarcophaga	1240	272.5	19.8	262	1	TRYU_DROME	P42279 drosophila
1168	280	20.4	267	2	Q8SYK8	Q8syk8 drosophila	1241	272.5	19.8	282	2	Q7PX30	Q7px30 anopheles g
1169	280	20.4	271	2	Q9V4W5	Q9v4w5 drosophila	1242	272.5	19.8	287	2	Q9VTV2	Q9vrv2 drosophila
1170	280	20.4	282	2	Q25395	Q25395 lumbricus r	1243	272.5	19.8	432	1	UROK_RAT	P29598 rattus norv
1171	280	20.4	336	2	Q7RTY5	Q7rt5 homo sapien	1244	272.5	19.8	537	2	Q804W8	Q804w8 fugu rubrip
1172	280	20.4	420	2	Q61E14	Q6ie14 rattus norv	1245	272.5	19.8	978	2	P91777	P91777 pacifastacu
1173	280	20.4	494	2	Q9VJD7	Q9vjd7 drosophila	1246	272	19.8	243	2	O01310	O01310 botryllus s
1174	279.5	20.3	745	2	Q9PVI3	Q9pyv3 cyprinus ca	1247	272	19.8	262	1	TRYT_DROME	P42278 drosophila
1175	279	20.3	242	2	Q6T374	Q6t374 eisenia foe	1248	272	19.8	262	2	Q9V5Y0	Q9v5y0 drosophila
1176	279	20.3	248	2	Q920S1	Q920s1 mus musculu	1249	272	19.8	288	2	Q8SX49	Q8sx49 drosophila
1177	279	20.3	267	2	Q9VA67	Q9va67 drosophila	1250	272	19.8	475	1	FA10_CHICK	P25155 gallus gall
1178	279	20.3	280	1	TRYZ_DROME	P42280 drosophila	1251	272	19.8	492	2	Q7Z155	Q7z155 chiromantes
1179	279	20.3	280	2	Q9V5X8	Q9v5x8 drosophila	1252	272	19.8	688	1	C1S_HUMAN	P09871 homo sapien
1180	279	20.3	319	2	Q9VRS5	Q9vrs5 drosophila	1253	272	19.8	688	2	Q8CFG8	Q8cf8 mus musculu
1181	279	20.3	329	2	Q9GL10	Q9gl10 ovis aries	1254	271.5	19.8	250	2	Q7PWE3	Q7pwe3 anopheles g
1182	279	20.3	385	2	Q25101	Q25101 herdmania m	1255	271.5	19.8	257	2	Q8IS83	Q8is83 aedes albop
1183	279	20.3	694	2	Q8R099	Q8r099 mus musculu	1256	271.5	19.8	262	2	Q9NB91	Q9nb91 agrotis ips
1184	279	20.3	694	2	Q6P6T1	Q6p6t1 rattus norv	1257	271.5	19.8	267	2	Q9V942	Q9v942 drosophila
1185	279	20.3	721	2	Q7ZT69	Q7zt69 lampetra ja	1258	271.5	19.8	272	2	Q9VRS3	Q9vrs3 drosophila
1186	278.5	20.3	269	2	Q7PWT2	Q7pwt2 anopheles g	1259	271.5	19.8	833	2	Q96442	Q96442 strongyloce
1187	278.5	20.3	326	2	Q7ZZ80	Q7zz80 brachydanio	1260	271	19.7	247	2	O70164	O70164 mesocricetu
1188	278.5	20.3	330	2	Q61E62	Q6ie62 rattus norv	1261	271	19.7	253	2	Q9XY50	Q9xy50 stenoccephal
1189	278.5	20.3	593	1	FA12_BOVIN	P98140 bos taurus	1262	271	19.7	275	2	Q7Z0B4	Q7z0b4 stomoxys ca
1190	278	20.2	239	2	Q9NKC5	Q9nkc5 drosophila	1263	271	19.7	1801	2	Q8WSJ2	Q8wsj2 bombyx mori
1191	278	20.2	474	2	Q7FZH7	Q7fzh7 anopheles g	1264	270.5	19.7	219	2	Q7PJ75	Q7pj75 anopheles g
1192	278	20.2	490	1	FA10_RABIT	O19045 oryctolagus	1265	270.5	19.7	245	2	Q8IE56	Q8ie56 rattus norv
1193	278	20.2	501	2	Q7QCVO	Q7qcvo anopheles g	1266	270.5	19.7	248	1	GRAD_MOUSE	P11033 mus musculus
1194	277.5	20.2	245	2	Q9BLI8	Q9bli8 lumbricus r	1267	270.5	19.7	256	1	TRYB_MANSE	P35046 manduca sex
1195	277.5	20.2	266	2	Q24091	Q24091 drosophila	1268	270.5	19.7	420	2	Q7Q235	Q7q235 anopheles g
1196	277.5	20.2	271	2	Q76519	Q76519 stomoxys ca	1269	270	19.7	253	2	O18440	O18440 helicoverpa
1197	277.5	20.2	845	2	Q9DGR1	Q9dgr1 xenopus lae	1270	270	19.7	297	2	Q7Q6U4	Q7q6u4 anopheles g
1198	277	20.2	252	2	Q76498	O76498 diaprepes a	1271	270	19.7	694	2	Q70542	Q70542 rattus norv
1199	277	20.2	272	2	Q82KGO	Q82kgo streptomyce	1272	269.5	19.6	248	1	GR22_RAT	Q06606 rattus norv

1273	269.5	19.6	339	2	Q6BDA8	Q6bda8 penaeus jap	1346	262	19.1	266	2	Q9VMX7	Q9vmx7 drosophila
1274	269	19.6	235	2	Q9GTk7	Q9gtk7 aedes albop	1347	262	19.1	272	2	Q8SZG4	Q8szg4 drosophila
1275	269	19.6	244	2	Q8MWR5	Q8mwr5 dermatophag	1348	262	19.1	390	2	Q7PVQ3	Q7pvq3 anopheles g
1276	269	19.6	375	2	Q9NAS8	Q9nas8 anopheles g	1349	262	19.1	427	2	Q7Q6T1	Q7q6t1 anopheles g
1277	269	19.6	389	2	Q7QGN4	Q7qgn4 anopheles g	1350	262	19.1	504	2	Q6PGW7	Q6pgw7 brachydanio
1278	269	19.6	445	2	Q7Q9S6	Q7q9s6 anopheles g	1351	261.5	19.0	259	2	Q4S048	Q4s048 anopheles g
1279	269	19.6	261.6	1	NDL_DROME	P98159 drosophila	1352	261.5	19.0	262	2	Q7PX38	Q7px38 anopheles g
1280	268.5	19.5	245	2	Q6DF10	Q6df10 xenopus tro	1353	261.5	19.0	297	2	Q7QNM1	Q7qnm1 anopheles g
1281	268.5	19.5	256	2	Q9Y842	Q9y842 metarhizium	1354	261.5	19.0	324	2	Q6BD08	Q6bd08 drosophila
1282	268.5	19.5	260	2	Q7Z0G4	Q7z0g4 phlebotomus	1355	261.5	19.0	366	2	Q70170	Q70170 mus musculus
1283	268.5	19.5	261	2	Q00344	Q00344 cochllobolus	1356	261.5	19.0	421	1	ACRO_HUMAN	P10323 homo sapien
1284	268.5	19.5	262	1	TRVY_DROER	P54628 drosophila	1357	261.5	19.0	669	2	Q7PWE1	Q7pwe1 anopheles g
1285	268.5	19.5	275	2	Q6GUD0	Q6gud0 culicoides	1358	261	19.0	239	2	P97595	P97595 rattus norv
1286	268.5	19.5	707	2	Q70W31	Q70w31 oncorhynch	1359	261	19.0	246	2	P97611	P97611 rattus norv
1287	268	19.5	182	2	Q6PLJ6	Q6plj6 penaeus jap	1360	261	19.0	262	2	Q7QFW4	Q7qfw4 anopheles g
1288	268	19.5	256	1	PRN3_HUMAN	P24158 homo sapien	1361	261	19.0	316	2	Q9VAC2	Q9vac2 drosophila
1289	268	19.5	270	2	Q9VKA9	Q9vka9 drosophila	1362	260.5	19.0	242	1	FIBC_LUMRU	P83298 lumbricus r
1290	268	19.5	277	2	Q6WN60	Q6wn60 brachiosio	1363	260.5	19.0	242	2	Q96687	Q96687 lumbricus b
1291	267.5	19.5	249	2	Q6IEB3	Q6ieb3 rattus norv	1364	260.5	19.0	242	2	Q8MX72	Q8mx72 eisenia foe
1292	267.5	19.5	255	2	O44332	O44332 manduca sex	1365	260.5	19.0	242	2	Q6T373	Q6t373 eisenia foe
1293	267.5	19.5	280	2	Q6GLK1	Q6glk1 xenopus lae	1366	260.5	19.0	245	2	Q7PFP6	Q7pfp6 anopheles g
1294	267	19.4	182	2	Q6PLJ5	Q6plj5 neocaridina	1367	260.5	19.0	264	2	Q9VT25	Q9vt25 drosophila
1295	267	19.4	262	2	Q8SZQ7	Q8szq7 drosophila	1368	260.5	19.0	298	2	Q7PZ90	Q7pzt90 anopheles g
1296	267	19.4	271	2	Q7PIA2	Q7pia2 anopheles g	1369	260.5	19.0	688	2	Q9PVT4	Q9pvt4 xenopus lae
1297	267	19.4	388	2	Q8I926	Q8i926 hyphantria	1370	260	18.9	257	2	Q8I8E2	Q8i8e2 aedes trise
1298	266	19.4	222	2	Q7S1G2	Q7s1g2 solenopsis	1371	260	18.9	282	2	Q7PVP7	Q7pvp7 anopheles g
1299	266	19.4	252	1	TRV1_DROME	P52905 drosophila	1372	260	18.9	302	2	Q8I1G9	Q8i1g9 drosophila
1300	266	19.4	254	2	Q9XY70	Q9xy70 rhizopertha	1373	259.5	18.9	252	2	Q61388	Q61388 mus musculu
1301	266	19.4	266	2	Q9VEM9	Q9vem9 drosophila	1374	259.5	18.9	275	2	Q66UC8	Q66uc8 culicoides
1302	266	19.4	273	2	Q8MTU7	Q8mtu7 drosophila	1375	259.5	18.9	309	2	Q6DH44	Q6dh44 brachydanio
1303	266	19.4	477	2	Q8MLC4	Q8mlc4 drosophila	1376	259.5	18.9	324	2	Q6BD05	Q6bd05 drosophila
1304	266	19.4	200	2	Q9GRG2	Q9grg2 tenebrio mo	1377	259.5	18.9	324	2	Q6BD06	Q6bd06 drosophila
1305	266	19.4	506	2	Q7PR64	Q7pr64 anopheles g	1378	259.5	18.9	324	2	Q6BD16	Q6bd16 drosophila
1306	265.5	19.3	322	2	Q6BD03	Q6bd03 drosophila	1379	259.5	18.9	511	2	Q9VZH5	Q9vzh5 drosophila
1307	265.5	19.3	434	2	Q9V7S7	Q9v7s7 drosophila	1380	259.5	18.9	546	2	Q8SXG6	Q8sxg6 drosophila
1308	265.5	19.3	444	2	Q9V4W6	Q9v4w6 drosophila	1381	259	18.9	248	1	GRAE_MOUSE	P08884 mus musculu
1309	265	19.3	251	2	Q9VQ99	Q9vq99 drosophila	1382	259	18.9	263	2	Q9V5X7	Q9v5x7 drosophila
1310	265	19.3	277	2	Q7QKR3	Q7qkr3 anopheles g	1383	259	18.9	279	2	Q7QE41	Q7qe41 anopheles g
1311	265	19.3	322	2	Q98G16	Q98g16 rhizobium l	1384	258.5	18.8	167	2	Q6URK9	Q6urk9 bothrops ja
1312	265	19.3	415	1	ACRO_PIG	P08001 sus scrofa	1385	258.5	18.8	248	2	Q6IE58	Q6ie58 rattus norv
1313	265	19.3	415	2	Q29015	Q29015 sus sp. pre	1386	258.5	18.8	285	2	Q69997	Q69997 streptomyce
1314	264.5	19.3	247	2	Q7PFF5	Q7pff5 anopheles g	1387	258.5	18.8	459	2	Q9V4W7	Q9v4w7 drosophila
1315	264.5	19.3	248	1	TRYP_FUSOX	P35049 fusarium ox	1388	258.5	18.8	522	2	Q8MQM9	Q8mqm9 drosophila
1316	264.5	19.3	256	1	TRYP_MANSE	P35045 manduca sex	1389	258.5	18.8	1089	2	Q8T3A0	Q8t3a0 ciona intes
1317	264.5	19.3	264	1	VDP_BOMMO	Q07943 bombyx mori	1390	258	18.8	267	2	Q9GP27	Q9gp27 drosophila
1318	264.5	19.3	369	2	Q6O6S3	Q6o6s3 callinectes	1391	258	18.8	269	2	Q7Q515	Q7q515 anopheles g
1319	264.5	19.3	719	2	Q9PVT2	Q9pvt2 triakis scy	1392	258	18.8	277	2	Q7PG95	Q7pg95 anopheles g
1320	264	19.2	176	2	Q15098	Q15098 homo sapien	1393	258	18.8	295	2	Q18445	Q18445 helicoverpa
1321	264	19.2	180	2	Q96A30	Q96a30 homo sapien	1394	258	18.8	300	2	Q7Q6U0	Q7q6u0 anopheles g
1322	264	19.2	301	2	Q7PXG5	Q7pxg5 anopheles g	1395	258	18.8	352	2	Q7KVM3	Q7kvm3 drosophila
1323	263.5	19.2	251	1	CAP7_HUMAN	P20160 homo sapien	1396	258	18.8	387	2	Q7RTV4	Q7rtv4 homo sapien
1324	263.5	19.2	256	2	Q6R561	Q6r561 ostrinia nu	1397	257.5	18.7	196	2	Q6VFC8	Q6vfc8 anopheles g
1325	263.5	19.2	258	2	Q9VMX9	Q9vmx9 drosophila	1398	257.5	18.7	248	2	Q6IE09	Q6ie09 rattus norv
1326	263.5	19.2	281	1	TRVY_DROER	P54630 drosophila	1399	257.5	18.7	254	2	Q0I136	Q0i136 metarhizium
1327	263.5	19.2	421	2	Q6ICK2	Q6ick2 homo sapien	1400	257.5	18.7	254	2	Q97098	Q97098 anopheles a
1328	263	19.1	180	2	Q6T775	Q6t775 homo sapien	1401	257.5	18.7	255	2	Q961Y0	Q961y0 galleria me
1329	263	19.1	241	2	Q7Q5E4	Q7q5e4 anopheles g	1402	257.5	18.7	259	2	Q97097	Q97097 anopheles a
1330	263	19.1	248	2	Q8IRE2	Q8ire2 drosophila	1403	257.5	18.7	274	2	Q6DHC9	Q6dhc9 brachydanio
1331	263	19.1	257	2	Q9VZT0	Q9vzt0 drosophila	1404	257.5	18.7	286	2	Q96900	Q96900 scolopendra
1332	263	19.1	272	2	Q7QIH5	Q7qih5 anopheles g	1405	257.5	18.7	326	2	Q7RTY6	Q7rty6 homo sapien
1333	263	19.1	289	2	Q945T9	Q945t9 phytophthor	1406	257	18.7	237	2	Q6LBN2	Q6lbn2 homo sapien
1334	263	19.1	295	2	Q9N6C6	Q9n6c6 heliothis z	1407	257	18.7	256	2	O18441	O18441 helicoverpa
1335	263	19.1	300	2	Q8IN70	Q8in70 drosophila	1408	257	18.7	284	2	Q8MLV8	Q8mlv8 drosophila
1336	263	19.1	405	2	Q8SZ60	Q8sz60 drosophila	1409	257	18.7	417	2	Q6JE90	Q6je90 homo sapien
1337	263	19.1	467	2	Q6IT09	Q6it09 pseudonaja	1410	256.5	18.7	196	2	Q6VF00	Q6vfd0 anopheles g
1338	262.5	19.1	256	1	TRVC_MANSE	P35047 manduca sex	1411	256.5	18.7	235	1	TRYD_HUMAN	Q9bzj3 homo sapien
1339	262.5	19.1	271	2	Q9VRS6	Q9vrs6 drosophila	1412	256.5	18.7	242	2	Q6NTB8	Q6ntb8 homo sapien
1340	262.5	19.1	281	2	Q8SYB5	Q8syb5 drosophila	1413	256.5	18.7	464	2	Q9NK82	Q9nk82 drosophila
1341	262.5	19.1	433	2	Q9QWF2	Q9qwf2 rattus sp.	1414	256	18.6	245	2	Q9XY47	Q9xy47 ctienocephal
1342	262.5	19.1	778	2	Q9V519	Q9v519 drosophila	1415	256	18.6	265	2	Q9XY55	Q9xy55 ctienocephal
1343	262	19.1	108	2	Q9CVU2	Q9cvu2 mus musculu	1416	256	18.6	267	2	Q9VRU0	Q9vru0 drosophila
1344	262	19.1	183	2	Q6ELJ7	Q6elj7 fenneropena	1417	256	18.6	282	2	Q7QCX2	Q7qcx2 anopheles g
1345	262	19.1	245	2	Q9VQ97	Q9vq97 drosophila	1418	256	18.6	403	2	Q9Ksq6	Q9ksq6 vibrio chol

1419	256	18.6	421	2	Q6ZMR5	Q6zmr5 homo sapien
1420	256	18.6	463	2	Q6IT10	Q6it10 pseudonaja
1421	255.5	18.6	240	2	Q6XII43	Q6xi43 drosophila
1422	255.5	18.6	254	2	Q6I8436	Q6i8436 helicoverpa
1423	255.5	18.6	273	2	Q7Z1633	Q7z1633 dermatophag
1424	255.5	18.6	431	2	Q7PV05	Q7pv05 anopheles g
1425	255	18.6	292	2	Q7PVQ5	Q7pvq5 anopheles g
1426	255	18.6	405	2	Q7PNC3	Q7pnc3 anopheles g
1427	254.5	18.5	254	2	Q6I8434	Q6i8434 helicoverpa
1428	254.5	18.5	278	2	Q6I8434	Q6i8434 helicoverpa
1429	254.5	18.5	357	2	Q7Q092	Q7q092 anopheles g
1430	254.5	18.5	357	2	Q7Q0X6	Q7qx6 anopheles g
1431	254.5	18.5	493	2	Q7PV62	Q7pv62 anopheles g
1432	254.5	18.5	523	2	Q9V819	Q9v819 drosophila
1433	254.5	18.5	524	2	Q8MR00	Q8mr00 drosophila
1434	254.5	18.5	827	2	Q7P288	Q7p288 anopheles g
1435	254	18.5	324	2	Q6BD11	Q6bd11 drosophila
1436	254	18.5	334	2	Q9VEA0	Q9vea0 drosophila
1437	253.5	18.4	282	2	Q641D4	Q641d4 antenonomus
1438	253	18.4	242	2	Q9XY59	Q9xy59 ctenocephal
1439	253	18.4	251	2	Q9VXC9	Q9vxc9 drosophila
1440	253	18.4	253	2	Q6W741	Q6w741 pediculus h
1441	253	18.4	272	1	SER3 DROME	P17207 drosophila
1442	253	18.4	287	2	Q675S0	Q675s0 oikopleura
1443	252.5	18.4	245	2	Q7Q2Q8	Q7q2q8 anopheles g
1444	252.5	18.4	254	2	Q7Q6954	Q7q6954 laccanobia o
1445	252.5	18.4	282	2	Q8WJDI1	Q8wjdi1 canis famli
1446	252.5	18.4	324	2	Q6BD09	Q6bd09 drosophila
1447	252	18.3	235	2	Q7PRK6	Q7prk6 anopheles g
1448	252	18.3	295	2	Q18450	Q18450 helicoverpa
1449	252	18.3	301	2	Q7Q6T0	Q7q6t0 anopheles g
1450	252	18.3	400	2	Q27081	Q27081 tachypneus
1451	251.5	18.3	186	2	Q6X655	Q6x655 marmota mon
1452	251.5	18.3	266	2	Q8MLC2	Q8mlc2 drosophila
1453	251.5	18.3	267	2	Q9VGB8	Q9vgb8 drosophila
1454	251.5	18.3	276	2	Q18443	Q18443 helicoverpa
1455	251.5	18.3	318	2	Q7QC37	Q7qc37 anopheles g
1456	251.5	18.3	418	2	Q7Q529	Q7q529 anopheles g
1457	251.5	18.3	520	2	Q8ING0	Q8ing0 drosophila
1458	251	18.3	285	2	Q7Q5K4	Q7q5k4 anopheles g
1459	251	18.3	405	2	Q8WQS8	Q8wqs8 apis mellif
1460	250.5	18.2	226	2	Q6XHU4	Q6xhu4 drosophila
1461	250.5	18.2	240	2	Q7PYJ1	Q7pyj1 anopheles g
1462	250.5	18.2	268	2	Q9VT24	Q9vt24 drosophila
1463	250.5	18.2	305	2	Q8MRL2	Q8mrl2 drosophila
1464	250.5	18.2	323	2	Q76920	Q76920 drosophila
1465	250	18.2	124	2	Q8C6G5	Q8c6g5 mus musculu
1466	250	18.2	203	2	Q9NB77	Q9nb77 heliothis z
1467	250	18.2	258	2	Q9VS86	Q9vs86 drosophila
1468	250	18.2	274	2	Q8WUG0	Q8wug0 glossina fu
1469	249.5	18.2	253	2	Q18442	Q18442 helicoverpa
1470	249.5	18.2	254	2	Q18447	Q18447 helicoverpa
1471	249.5	18.2	258	2	Q7Q2P0	Q7q2p0 anopheles g
1472	249.5	18.2	269	2	Q7PWI5	Q7pwi5 anopheles g
1473	249.5	18.2	274	2	Q9VRS7	Q9vrs7 drosophila
1474	249.5	18.2	282	2	Q18655	Q18655 plodia inte
1475	249.5	18.2	327	2	Q8MS77	Q8ms77 drosophila
1476	249.5	18.2	362	2	Q6LUJ1	Q6luj1 photobacter
1477	249.5	18.2	520	2	Q8SY93	Q8sy93 drosophila
1478	249	18.1	253	2	Q9NGY5	Q9ngy5 heliothis v
1479	249	18.1	305	2	Q7Q6S4	Q7q6s4 anopheles g
1480	249	18.1	388	2	Q966V2	Q966v2 halocynthia
1481	249	18.1	714	2	Q7PWE5	Q7pwe5 anopheles g
1482	248.5	18.1	296	2	Q917I1	Q917i1 drosophila
1483	248.5	18.1	381	2	Q8MQY4	Q8mqy4 drosophila
1484	248.5	18.1	746	2	Q01654	Q01654 halocynthia
1485	248	18.0	141	2	Q6GKZ6	Q6gkz6 drosophila
1486	248	18.0	257	2	Q8IT49	Q8it49 pyrocoelia
1487	248	18.0	257	2	Q945U0	Q945u0 phytothor
1488	248	18.0	258	2	Q9VZS9	Q9vzs9 drosophila
1489	248	18.0	277	2	Q7Q4I1	Q7q4i1 anopheles g
1490	248	18.0	277	2	Q7QNM2	Q7qnm2 anopheles g
1491	248	18.0	367	2	Q7O169	Q7o169 mus musculu
1492	248	18.0	374	2	Q80YD5	Q80yd5 mus musculu
1493	248	18.0	392	2	Q9VMZ3	Q9vmz3 drosophila
1494	248	18.0	401	2	Q6LH17	Q6lhi17 photobacter
1495	247.5	18.0	260	2	Q9U4I4	Q9u4i4 plodia inte
1496	247.5	18.0	291	2	Q6V1Y9	Q6v1y9 lygus lineo
1497	247	18.0	243	2	Q7M4I3	Q7mai3 megabombus
1498	247	18.0	278	2	Q7Q8Q5	Q7q8q5 anopheles g
1499	247	18.0	350	2	Q9VCJ9	Q9vcj9 drosophila
1500	247	18.0	360	2	Q9W1X6	Q9wix6 drosophila

## ALIGNMENTS

## RESULT 1

KLKC\_HUMAN STANDARD; PRT; 248 AA.

AC Q9UKR0; Q9UKR1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)  
DE (KLK-L5) (UNQ669/PRO1303).  
GN Name-KLK12; Synonyms=KLK15;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20118156; PubMed=10652563;  
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4";  
RL Anticancer Res. 19:2843-2852 (1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;  
RT "Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5)";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepir B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130 (2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaud C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RL Genome Res. 13:2265-2270 (2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX PubMed=15057824; DOI=10.1038/nature02399;  
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E., Caenepeel S., Carrano A.V., Caciile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,

RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Layton L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Uetazewska A.,  
RA Furey T.S., DeLong P., Dickson M., Gordon D., Eichler E.B.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9UKR0-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
CC -|- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
CC subfamily.  
CC  
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CC  
CC EMBL; AF135025; AAD26426.2; -;  
CC EMBL; AF135025; AAF06065.1; -;  
CC EMBL; AF243527; AAG33365.1; -;  
CC EMBL; AY358524; AAQ88888.1; -;  
CC EMBL; AC011473; AAG23258.1; -;  
CC HSSP; P00760; 1EZX.  
CC MEROPS; S01.020; -;  
CC Genew; HGNC:6360; KLIK12.  
CC MIM; 605539; -;  
CC GO; GO:0005576; C:extracellular; NAS.  
CC GO; GO:004252; P:serine-type endopeptidase activity; NAS.  
CC GO; GO:006508; P:proteolysis and peptidolysis; NAS.  
CC InterPro; IPR009003; Pept\_Ser\_Cys.  
CC InterPro; IPR001254; Peptidase\_S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC Pfam; PF00089; Trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC SMART; SM00020; TRYPSIN\_DOM; 1.  
CC PROSITE; PS50240; TRYPSIN\_DOM; 1.  
CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
CC Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal.  
KW SIGNAL. 1 17 Potential.  
FT CHAIN 18 248 Kallikrein 12.  
FT ACT\_SITE 62 62 Charge relay system (By similarity).  
FT ACT\_SITE 108 108 Charge relay system (By similarity).  
FT ACT\_SITE 200 200 Charge relay system (By similarity).  
FT DISULFID 28 161 By similarity.  
FT DISULFID 47 63 By similarity.  
FT DISULFID 133 235 By similarity.  
FT DISULFID 140 206 By similarity.  
FT DISULFID 172 186 By similarity.  
FT DISULFID 196 222 By similarity.  
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 236 248 KYVDWRIMRN -> NSTLVGLGTSWNFNSQPP (in  
FT isoform 2).  
FT SIGNAL. 248 AA; 26733 MW; BB473E98F8BAF703 CRC64;  
SQ /FTIGSVSP\_005403.

Query Match 100.0%; Score 1374; DB 1; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.5e-102;  
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGLSIFLLCVLGLSQAATPKIFNGTEGRNSQPMQVGLFEGTSRCCGVLIDHRWLTA 60  
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTEGRNSQPMQVGLFEGTSRCCGVLIDHRWLTA 60  
QY 61 AHCSGRVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVYGASTSHEDHLRLRLPVRV 120  
DB 61 AHCSGRVWVRLGHSLSQLDWTEQIRHSGFSVTHPGVYGASTSHEDHLRLRLPVRV 120  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHNPRNPFDDLLQCLNLSIVSHATGCHVYPGRI 180  
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGIITHNPRNPFDDLLQCLNLSIVSHATGCHVYPGRI 180  
QY 181 TSNMVCAGVPGQDACQSDSGGLVCGGVLOGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240  
DB 181 TSNMVCAGVPGQDACQSDSGGLVCGGVLOGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240  
QY 241 IRMINRN 248  
DB 241 IRMINRN 248  
RESULT 2  
Q9CV76 PRELIMINARY; PRT; 234 AA.  
ID Q9CV76  
AC Q9CV76; TREMBLrel. 17, Created  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 26, Last annotation update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
DE library, clone:231008B01 product:similar to KALLIKREIN 12 (EC  
DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN S) (KLU-L5) (Fragment).  
GN Name=KLIK12;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RA The FANTOM Consortium,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
RN [5]



RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carrano A.V.,  
RT "Sequence analysis of chromosome 19q13.4";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and  
CC hippocampal plasticity.  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O60259-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O60259-2; Sequence=VSP\_005401;  
CC -!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the  
CC pancreas while isoform 2 is expressed in adult brain and  
CC hippocampus. Both forms are also found in fetal brain and  
CC placenta. Not detected in kidney, spleen, liver and lung.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
CC subfamily.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AB009849; BAA28673.1; -;  
CC EMBL; AB012761; BAA28676.1; -;  
CC EMBL; AB010780; BAA88684.1; -;  
CC EMBL; AB008390; BAA82665.1; -;  
CC EMBL; AB008927; BAA82666.1; -;  
CC EMBL; AF055982; AAD56050.1; -;  
CC EMBL; AF095742; AAD25979.1; -;  
CC EMBL; AF095743; AAD29574.1; -;  
CC EMBL; AF243527; AAG33361.1; -;  
CC EMBL; AY359036; AAG89395.1; -;  
CC EMBL; AC011473; AAG23254.1; -;  
CC HSSP; P00760; 1EZX.  
CC MEROPS; S01.244; -;  
CC Genew; HGNC:6369; KLK8.  
CC MIM; 605644;  
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.  
CC GO; GO:0007399; P:neurogenesis; TAS.  
CC InterPro; IPR009003; Pept\_Ser\_Cys.  
CC InterPro; IPR001254; Peptidase\_S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC Pfam; PF00089; Trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC PROSITE; PS00240; TRYPSIN\_DOM; 1.  
CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
CC PROSITE; PS00135; TRYPSIN\_SRR; 1.  
CC KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal; Zymogen.  
FT SIGNAL 1 28 Potential.  
FT PROPEP 29 32 By similarity.  
FT CHAIN 33 260 Neuropsin.  
FT ACT\_SITE 73 73 Charge relay system (By similarity).  
FT ACT\_SITE 120 120 Charge relay system (By similarity).  
FT ACT\_SITE 212 212 Charge relay system (By similarity).  
FT DISULFID 39 173 By similarity.  
FT DISULFID 58 74 By similarity.  
FT DISULFID 145 246 By similarity.  
FT DISULFID 152 218 By similarity.  
FT DISULFID 184 198 By similarity.  
FT DISULFID 208 233 By similarity.  
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
FT VARSPLOC 23 23 A -> AACGSLDILLTKLYAENLPCVHLNLPQWPSQPSHCPRG

FT WRSNPLPPAA (in isoform 2).  
FT /FTId=VSP\_005401.  
SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C83B660 CRC64;  
Query Match 45.9%; Score 630.5; DB 1; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.3e-42;  
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;  
QY 5 IFLLL--CVLGLSQATPKIFNGTECGRNSOPWQGLFEGTSLRCGGVLIDHRWVLTAA 61  
DB 13 MFLLLGGAWAGHSRAQEDKVLGHECQHPQWQAALFQGQLLCGGVLVGNWVLTAA 72  
QY 62 HCGSRYYVRLGEHSLSDLWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRLPVRV 120  
DB 73 HCKPKYTVRLGDHSLQNKDGPEQIPVQSIHPHCYNSDVEDHNDMLQLQDRQASL 132  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIINHPNPFPDILLCLNLISVSHATCGVYPGRI 180  
DB 133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSRENFPDITLNCVAEVKIFPKKCEDAYPGQI 192  
QY 181 TSNMVACAGVPGQDACQDGGPLVCGGVLOGLVSWGSGVPCGQDGIQGVYTIQKYVDW 240  
DB 193 TDGMVACAGSSKGADTCQDGGPLVCDALQGITSWGSDFCGRSDKFGVYTNICRYLDW 251  
QY 241 IRMIM 245  
DB 252 IKKII 256  
RESULT 4  
QIWI69 PRELIMINARY; PRT; 260 AA.  
AC QIWI69;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Kallikrein 8, isoform 1 preproprotein.  
GN Name=KLK8;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
DB EMBL; BC040887; AAH40887.1; -;





DR	InterPro; IPR001254; Peptidase S1.
DR	InterPro; IPR001314; Peptidase_SIA.
DR	Pfam; PF00089; Trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
KW	Serine protease; Signal; Zymogen.
FT	SIGNAL 1 28 Potential.
FT	PROPEP 29 32
FT	CHAIN 33 260
FT	ACT_SITE 73 73 Neuropein.
FT	ACT_SITE 120 120 Charge relay system (By similarity).
FT	ACT_SITE 212 212 Charge relay system (By similarity).
FT	DISULFID 39 173 Charge relay system (By similarity).
FT	DISULFID 58 74
FT	DISULFID 145 246
FT	DISULFID 152 218
FT	DISULFID 184 198
FT	DISULFID 208 233
FT	CARBOHYD 110 110 N-linked (GlcNAc.. ) (Potential).
FT	STRAND 34 34
FT	STRAND 37 38
FT	TURN 41 42
FT	TURN 45 46
FT	TURN 47 52
FT	TURN 53 54
FT	TURN 55 64
FT	TURN 55 66
FT	TURN 67 70
FT	HELIX 72 74
FT	STRAND 80 83
FT	STRAND 87 87
FT	STRAND 88 89
FT	STRAND 96 98
FT	STRAND 100 105
FT	TURN 107 108
FT	TURN 114 115
FT	TURN 118 119
FT	STRAND 122 126
FT	STRAND 140 141
FT	TURN 148 149
FT	STRAND 151 156
FT	STRAND 170 170
FT	STRAND 172 178
FT	HELIX 181 187
FT	TURN 189 191
FT	TURN 194 195
FT	STRAND 196 200
FT	TURN 202 203
FT	STRAND 206 206
FT	TURN 209 210
FT	TURN 212 213
FT	STRAND 215 218
FT	TURN 219 220
FT	STRAND 221 228
FT	STRAND 235 235
FT	TURN 236 237
FT	STRAND 238 238
FT	STRAND 240 244
FT	HELIX 245 256
SEQ	SEQUENCE 260 AA; 28523 MW; BE5F6F6BE37CD60E CRC64;
Query Match	45.3%; Score 622.5; DB 1; Length 260;
Best Local Similarity	49.0%; Pred. No. 5.6e-42;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps	
QY	5 IFLLICV--LGLSOAATPKIFNGTECGRNSQPWVGLEFGTSLRCGGVLIDHRWV
DB	13 LILLLFMGANAGLTRAQSCLLEGRECTIPHSQPWAALFQGERLICGGVLVDGRWV
QY	62 HCSGRYVWRVLRGEHLSQLDWTEQIRHSGFSVTHPGYLGA--TSHEHDRLRLRLRL





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QY 191 -PGDACCQDSCGGLVCGGLVGLVSWGSGVPCGQDGPVGVYICKYVDWIRMRNN 248
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
198 GRGAESCEGSGPLVCGGILGVSWGDV-PCDNTTKFVGTVKCRVYKWIETMKRN 255

RESULT 9
Q632F2 PRELIMINARY; PRT; 250 AA.
AC Q632F2
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Glandular kallikrein 11 precursor.
GN Name=Klk11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
RA Olsson A.Y., Lilja H., Lundwall A.;
RT "Taxon-specific evolution of glandular kallikrein genes and
RT identification of a progenitor of prostate-specific antigen.";
RL Genomics 84:147-156(2004).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ third party annotation (TPA) entry.
KW EMBL; BK001364; DAA05600.1; -.
KW Signal.
FT SIGNAL. 1 18 Potential.
FT CHAIN 22 250 Glandular kallikrein 11.
SQ SEQUENCE 250 AA; 27630 MW; 247B29D3F0DEF8F1 CRC64;

Query Match 44.4%; Score 610; DB 2; Length 250;
Best Local Similarity 46.7%; Pred. No. 5.4e-41;
Matches 115; Conservative 37; Mismatches 90; Indels 4; Gaps 3;

QY 6 FULLCVLGLSOAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRVWLTAACHSG 65
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
6 FTALAVTVGHVGGETRIIKGYECRPHSQPWQVALFQKTRLLCGATLIAPKMLLTAACHCK 65

QY 66 SHYWRVLRGHSLSQLDWTEQIRHSGFSVTHPGYVGLA--STSEHDLRLRLRLPVRVTS 123
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
66 PHYVILLGHELEKTDGCGQRMMATESFPHPGFFNSLPNKHNRNIMLVKMSAPFITRA 125

QY 124 VQPLPLNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATGCHVYPCRTSN 183
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
126 VRPLTSLLCVTAAGTSLISGWTGSSPOLRPLPHSLRCANVSIIGHKECERAYPGNITDT 185

QY 184 MYCAG-GVPGDACCQDSCGGLVCGGLVGLVSWGSGVPCGQDGPVGVYICKYVDWIR 242
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
186 MLCASVRKEGKDCQDSCGGLVCGGLVGLVSWGSGVPCGQDGPVGVYICKYVDWIR 244

QY 243 MTMRNN 248
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
245 EVMRNN 250

RESULT 10
Q8CGR4 PRELIMINARY; PRT; 254 AA.
AC Q8CGR4
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Proctin.
GN Name=Klk15; Synonyms=KLK15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
```

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RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AV152434; AAN78422.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.237; -.
DR MGD; MGI:2447533; Klk15.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEBDD01861 CRC64;

Query Match 44.3%; Score 608; DB 2; Length 254;
Best Local Similarity 49.0%; Pred. No. 7.9e-41;
Matches 124; Conservative 30; Mismatches 77; Indels 22; Gaps 7;

QY 5 IFLLLCVLGLSOAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRVWLTAAH 62
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
1 MLLLAFLVLLVSAADQDKVLEGECVPHSQPWQVALFERGFNCAGFLISPRVWLTAAH 60

QY 63 CSGSRVYWRVLRGHSLSQLDWTEQIRHSGFSVTHPGYVGLASTSHEDLRLRLPVRVTS 122
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
61 CQTRFMRVLRGHEHLRKFDPGLASVSRIIPHPGY--EARTHHDIMLLRFLKPARLTA 118

QY 123 SVQPLPLNDCATAGTECHVSGWGITNHPN-----FPDLQCLNLSIVSHAT 171
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
119 YVRPVALPRRCPLIGEDCVVSGWGLLS--DNNFGATGSKSHVRLPDTLRCANISISEAS 177

QY 172 CHGVYPRGITSNMVCA---GGVPGDACCQDSCGGLVCGGLVGLVSWGSGVPCGQDGP 228
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
178 CNKDYPRVRLPTWVCAGVEGG--GTDSCGDSGGPLVCGGLVGLVSWGDV-PCDTTTRP 234

QY 229 GVYTYICKYVDWI 241
Db |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
235 GVYTKVCSYLEWI 247

RESULT 11
Q8IXD7 PRELIMINARY; PRT; 275 AA.
AC Q8IXD7
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Variant form hippostasin/KLK11.
GN Name=KLK11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB078780; BAC54105.1; -;  
 DR HSSP; P00760; 1EZX.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00089; Trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYP SIN.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolyase; Protease; Serine protease.  
 SQ SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;  
 Query Match 43.7%; Score 601; DB 2; Length 275;  
 Best Local Similarity 44.2%; Pred. No. 3.1e-40;  
 Matches 121; Conservative 35; Mismatches 88; Indels 30; Gaps 5;  
 QY 3 LSTFLLCVLGSLQAATPKIFNGTEGRNSQPQVGLFEGTSLRCGGVLIDHRWVLAH 62  
 DB 4 LQILLALATGLVGGT-RIIKGFCKPHSQPQAALEKTRLLCGATLIAPRWLLTAH 62  
 QY 63 CSG-----SRVVRGLGEHSLSQLDWTQIRHSGFVSHPG 97  
 DB 63 CLKPWSLSTPHVSPLSSNYCLSHLSRYIVHLGQHNLOKESGCEGTRTATESFPHG 122  
 QY 98 YLGA--STSGHEHDLRLRLRPVRTSSVQPLPLPNDCATAGTECHVSGWGITNHPNPF 155  
 DB 123 FNNSLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSLISGSGTSSPQLRL 182  
 QY 156 PLLQLCLNLSIVSHATGHVYGRITSNMVCAG-GVPGQDACCQDSGGPLVCGGVQLGV 214  
 DB 183 PHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCQDSGGPLVCGNQLGII 242  
 QY 215 SWGSGVPCQGDGPGVYVYICKYVDWIRMENN 248  
 DB 243 SWGQ-DPCAITRKPQGVYICKYVDWIMQETMKN 275  
 RESULT 12  
 Q6IS10 PRELIMINARY; PRT; 255 AA.  
 ID Q6IS10  
 AC Q6IS10  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)  
 DE Kallikrein 15, isoform 4 preproprotein.  
 GN Name=KLK15;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RC Director MGC Project;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; BC069518; AAH69518.1; -;  
 DR EMBL; BC069480; AAH69480.1; -;  
 DR HSSP; P00761; 1AKS.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00089; Trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYP SIN.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 KW Hydrolyase; Protease; Serine protease.  
 SQ SEQUENCE 255 AA; 28016 MW; 1581B784D4A39C4F CRC64;  
 Query Match 43.6%; Score 599; DB 2; Length 255;  
 Best Local Similarity 46.9%; Pred. No. 4.2e-40;  
 Matches 120; Conservative 32; Mismatches 86; Indels 18; Gaps 6;  
 QY 8 LLCVLGLSQAAT----PKIFNGTEGRNSQPQVGLFEGTSLRCGGVLIDHRWVLAH 63  
 DB 3 LLLTLTSLFLASTAQDGLLEGDECAPHSQPQVALYERGRFNCASLISPHWVLSAAHC 62  
 QY 64 SGRVVRVGLGEHSLSQLDWTQIRHSGFVSHPGQDACCQDSGGPLVCGGVQLVSWGSGVPCQDGIGVYT 123  
 DB 63 QSRFVRVRLGEHNLKRDGPQLRTTSRVIPHPY--EARSHRNDIMLRLVQAPALNPQ 120  
 QY 124 VOPLPLPNDCATAGTECHVSGWGITNH-----PRN--PFDDLLQLNLSIVSHATCH 173  
 DB 121 VRPAVLPTRCPHGECACVVGSLVSHNEPCTAGSPRSQVSLPDLHCANISIIISDTSCD 180  
 QY 174 GYVPGRTSNMVCAGGV-PGQDACCQDSGGPLVCGGVQLVSWGSGVPCQDGIGVYT 232  
 DB 181 KSYPGRLTNTMVCAGARGAEGSCEGDSGGPLVCGGVQLVSWGSDV-PCDNTTKPGVYT 239  
 QY 233 YICKYVDWIRMENN 248  
 DB 240 KVCHYLEWIRETMKN 255  
 RESULT 13  
 KLKF\_HUMAN STANDARD; PRT; 256 AA.  
 ID KLKF\_HUMAN  
 AC Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HB09;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).  
 GN Name=KLK15;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RC PubMed=1101966; DOI=10.1074/jbc.M005432200;  
 RA Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;

RT Molecular cloning of the human kallikrein 15 gene (KLK15). Up-regulation in prostate cancer.";  
RL J. Biol. Chem. 276:53-61(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
RA Can L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepir B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN [3]  
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;  
RA Dhanich M.E., Spiess M.;  
RL "A novel serine proteinase-like sequence from human brain.";  
RN Biochim. Biophys. Acta 1218:225-228(1994).  
RN [4]  
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).  
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
RA Hillman R.T., Green R.E., Brenner S.E.;  
RT "An unappreciated role for RNA surveillance.";  
RL Genome Biol. 5:RSEARCH008.1-RESEARCH008.16(2004).  
CC -!- FUNCTION: Protease whose physiological substrate is not yet known.  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q9H2R5-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9H2R5-2; Sequence=VSP\_005405;  
CC Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=3;  
CC IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407;  
CC Name=4;  
CC IsoId=Q9H2R5-4; Sequence=VSP\_005404;  
CC -!- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon testis and kidney.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; AF242195; AAG09469.1; -;  
CC EMBL; AF242195; AAG09470.1; -;  
CC EMBL; AF242195; AAG09471.1; -;  
CC EMBL; AF242195; AAG09472.1; -;  
CC EMBL; AF243527; AAG33354.1; -;  
CC EMBL; X75363; CA53145.1; ALT\_SEQ.  
CC HSP; P00760; IEZX.  
CC MEROPS; S01.081; -;  
CC Genew; HGNC:20453; KLK15.  
CC GO; GO:0005576; C:extracellular; NAS.  
CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
CC GO; GO:0005508; P:proteolysis and peptidolysis; NAS.  
CC InterPro; IPR009003; Pept\_Ser\_Cys.  
CC InterPro; IPR001254; Peptidase\_S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC Pfam; PF00089; Trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC SMART; SM00020; TRY\_SP; 1.  
CC PROSITE; PS0240; TRYPSIN\_DOM; 1.  
CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
CC PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NEG.

KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
FT SIGNAL; Zymogen. 1 16  
FT PROPEP 17 21 Potential.  
FT CHAIN 22 256 Activation peptide (Potential).  
FT ACT\_SITE 62 62 Kallikrein 15.  
FT ACT\_SITE 106 106 Charge relay system (By similarity).  
FT ACT\_SITE 209 209 Charge relay system (By similarity).  
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 122 206 Missing (in isoform 4).  
FT VARSPLIC 122 256 Missing (in isoform 2).  
FT VARSPLIC 161 161 Missing (in isoform 3).  
FT VARSPLIC 162 256 Missing (in isoform 3).  
FT CONFLICT 147 160 SHNEPDTAGSPRSQ -> PLSSP (in Ref. 2).  
SQ SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;  
  
Query Match 43.6%; Score 599; DB 1; Length 256;  
Best Local Similarity 47.1%; Pred. No. 4.2e-40;  
Matches 121; Conservative 32; Mismatches 88; Indels 16; Gaps 6;  
  
QY 5 IFLLCLVLGLSOAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62  
DB 3 LLLTLTSLASTAAQDGKLLGDECAPHSQWQVALYERGFNCGLSLSPHWVLSAAH 62  
  
QY 63 CSGSRVWRLGHSLSQLDWTEIQIHSGFSVTHPGYLGASTSHEHDLRLRLPLRVVTS 122  
DB 63 COSRFMRVRLGHNLRKRDGPQLRTTSRVIPHPRY--EARGHRNDIMLLRLVQPARLNP 120  
  
QY 123 SVQPLPLPNDCATAGTECHVSGWGITNH-----PRN--PPDLOCNLNLSIVSHATC 172  
DB 121 QVRPAVLPTCPHPGEACVWVGSLVSHNEPCTAGSPRSQVSLPDTLHKANISIIDTSC 180  
  
QY 173 HGVPYGRITSNMVCAGGV-PGQACQSGSGGLVCGVLPGLVQVSGVPGCGQDGPVGY 231  
DB 181 DKSYFGLRTNTWVCAGAEGRGAESCEGDSGLVCGGILQGVSGWGV-PCDNTTKPGVY 239  
  
QY 232 TVICKYVDWIRMN 248  
DB 240 TKVCHYLEWIRETKRN 256  
  
RESULT 14  
QYQYN4 PRELIMINARY; PRT; 249 AA.  
AC Q9QYN4; DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Hippocastin.  
GN Name=2310015108Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;  
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;  
RT "cDNA cloning and tissue-specific splicing variants of mouse hippocastin/TLSP (PRSS20).";  
RL Biochim. Biophys. Acta 1494:206-210(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Yamaguchi N., Mitsui S.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL; AB016226; BRA88825.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGD; MGI:192997; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SBR; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9F9CB457D727D5 CRC64;

Query Match 43.5%; Score 597.5; DB 2; Length 249;
Best Local Similarity 47.0%; Pred. No. 5.4e-40;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;

QY 1 MGLSIFLLCVLGLSQAATPKLFGTECGRNQPMQVGLFEGTSLSCGGVLIIDHRVLT 60
Db 1 MIURLTALALVTGHVGGET-RIIKGYECRPHSQPMQVGLFQKTRLLCGATLAPKWLTA 59

QY 61 AHCGSGRYVVRGLGHSLSQDWTQIRHSGFSVTHPGYLCA--STSHEHDLRLRLRLPV 118
Db 60 AHCRKPHYVILLGEHNLEKTDGCEQRMRATESFPHPDFNLSLPNKDRNDIMLVKMSPV 119

QY 119 RVTSSVQPIPLPNDCAATAGTECHVSQWGTNHPNRPFDLPOLLOCLNLSIVSHATCGVY 178
Db 120 FETRAVQPIPLPHCAAGTSCLLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPG 179

QY 179 RITSNMVACG-GVPGDAGCGSGPLVCGVGLGVLSWGSVPCQDGIQGVYTVICKY 237
Db 180 NITDTMLCASVKEGKDCQSGSGLVLCVNGSLQGIISWGQ-DPCAIVTRKPGVYTVICKY 238

QY 238 VDWIRMIRNN 248
Db 239 FNIWEHVEMNN 249

RESULT 15
Q9QYN3 PRELIMINARY; PRT; 276 AA.
ID Q9QYN3
AC Q9QYN3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hippostasin prostate type (Mus musculus adult male tongue cdna, RIKEN
DE full-length enriched library, clone:2310015108 product:protease,
DE serine, 20, full insert sequence) (Mus musculus adult male tongue
DE cdna, RIKEN full-length enriched library, clone:2310040F07
DE product:protease, serine, 20, full insert sequence).
GN Name:2310015108Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hippostasin/TLSP (PRSS20)".
RL Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Yamaguchi N., Mitui S.;
RT Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.
RN [3]
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
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RP SEQUENCE FROM N.A.
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RA RIKEN FANTOM Consortium;
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RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
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RT 60,770 full-length cDNAs.";
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RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11078861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
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RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB016227; BAA36955.1; -.
DR EMBL; AK009360; BAB26241.2; -.
DR EMBL; AK009720; BAB26461.2; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.257; -.
DR MGD; MGI:192997; 2310015108Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
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